

Faster Gas-Phase Protein Sequencing

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WARF: P04178US

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The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing a method for sequencing polypeptides that combines the powers of mass spectrometry and Edman degradation chemistry.

Overview

Determining the amino acid sequence of any given protein or polypeptide is a formidable task. The first major technology to emerge for this purpose was the Edman degradation method, which sequences a target residue-by-residue and has been in use for more than 50 years. The method works well for de novo sequencing (when no reference sequence is available) but is slow. Sensitivity also is an issue for proteins that exist at low levels in the cell.

The Edman degradation method can be combined with mass spectrometry (MS) - a modern analytical technique that determines the mass "fingerprint" of a protein and matches it in a database of known proteins. Although the two methods can be coupled in several different ways, slow processing speed and sensitivity remain issues. Part of the problem is that MS is used solely as a means for detection and the Edman reaction does not take place within the mass spectrometer itself.

The Invention

UW-Madison researchers have developed a sequencing method that combines the time-tested de novo capability of Edman degradation chemistry with the speed and sensitivity of mass spectrometry.

In the new process, a protein or polypeptide molecule is introduced into a mass spectrometer and allowed to accumulate in the linear ion trap. Edman degradation reactions then are conducted in gas phase (within the linear ion trap) by introducing chemical reagents. After each cycle the product ions are selectively transmitted through the mass spectrometer to determine their mass-to-charge ratios. The chemical identities of the amino acid residues are determined based on the mass spectra thus generated.

Applications

· De novo sequencing of proteins and peptides

Key Benefits

- · High speed and sensitivity
- · Manipulation of gas-phase ions is clean and fast.
- · Sequence information can be obtained for any protein spot detectable on a gel.

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• Lloyd Smith

Related Technologies

WARF reference number P08040US describes an MS technique that enables real-time identification of unknown peptides.

Tech Fields

<u>Analytical Instrumentation, Methods & Materials : Mass spectrometry</u>

For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854

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