Mass Spectrometry Data Acquisition Method Enables More Reliable Large-Scale Protein Quantitation

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Inventors: Joshua Coon, Craig Wenger, Douglas Phanstiel

The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing an improved method to obtain protein quantitation using mass spectrometry.

Overview

Quantitative analysis in chemistry is the determination of the absolute or relative abundance of substances present in a sample. For biological samples, quantitative analysis performed via mass spectrometry can determine the relative abundance of peptides and proteins. The accepted methodology for performing mass spectrometry quantitation is accomplished using a mass spectrometer capable of MS/MS fragmentation.

The quantitation process typically involves isobaric tagging of peptide precursors, which provides the relative abundance of peptides when combined with post-acquisition software. However, when a peptide precursor is selected for tandem mass spectrometry, interfering species with similar mass-to-charge ratios can be co-isolated and subjected to activation. These species often are other isobarically tagged peptides with different relative quantitation, which disrupt the quantitative measurement of the peptide of interest and make much of the data unusable. Currently, correction for precursor interference can only be performed using post-acquisition software. A method that corrects for precursor interference during data acquisition is desirable.

The Invention

UW–Madison researchers have developed a platform for analyte quantitation that prevents the acquisition of mass spectra that will not result in usable data due to interference by modifying the data acquisition software. During the automated precursor selection process, candidate precursors with significant interference are rejected until a suitable replacement is found. This method enables increased quantitation accuracy while maintaining high levels of throughput.

Specifically, a distribution of precursor ions from an analyte is analyzed using mass spectrometry to identify a precursor peak in the ion mass spectrometry data corresponding to a precursor ion. The data allows determination of the amount of interference within a preselected range about the precursor peak. Then, an adjusted range of ions may be selected for analysis such that the amount of interference is less than a selected value.

Applications

- Rapid, large-scale quantitative analysis of analytes containing proteins or peptides

Key Benefits

- Corrects for precursor interference in the acquisition phase

- Minimizes the amount of data acquired with unreliable quantitation
- Allows more efficient use of the mass spectrometer

Additional Information

For More Information About the Inventors

- Joshua Coon

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