Identifying Related Peak Sets to Boost Mass Spectrometry Throughput

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WARF: P120336US01

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The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in an algorithm that identifies related peak sets in MS1 spectra and improves the success rate for properly quantitating multiplexed samples.

Overview

Tandem mass spectrometry (MS/MS) is a technique capable of identifying large numbers of proteins in complex biological samples. In the process, peptides are ionized and an initial survey scan (i.e., a first mass spectrum or MS1) reveals peptide mass and charge state. The most intense ionized peptides (called 'precursor ions') are selected for a second scan (MS2), isolated and fragmented. The MS2 fragmentation patterns are compared to a database to identify the peptide or protein of origin.

To quantify peptides or proteins, e.g., to compare the amount of a particular protein in several different samples, MS/MS can be combined with stable isotope labeling. Depending on the labeling technique, the process can employ MS1 data (limited to three samples at once) or MS2 data (limited to eight samples at once). Combining techniques would enable an even greater number of samples to be analyzed simultaneously. For example, bio-duplicates could be distinguished in MS1 using light and heavy isotopes, and then analyzed at six different time points in MS2. This would allow the multiplexed analysis of 12 samples at one time.

Unfortunately, the potential of such experiments has been limited. This is because, as noted, most MS/MS systems select only the most intense precursor ions for MS2. If a group of peaks in the MS1 spectrum are not among the most intense, then not all peaks will be selected for MS2. This precludes true quantitative comparison among the different samples. Even if all peaks in a group are eventually selected, fluctuating conditions can degrade accuracy.

The Invention

UW–Madison researchers have developed an algorithm for identifying related peak sets from MS1 spectra data.

First, an intensity peak is selected from the MS1 data and its peak location is identified. Based on intensity values associated with all potentially related peak locations, an intensity score is calculated. This score determines whether or not the peak locations form a related set. Related peaks may optionally be selected for MS2 processing.

Applications

- Quantitative proteomics

Key Benefits

- Superior throughput
- Related peptides are processed within one second of each other.
- Improves the consistency and repeatability of an experiment

Stage of Development

Compared to a conventional method called Data Dependent Acquisition (DDA), the new algorithm found 84 percent of a possible 3546 detections. DDA found only 33 percent of a possible 4530.

Additional Information

For More Information About the Inventors

- Joshua Coon

Related Technologies

- WARF reference number P130032US01 describes neutron-encoded mass tags that enable more accurate proteomic quantification in a large number of samples.

Tech Fields

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