



HIGH THROUGHPUT INFUSION PEPTIDE MAPPING

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The Invention

UW-Madison researchers have developed a high throughput peptide mapping platform by combining a plate-based sample preparation method with direct injection MS analysis. Protein samples are cleaned, reduced, alkylated, digested, and acid quenched in a filter plate. Prepared samples are then sequentially introduced using an automated infusion system (e.g., NanoMate®) directly into the mass spectrometer (i.e., high resolution orbitrap without liquid chromatography(LC)). The result is an effective assay for identifying site specific modifications in therapeutically relevant peptides (e.g., monoclonal antibodies).

Their method showed high fidelity to LC based methods (>90% sequence coverage) for methionine and tryptophan oxidation, asparagine glycosylation, protein n-terminal pyrolysis, clipping, amino acid sequence variants, and succinimide intermediates of asparagine deamidation and aspartic acid isomerization. Adding targeted ultrahigh resolution MS2 scans (500,000 resolving power at 200 m/z) into the scan sequence enabled measuring site-specific deamidation.

All told, this approach has the potential to significantly reduce the time and overhead for generating peptide maps, an area of characterization that is expected to see significant increases in demand, as biosimilars and other peptide-based therapeutics become more prevalent.

Additional Information

For More Information About the Inventors

- [Joshua Coon](#)

Tech Fields

- [Analytical Instrumentation, Methods & Materials : Mass spectrometry](#)
- [Drug Discovery & Development : Other drug discovery & development](#)

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