

Parallel accumulation – serial fragmentation combined with data-independent acquisition (diaPASEF):

Bottom-up proteomics with near optimal ion usage

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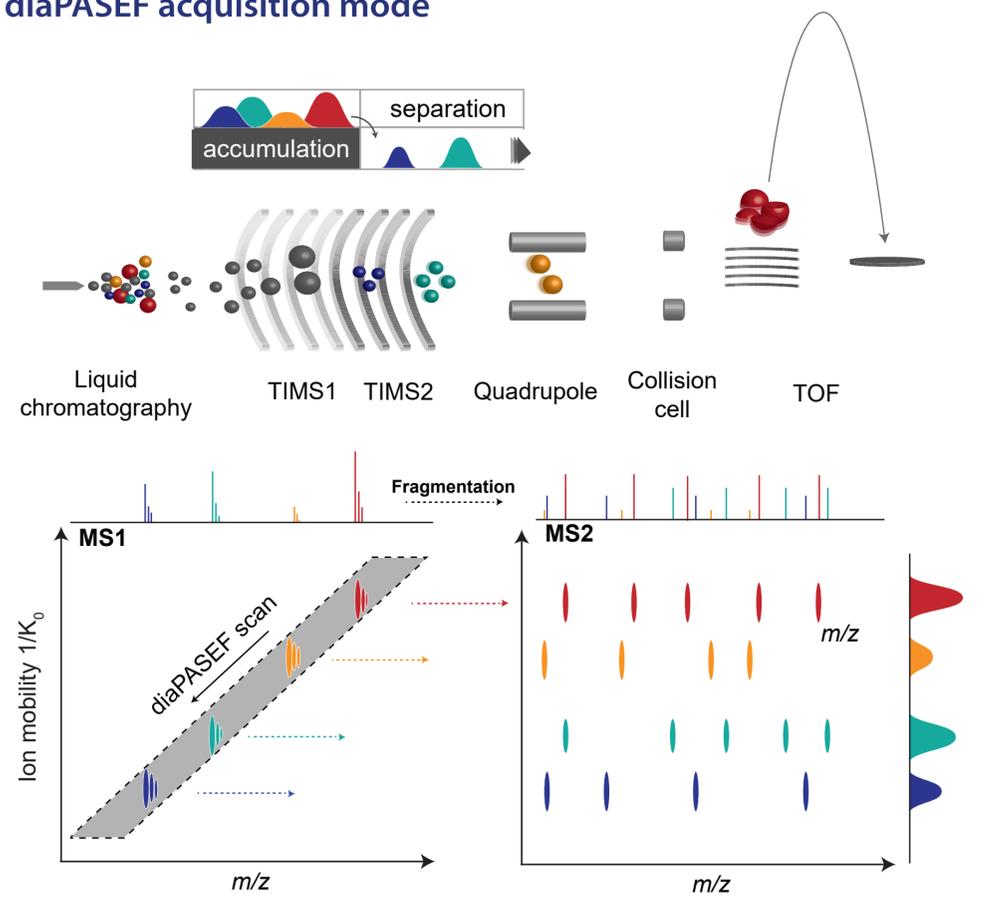
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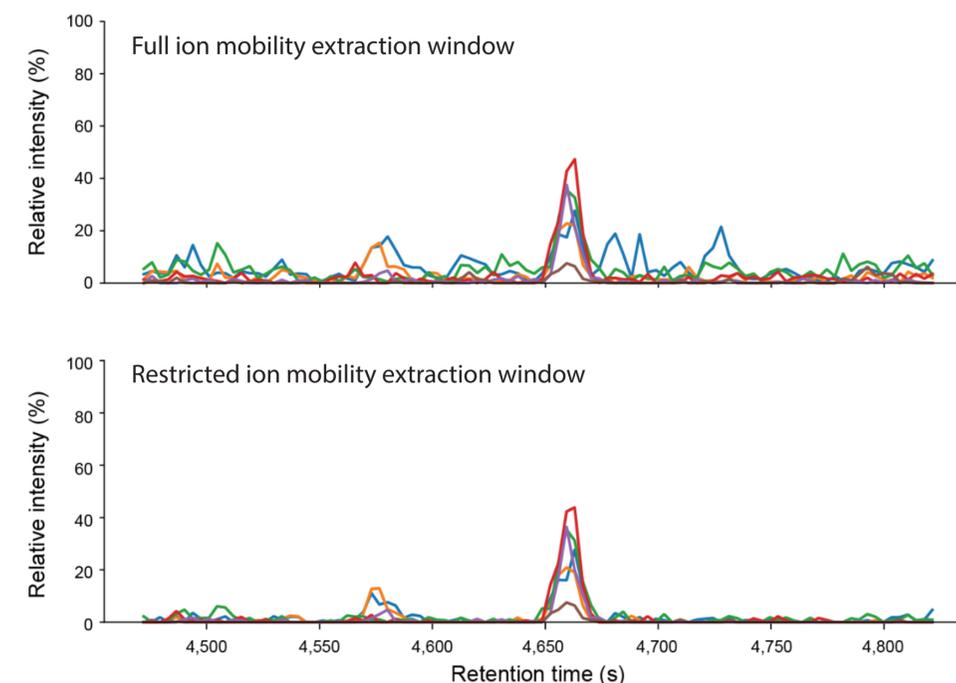


MAX-PLANCK-GESELLSCHAFT

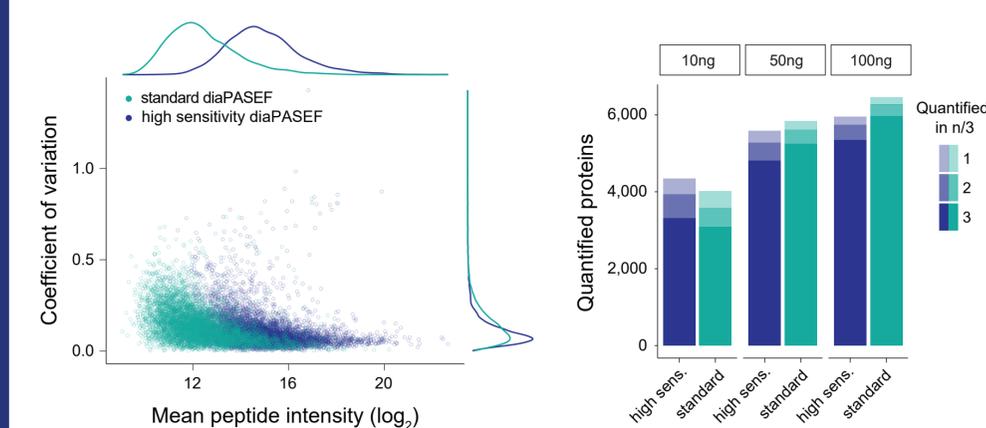
diaPASEF acquisition mode



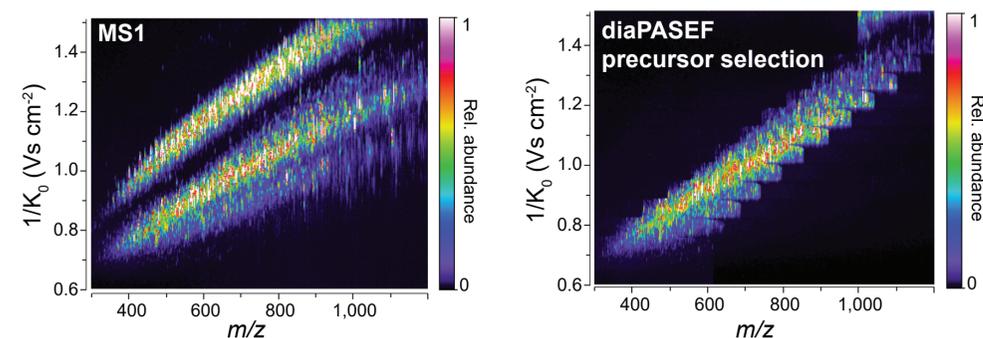
Ion Mobility-Aware Targeted Data Extraction



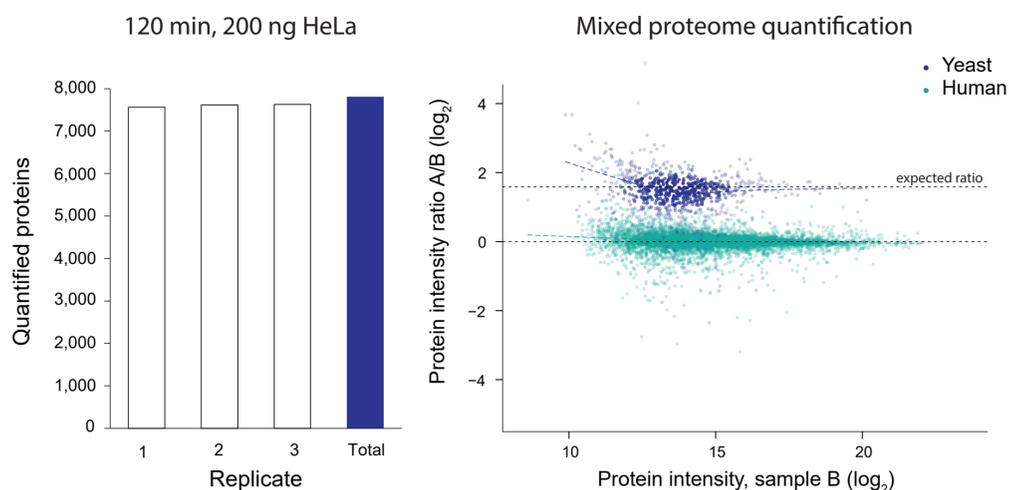
High-sensitivity Proteome Analysis



Correlation of Peptide Ion Mobility and Mass



Single Run Proteome Quantification



Highlights

Standard DIA acquisition schemes utilize only a few percent of the ion current by cycling through segments of the precursor m/z range.

diaPASEF makes use of the correlation of molecular weight and ion mobility in a trapped ion mobility mass spectrometer (timsTOF Pro).

Synchronizing ion mobility separation and precursor selection allows to sample up to 100% of the peptide precursor ion current.

Ion mobility-aware targeted data extraction increases the specificity for precursor identification.

Single run analysis of whole proteome digests and mixed organism samples demonstrates deep proteome coverage and exceptional sensitivity.

Learn more:

Meier *et al.*, *bioRxiv* 2019

<http://biorxiv.org/content/10.1101/656207v2>

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