



Faster Gas-Phase Protein Sequencing

[View U.S. Patent No. 8,628,974 in PDF format.](#)

WARF: P04178US

Inventors: Lloyd Smith, Michael Westphall, Xiaoyu Chen, Brian Frey

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.

We use cookies on this site to enhance your experience and improve our marketing efforts. By continuing to browse without changing your browser settings to block or delete cookies, you agree to the storing of cookies and related technologies on your device. [See our privacy policy.](#)

For More Information About the Inventors

OK



WARF
Wisconsin Alumni Research Foundation

| info@warf.org | 608.960.9850

- [Lloyd Smith](#)

Related Technologies

- [WARF reference number P08040US describes an MS technique that enables real-time identification of unknown peptides.](#)

Tech Fields

- [Analytical Instrumentation, Methods & Materials : Mass spectrometry.](#)

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

We use cookies on this site to enhance your experience and improve our marketing efforts. By continuing to browse without changing your browser settings to block or delete cookies, you agree to the storing of cookies and related technologies on your device. [See our privacy policy.](#)

OK



WARF
Wisconsin Alumni Research Foundation

| info@warf.org | 608.960.9850