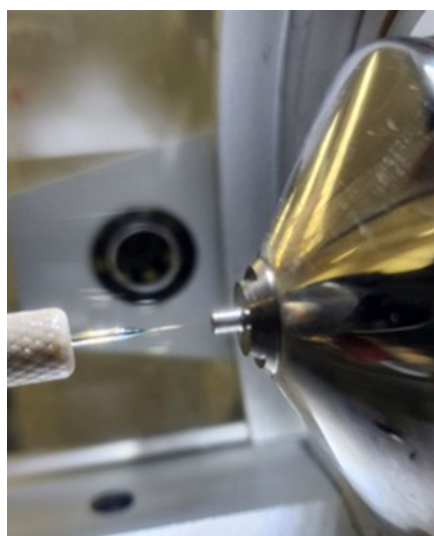


Accurate and comprehensive analysis of top-down mass spectra for the discovery of protein modifications

PrecisIION is an analytical workflow and GUI-based software package enabling exhaustive, mechanism-informed interpretation of native top-down mass spectra. It combines unprecedented fragment-assignment logic, enhanced deconvolution routines, a hierarchical matching engine, and novel modification-discovery methods, enabling fully de novo spectral interpretation without reliance on incomplete proteoform databases.

Applications: Top-down mass spectrometry



Features

Novel mechanism-based fragment-assignment workflow

Benefits

Delivers a step-change in interpretability by identifying sequence ions that current native TDMS pipelines systematically miss, especially in discovery-mode experiments

Features	Benefits
Advanced deconvolution routines optimised for native spectra	Produces cleaner, more reliable precursor and fragment mass assignments, enabling confident interpretation even for complex or partially unknown protein assemblies
De novo assignment of proteoforms without reliance on prior knowledgebases	Enables discovery of unexpected proteoforms, post translational modifications, chemical adducts, and sequence variants, unlocking biological insights inaccessible to database-dependent tools
Purpose-built for native top-down mass spectrometry as it enters mainstream analytical use	Increases the fraction of interpretable spectral information by more than threefold in typical datasets, transforming native TDMS from a niche technique into a powerful discovery-grade platform

Awaiting patent and Available for

- Co-development
- Consulting
- Licensing

To find out more, contact enquiries@innovation.ox.ac.uk and quote the project number.

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