

PEPTIDE SEQUENCING USING CHEMICALLY ASSISTED FRAGMENTATION (CAF) -MALDI

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Sequence information from proteins and peptides is fundamental, for understanding of physiological and biochemical processes at the molecular level.

Such information can be readily obtained using the Ettan[®] CAF-MALDI sequencing kit in conjunction with Ettan MALDI ToF Pro mass spectrometer (MS). The chemistry, based on a new class of water-stable sulfonation reagents, eliminates the most common problems associated with PSD. It greatly improves the fragmentation efficiency of the peptides and also simplifies the interpretation of their fragmentation spectra.

Convenient derivatisation protocols have been developed and optimized, enabling fast, simple, and robust sample preparation.

The special features of the Ettan MALDI-ToF Pro MS and the Ettan CAF-MALDI sequencing kit allows:

- identification of increased number of proteins by MALDI
- rapid, sensitive and precise peptide sequencing by MALDI
- characterization of phosphorylation sites by MALDI

Several examples, using CAF-MALDI for protein identification, peptide sequencing and characterization of phosphorylated amino acid residues will be presented.

References:

1. Keough, T. *et al.*, A method for high-sensitivity peptide sequencing using post-source decay matrix-assisted laser desorption ionization mass spectrometry. *Proc. Natl. Acad. Sci. USA*. **96**, 7131-7136 (1999).
 2. Liminga, M., *et al.*, Water-stable chemistry for improved amino acid sequencing by derivatization post-source decay (dPSD) using Ettan MALDI-ToF with a quadratic field reflectron. *Proc. 49th Conf. Mass Spectrometry and Allied Topics*, Chicago, IL (2001).
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