PASEF-Melodies: Orchestrating Precision Proteomics with timsTOF

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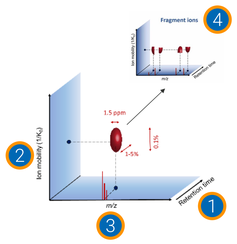
Introduction

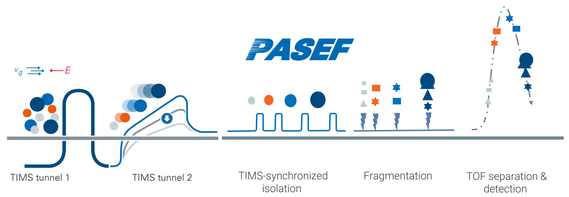
Trapped Ion Mobility Spectrometry (TIMS) adds an orthogonal 4th dimension, allowing biomolecules to be distinguished by collision cross section (CCS). This increases selectivity and supports higher-confidence identification by reducing interference, focusing the signal, and enabling TIMS-cleaned MS/MS. For bioinsights, TIMS helps disentangle complex molecular mixtures into interpretable layers.

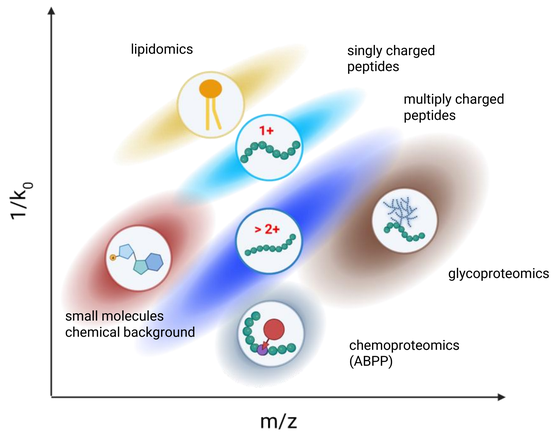
4 Dimensions of Selectivity

1. **Retention time** (LC separation)
2. **Mobility** value **CCS** (collision cross section): routinely measured in PASEF experiments
3. **MS**[1]: accurate mass (*m/z*)
4. **TIMS-cleaned MS/MS**: high-quality fragmentation data

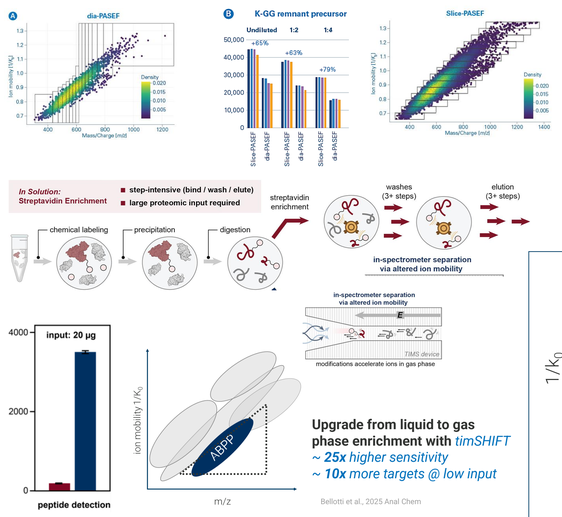


PASEF couples TIMS mobility separation with synchronized precursor isolation and fast TOF detection to maximize ion usage and sampling efficiency.

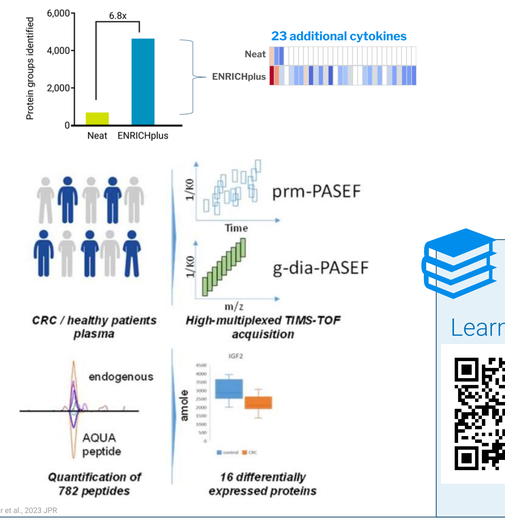




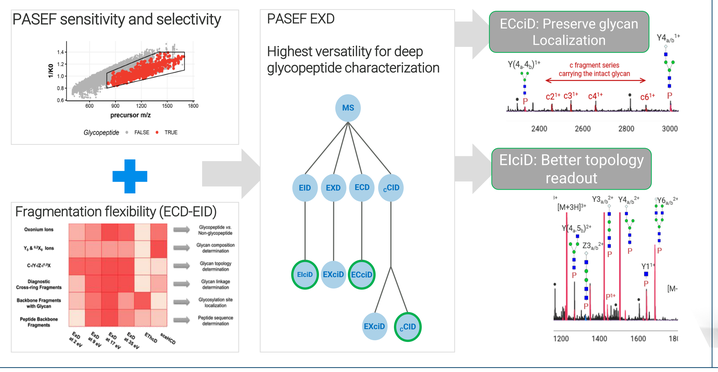
Chemoproteomics: **timSHIFT** enabled ABPP tackles the "needle-in-a-haystack" problem of rare modified peptides by shifting them in mobility and using a TIMS polygon to target that population—enabling a simpler, more sensitive workflow; TPD/ubiquitinomics benefits from **Slice-PASEF** with improved depths, revealing on/off-target ubiquitination and turnover pathways.



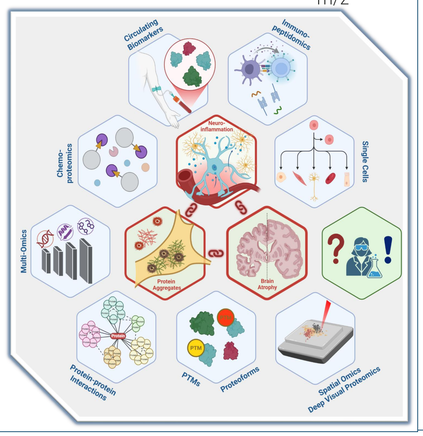
Biomarker discovery requires robustness at scale. CCS/ TIMS-enabled dia-PASEF enables reproducible, large-cohort discovery with continuous QC (TwinScape + iRT). **prm-PASEF** delivers fast, sensitive validation panels and **guided dia-PASEF** quantifies known targets during discovery.



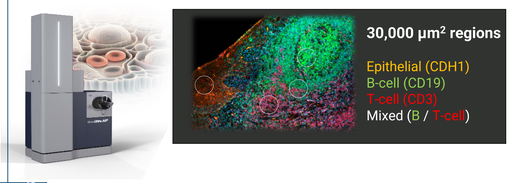
PTMs an proteoforms: For instance, **glyco-PASEF®** + **GlycoScape™** deploy TIMS/PASEF selectivity to enable high-sensitivity glycopeptide discovery and CCS-based separation of isomeric species, while timsOmni **ExD** allows ECciD to reveal glycan localization and EIciD to map glycan topology.

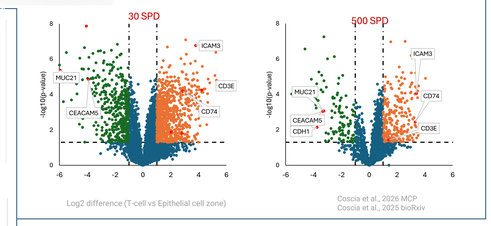


Diseases comprise many facets. Neurodegeneration for instance is associated with neuroinflammation, toxic protein aggregates, and brain atrophy. Tailored investigations are key to dissect disease mechanism and to gain translational insights.

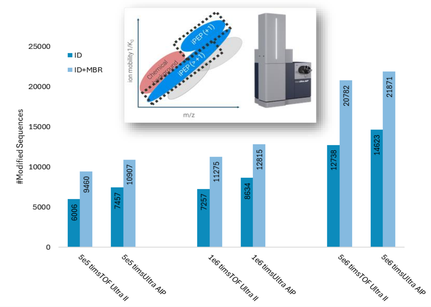


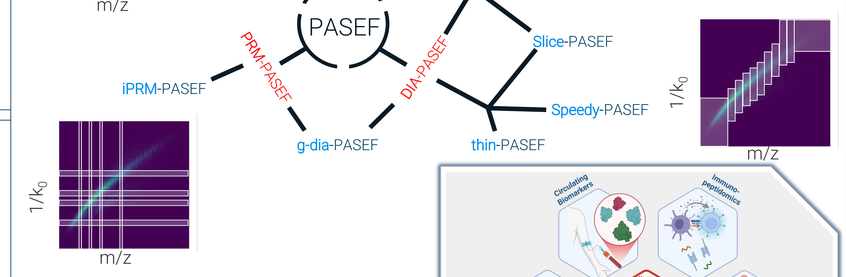
Single Cell and Spatial Omics: Atrophy and pathology unfold across tissue geography—region by region, cell type by cell type. Deep Visual Proteomics on timsUltra AIP combines single-cell sensitivity with high-throughput spatial acquisition, delivering thousands of proteins per region in minutes and enabling pathology maps that resolve microenvironment shifts, degeneration patterns, and cell-type composition across the tissue.





Immunopeptidomics: To study cell-Immune interfaces combining TIMS selectivity with tailored acquisitions like thunder-PASEF retains both +1 and >+1 immunopeptidos and filters out chemical noise, enabling deeper antigen discovery from limited input.





Learn More

- TIMS/CCS adds 4D selectivity and TIMS-cleaned MS/MS to reduce interference and boost confidence.
- PASEF on timsTOF maximizes ion usage via synchronized mobility separation + fast TOF detection for efficient depth/throughput.
- One platform, many modalities: dia-/prm-PASEF (discovery → validation), timSHIFT (chemoproteomics/ABPP), Slice-PASEF (ubiquitinomics/TPD), thunder-PASEF (immunopeptidomics), glyco-PASEF / PTM & proteoform extensions via timsOmni and many more…

PASEF: Run Fast, Run Deep, Run Confident

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