Increasing Peptide and Protein Identifications with Prioritized Mass Spectrometry

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WARF: P110191US01

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The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing a probability-based method for tandem mass spectrometry that utilizes multiple ion properties to prioritize analysis and promote protein identifications.

Overview

As resources shift from genome sequencing to understanding and characterizing expressed genes and protein function, reliable and rapid tools for the analysis of protein composition are increasingly vital. Determining the unique, constituent amino acid structure of proteins is achieved by mass spectral instruments, which can ionize, separate and fragment tens of thousands of molecules in tandem scan events (MS/MS).

Identifying proteins and peptides from the resulting plot of mass-to-charge (m/z) intensity peaks, however, may compromise investigation. For complex mixtures not all peaks can be selected within an elution window, and many of the selections do not lead to successful identifications. Commonly, peaks are designated for consideration in order of decreasing intensity.

A more refined approach is needed, increasing protein and peptide identifications by interrogating the ions formed during the first MS analysis, called precursor ions, in order not of diminishing peak intensity, but prospect of success.

The Invention

UW–Madison researchers have developed a universally compatible, computationally based method in which multiple precursor ion attributes—such as mass, intensity, m/z ratio and charge state, as well as results obtained from previous scans—are used to calculate the likelihood of identification, thus prioritizing subsequent analysis.

The method comprises MS/MS analysis of a sample (or training sample) containing proteins and peptides, with one or more compounds optionally labeled with isobaric tags. Established procedure for analyte ionization and mass-to-charge separation generates precursor ions. The ions then are detected and analyzed for information related to two or more physical properties (mass, charge state, etc.) and directed for MS^2 dissociation—selecting and/or allotting resources to the most identifiable ions as determined by the algorithm. Segregated and detected for mass and abundance, the fragmented ions provide further characteristic data used to identify the compounds. Additionally, the process permits novel, or first-time, identification of precursor ions during an experiment or within an ID database.

Enabling prioritized, probability-focused mass spectrometry, the innovative software achieves increased sample identification with little or no time increase and requiring no additional hardware.

- Implementation on existing MS platforms as software upgrades
- Expanding proteomic databases

- Developing sequence information pertinent to fundamental research, biologics and medicine

Key Benefits

- Increased peptide and protein identifications
- Compatible with all mass spectrometry instruments
- Real-time analysis without added hardware

Stage of Development

When the algorithm was trained on the sample of interest, the researchers showed 14 and 25 percent increases in unique identifications for yeast lysate and human tryptic digest, respectively.

Additional Information

For More Information About the Inventors

- Joshua Coon

Related Technologies

- For more information on real-time tandem mass spectrometry using improved electron transfer dissociation (ETD) techniques for ion fragmentation, see WARF reference number P08040US.

Publications

- McAlister G.C., Phanstiel D.H., Wenger C.D., Lee M.V. and Coon J.J. 2010. Analysis of Tandem Mass Spectra by FTMS for Improved Large-Scale Proteomics with Superior Protein Quantification. Anal. Chem. 82, 316-322.

Tech Fields

- Analytical Instrumentation, Methods & Materials : Mass spectrometry
- Research Tools : Genomics & proteomics

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