SpiralTOF™

Introduction of the JMS-S3000 SpiralTOF™

Analysis of Bovine Serum Albumin

Introduction:

The JMS-S3000 "SpiralTOF™" is a MALDI-TOF MS incorporating an innovative SpiralTOF™ ion optics system (Fig. 1). JEOL's patented technology[1] achieves a spiral ion trajectory of 17m within a compact 1m space. The ions are sent through four sets of layered toroidal electric fields, which are implemented by four pairs of cylindrical electrodes and nine Matsuda plates that are incorporated within every pair of cylindrical electrodes. Ions are accelerated to 20 kV in the ion source and fly sequentially through the layered toriodal electric fields to reach the detector (Fig. 2). With the extended flight distance, the JMS-S3000 SpiralTOF™ achieves high mass resolving power and high mass accuracy over a wide mass range.

However, ions with a very short lifetime or that undergo spontaneous dissociation during their flight (e.g., protonated molecules of high-mass proteins, multiply-phosphorylated peptides, etc.) cannot be detected by either the SpiralTOF™ or a conventional reflectron TOF. Considering the wide application of the MALDI technique, a mass analyzer that can detect such short-lived ions is necessary in addition to the SpiralTOF™. A Linear TOF option is available for the JMS-S3000 in order to satisfy this requirement (Fig. 2). In this application note, the analysis of the tryptic digest of bovine serum albumin (BSA) is shown as a Spiral mode example while the analysis of intact BSA is shown as a Linear mode example.

Figure 1. JMS-S3000 SpiralTOF™.

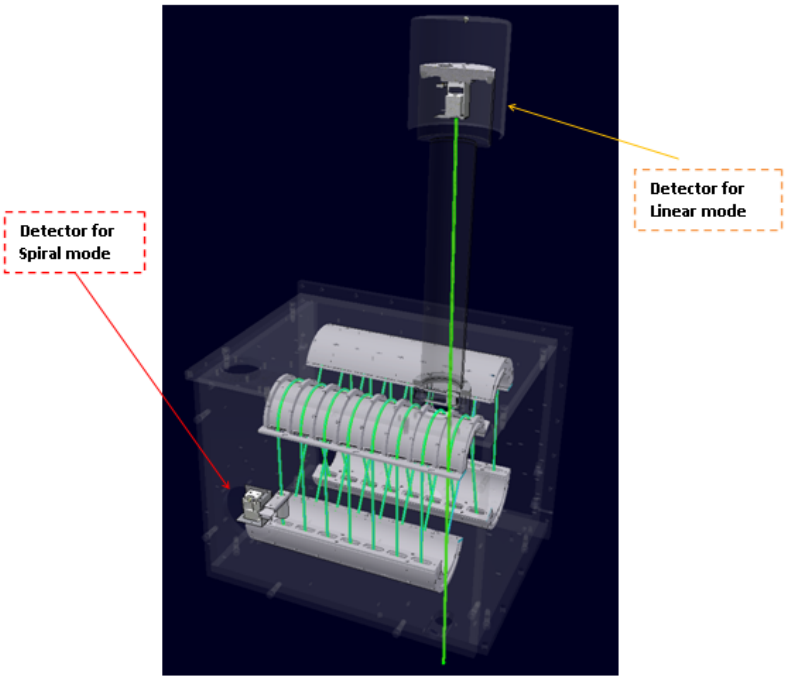

Figure 2. Ion trajectories of the JMS-S3000 SpiralTOF™.

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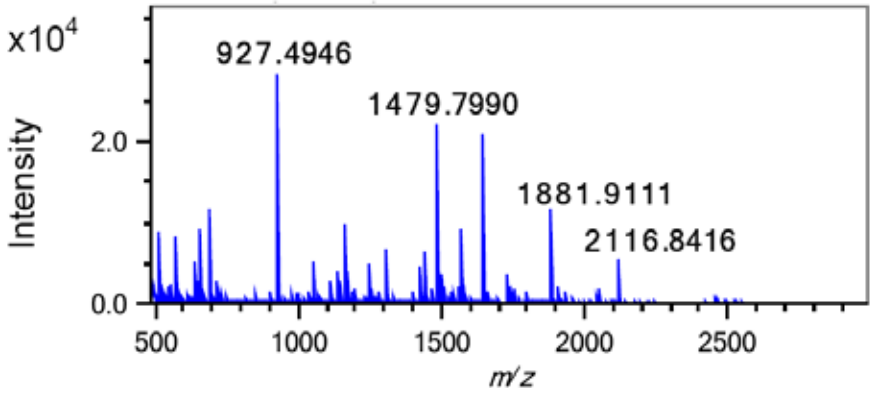

Figure 3. Mass spectrum for the tryptic digest of BSA (equivalent to 25 fmol of the protein).

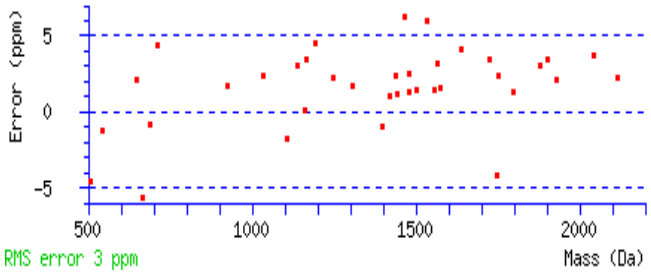

Figure 4. Mass error plot from the MASCOT PMF search result.

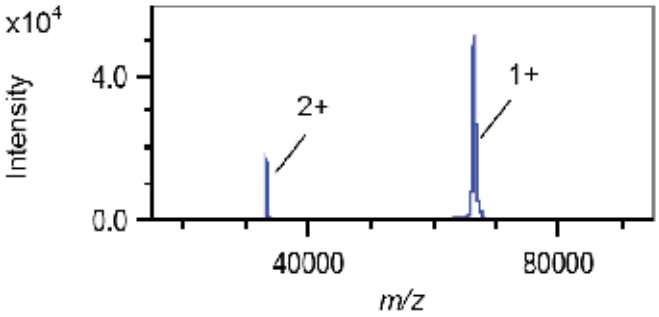

Figure 5. Mass spectrum of the intact BSA protein (2.5 pmol).

Methods:

The tryptic digest of BSA was analyzed in SpiralTOF mode. An external mass calibration was used for this data. The intact BSA was analyzed using the Linear TOF mode. The data was acquired automatically by using the msTornado™ Control, which is the instrument control and data acquisition software for the JMS-S3000.

Results and discussion:

The mass spectrum of the tryptic digest equivalent to 25 fmol of BSA is shown in Fig. 3. The peak list from this mass spectrum was submitted to the MASCOT peptide mass fingerprint (PMF) search, and the protein was identified as BSA. The mass error plot of all matched peptides is shown in Fig. 4. The RMS error was 3 ppm. The mass spectrum of the intact BSA acquired in Linear mode is shown in Fig. 5. Single- and double-charge protonated molecular ion peaks were observed at the *m/z* values expected for the primary structure of this protein.

Conclusions:

A mass spectrum of the tryptic digest of BSA with very high mass accuracy was obtained using Spiral mode. Using the MASCOT PMF search method, a peptide mass tolerance set as narrow as 10 ppm can lead to highly reliable protein identification with very few false positives. Additionally, the molecular weight of an intact protein was readily obtained by using the JMS-S3000 Linear mode.

References:

[1] US patent US7504620, Japanese patent application JP2006-12782