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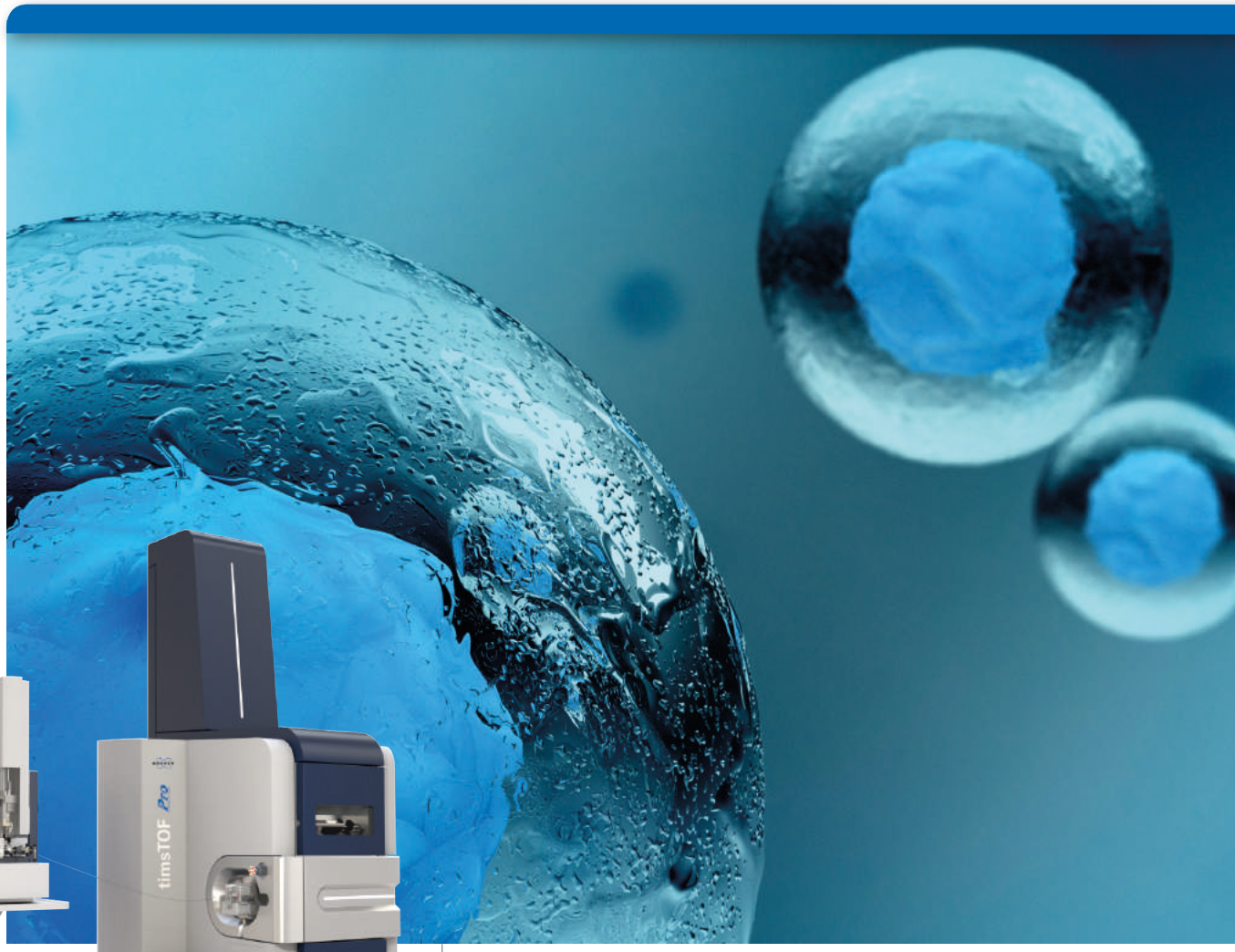





# timsTOF Pro

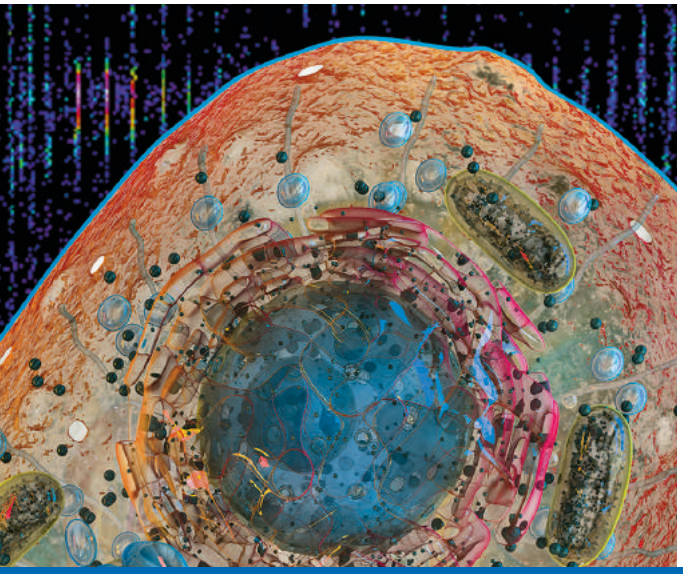
- Powered by PASEF

TIMS-QTOF MS

Innovation with Integrity

# timsTOF Pro

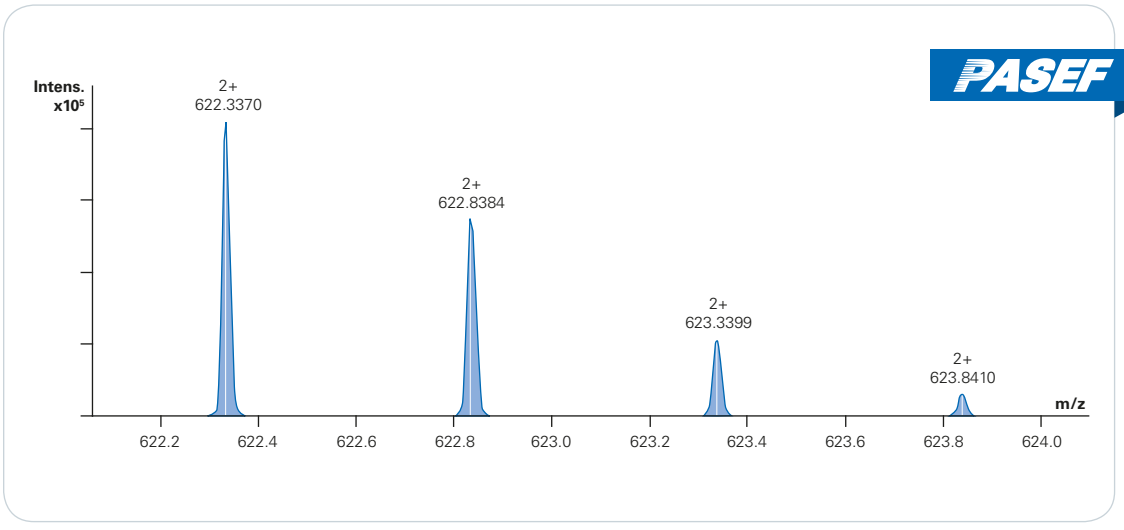
The new standard for high speed, high sensitivity shotgun proteomics



*The timsTOF Pro with PASEF technology delivers revolutionary improvements in scan speed, coupled with enhanced specificity and high sensitivity. It does so while simultaneously maintaining ultra-high resolution for both precursors and MS/MS spectra. This unique performance quintet gives scientists the tools to dig deeper into the complex biology of the deep proteome.*

## Novel dual TIMS design delivers near 100% duty cycle

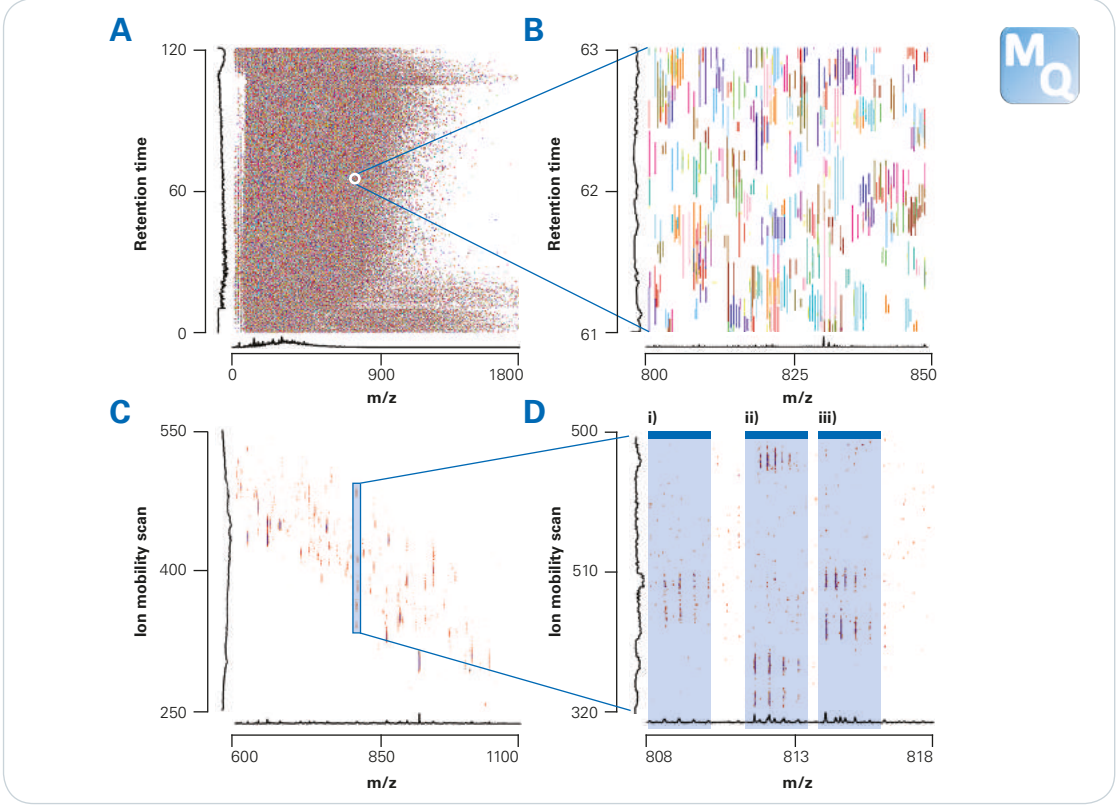
The novel design allows incoming ions to be accumulated in parallel in the first section and for ions to be released dependent on their mobility from the second section of the dual TIMS analyzer in a process called parallel accumulation serial fragmentation or PASEF. This allows for near 100% duty cycle.




High mass resolving power independent of sequencing speed. Measurements were performed with a resolving power of 50,000 (FWHM @ m/z 1222)

# PASEF digs deeper into the proteome

**PASEF** delivers unmatched effective MS/MS acquisition rates and sensitivity by interfacing the time focusing power of the TIMS dimension with ultra-high resolution QTOF technology. Due to the sensitivity gains from PASEF, it is possible to analyze samples with low cell populations and shorter gradients can be used while identifying more peptides and their post-translational modifications (PTMs).




**Power of TIMS separation:** (A) Shotgun proteomics data feature two dimensions at the MS level, the m/z and the retention time (MaxQuant viewer). Illustration of the extremely high complexity of shotgun proteomics data from a HeLa digest over a 90 min gradient. (B) A large number of co-eluting peptides that only differ slightly in mass within a 2 min retention time slice. (C) Within a 2 Th isolation window peptides are not distinguishable based on their m/z. (D) But peptides can be separated based on their trapped ion mobility.

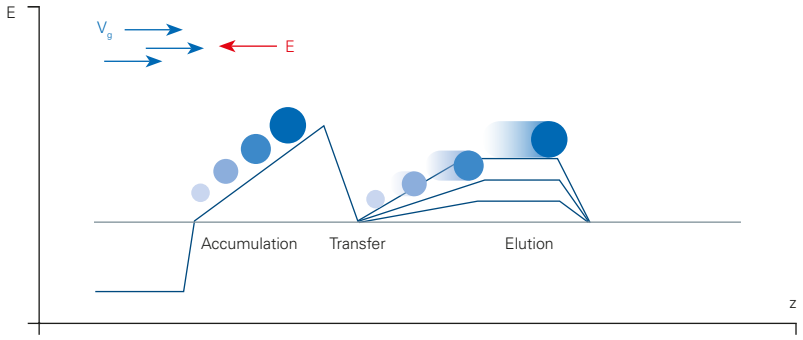
***Prof. Dr. Matthias Mann, Director Department of Proteomics and Signal Transduction, Max-Planck-Institute of Biochemistry, Germany***

*"We now know that the peptide mixtures are still extremely complex when analyzing them in two dimensions (retention time and m/z). Adding one more dimension should in principle get us a long way ahead. In addition to the additional dimension of separation, the timsTOF Pro gives us extremely high speed and sensitivity to get deeper into the proteome and using less sample material."*

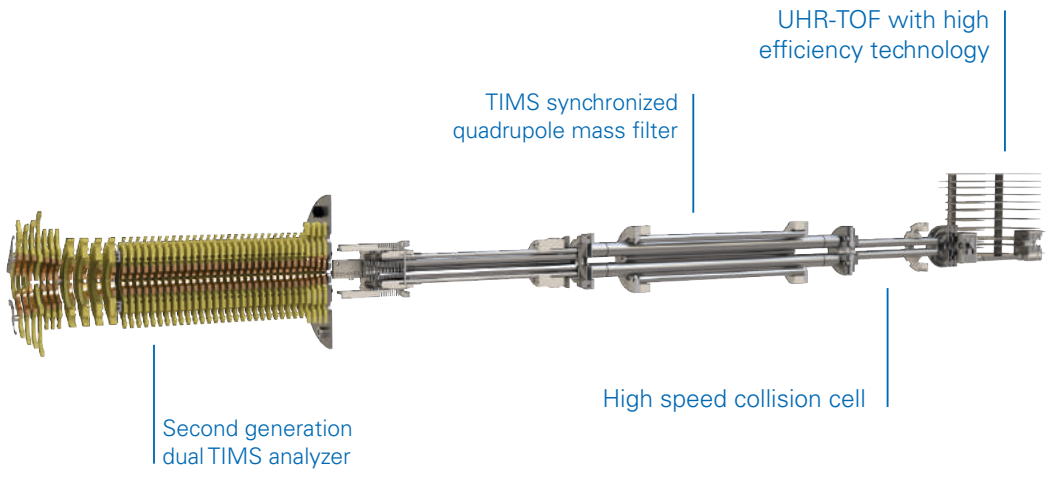
# Enabling record breaking speed with PASEF

The timsTOF Pro was engineered by Bruker experts for scientists to enable breakthrough discoveries in shotgun proteomics. Using parallel accumulation, all ions that enter the timsTOF Pro can be analyzed. In addition, higher ion transmission is provided by the newly designed TIMS synchronized quadrupole. The high speed collision cell and ultra-high resolution TOF enables high MS and MS/MS spectra quality at high speeds.

## Parallel accumulation

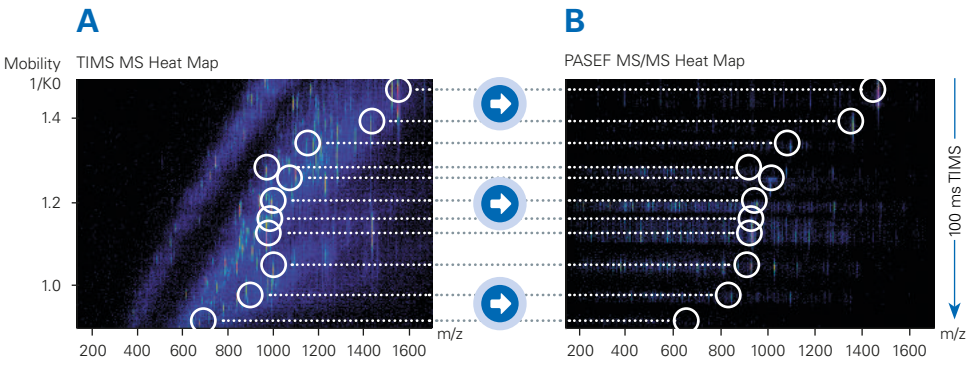



## Optimized for shotgun proteomics



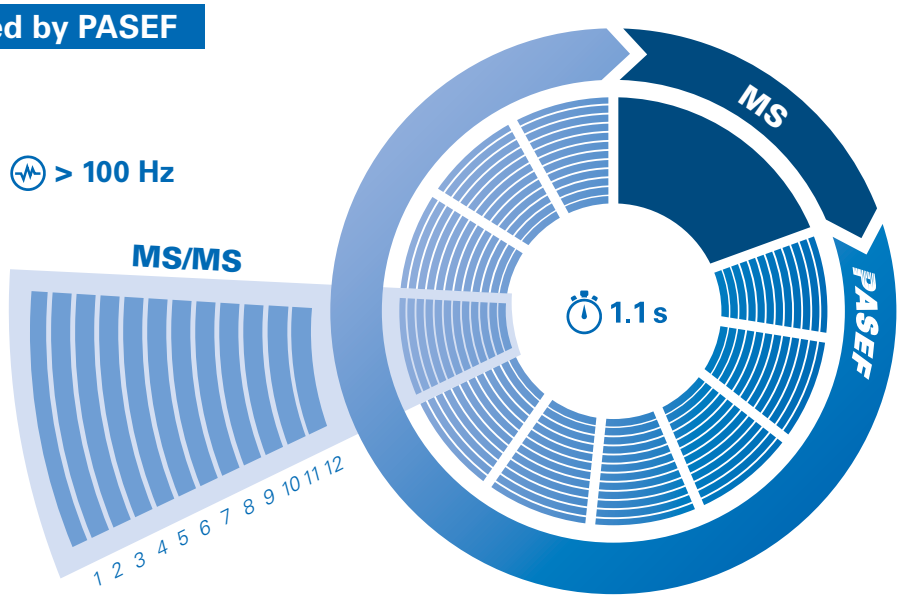

**Schematic of the timsTOF Pro.** All ion optics have been optimized to enhance proteomics performance, including an enhanced quadrupole synchronized with the TIMS analyzer to enable time-focusing, a high speed collision cell and an actively cooled temperature controlled flight tube.

## Time focusing




**The principle of PASEF acquisition:** Peptide ions are separated using trapped ion mobility spectrometry, eluted (~ 100 ms) and detected in the QTOF, generating the TIMS MS heat map (A). For acquisition of PASEF MS/MS spectra (B) the same TIMS separation is used with the quadrupole isolating a certain ion species only during its mobility elution time and immediately shifting to next precursor. Parent and fragment spectra are aligned by mobility values.

## Powered by PASEF

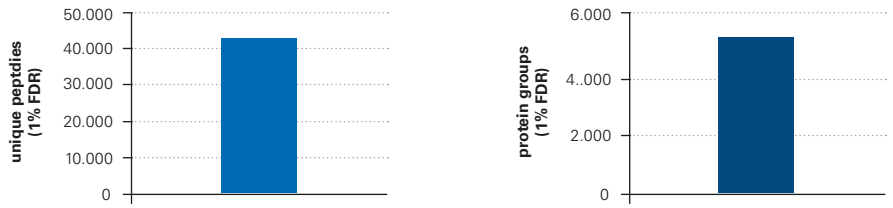



**Parallel accumulation serial fragmentation (PASEF) cycle time:** By synchronizing the quadrupole with the TIMS elution time, an average of 12 precursors can be fragmented within a 100 ms timescale. Intelligent software targets low-level precursors multiple times for PASEF MS/MS fragmentation.

# timsTOF Pro for high sensitivity shotgun proteomics

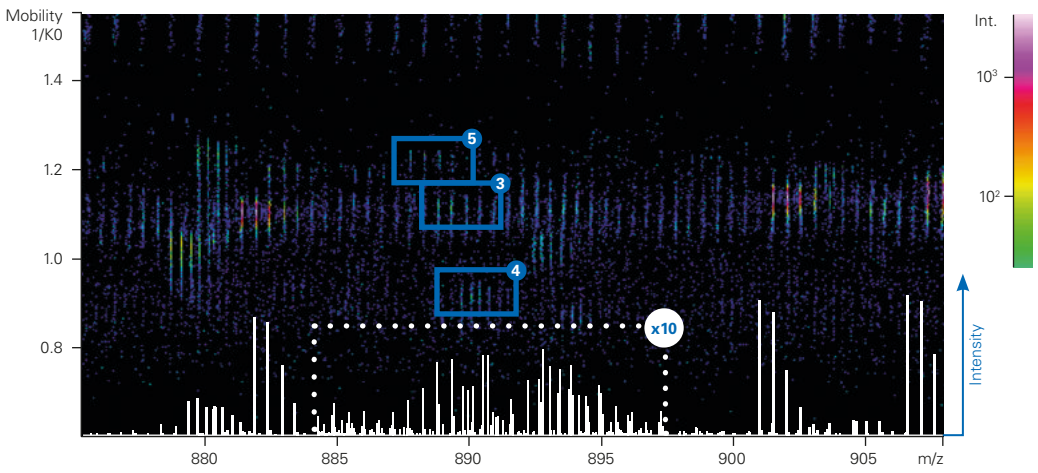
Recent advances in proteomic technologies have made MS-based proteomics a central research tool. However, truly complete proteomes are still elusive, mainly due to the high complexity and dynamic range of biological samples. Analyses using low sample amounts or where a range of post-translational modifications (PTMs) need to be located additionally remain challenging. With the timsTOF Pro, deep proteome coverage can be achieved without the need for large sample amounts ( > 1 µg), reducing the sample preparation costs and making it very attractive for clinical proteomics when sample amounts are limited. Moreover, cleaner MS/MS spectra can be generated by the additional dimension of separation.

## New proteome coverage depths using low sample amounts




**Same depth by using 1/10 of a common sample amount:** Number of identified unique peptides and protein groups using only 200 ng of HeLa digest within a 90 min gradient.

## Higher specificity and sensitivity with TIMS

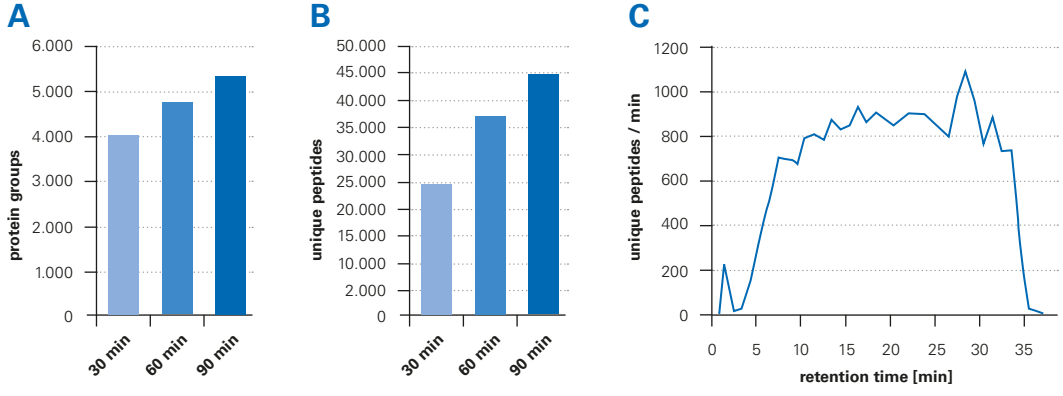



**Improved spectra quality with the timsTOF Pro:** The two dimensions of separation currently available in most LC-MS systems used for proteomics (retention time and m/z) are not enough to distinguish co-eluting peptides that only differ slightly in m/z (white mass spectrum). By applying TIMS, peptide ions can be clearly separated from each other (marked in blue) due to an additional dimension of separation (size-to-charge), resulting in higher specificity and sensitivity. Low level precursors can be targeted multiple times (blue numbers) to enable higher identification rates.

# Higher throughput and more PTMs revealed using PASEF

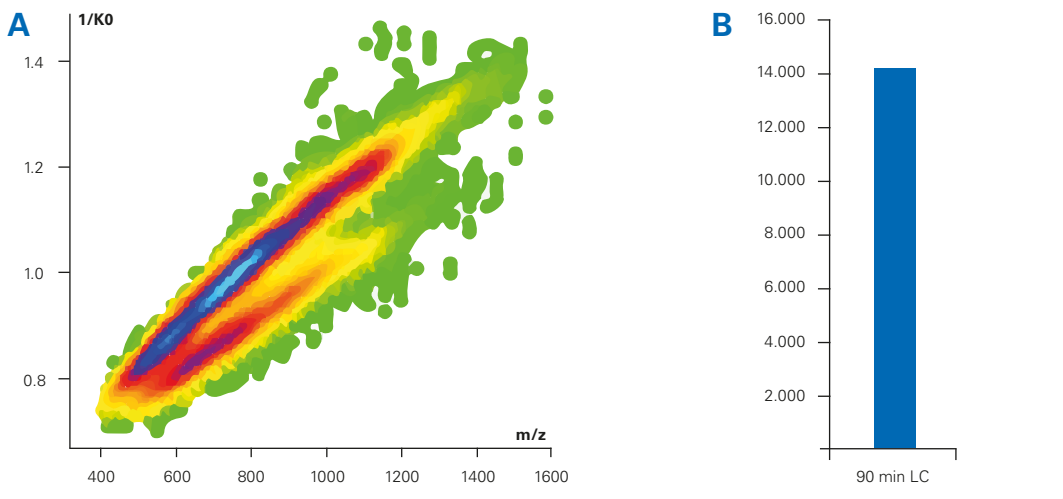
Due to the extremely high data acquisition speed provided by PASEF on the timsTOF Pro without a loss in sensitivity and resolution, typical proteomic analyses can be performed even faster, increasing the throughput of biological experiments tremendously. In addition, PTMs can be better separated from each other using TIMS resulting in a higher identification rate.

## Deep proteome coverage using short gradients




**Deep proteome coverage with short gradients:** Number of identified proteins groups (A) and unique peptides (B) using different gradient lengths (30 min, 60 min and 90 min) with 100 ng of HeLa digest indicating high depth and sensitivity. (C) Number of unique peptides/min with identification rates of ~ 1100 /min at maximum.

## High number of phosphopeptide identifications




**Deep phosphoproteomics analysis:** (A) Density heat map of phosphopeptide features using a 90 min gradient (only multiply charged precursors are shown, singly charged species are excluded). (B) Number of unique phosphopeptides identified in a 90 min gradient run using only 1/10 of sample required for LC-MS systems.

# timsTOF Pro

**Specificity**
**Sensitivity**
**Speed**

The New Standard for Shotgun Proteomics

**PASEF**

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***Prof. Dr. Jürgen Cox, Group Leader Computational Systems Biochemistry, Max-Planck-Institute of Biochemistry, Germany***

*"We have been impressed with the quality of the data that we've seen and therefore we expect that the performance of the timsTOF Pro with the PASEF technology will make it very popular among proteomics researchers."*

## List of timsTOF patents

**TIMS cell (BIL 031/08)**, Title: "Apparatus and method for parallel flow ion mobility spectrometry combined with mass spectrometry", Issued: US7838826B1; US 8288717B2

**Temporal Zoom, IMEX (BDAL 293/11)**, Title: "Spectrum Acquisition Modes For Ion Mobility Spectrometers Using Trapped Ions", Issued: US8766176B2; GB2490387B, Pending: DE102012004398A1

**Spatial Zoom (BRE 399/15, BRE 404/15)**, Title: "Spatial zoom mode for accumulative trapped ion mobility spectrometry", Issued: US9304106B1; US9546980B1, Pending: EP3054475A1; EP3165913A1; US20170125234A1; CN105869980A; CN107039231A

**Parallel Accumulation TIMS (BRE 398/15)**, Title: "Trapping ion mobility spectrometer with parallel accumulation", Issued: US9683964B2, Pending: EP3054473A1; CN105869983A

**Parallel Accumulation - Serial Fragmentation, PASEF (BRE 405/15)**, Title: "Acquisition of fragment ion mass spectra of ions separated by their mobility", Pending: EP3165914A1; US20170122906A1; CN107037170A

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