New prm-PASEF® for highly multiplexed targeted acquisition in clinical samples.

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Results
Fig. 1: prm-PASEF, a new highly parallelized acquisition method
a) Selection of the targeted peptide precursor ions during a single PRM-PASEF event.
Up to 11 precursors can be selected within a 100ms IMS scan and consecutively fragmented in the collision cell.
High selectivity in the precursor’s selection is obtained by combining the ion mobility (green bars) with the quadrupole isolation windows (blue bars)
b) Representation of PASEF-PRM isolation windows in the ion mobility (1/K₀) and chromatography retention time (s) dimensions
c) Visualization of the MS cycle time across the chromatography separation (1 frames =100ms)

Conclusions
• prm-PASEF takes advantage of the trapped ion mobility technology for the targeted proteomics analysis.
• The sensitivity and selectivity of the acquisition method is improved by the ion mobility filtering and time focusing effect that happens during a PASEF acquisition.
• The high multiplexing capacity of the prm-PASEF maximizes the number of peptides quantified in a single analysis while keeping an excellent chromatographic peak profiling.
• prm-PASEF delivers accurate quantitation for a large number of targets over sharp chromatographic peaks and is compatible with high-throughput chromatography for the screening of large clinical sample collections.

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