



NEWS RELEASE

Bruker Introduces PaSER™ Software for ‘Run and Done’ 4D- Proteomics™ and TIMS/PASEF Method Wins HUPO 2020 Award

10/19/2020

- HUPO 2020 Science and Technology Award for Commercialization of TIMS Technology
- True Single Cell 1,000 Protein Group Results from Mann Lab leverage dia-PASEF® and further improvements in ultra-low flow Evosep chromatography and modified TIMS/PASEF set-up
- Significant Improvements in Quantitative Targeted 4D-Proteomics with prm-PASEF®
- Licensing of PhoX cross-linker from Heck Lab enables caps-PASEF structural proteomics

BILLERICA, Mass.--(BUSINESS WIRE)-- At the virtual 19th Human Proteome Organization World Congress (hupo2020.org), **Bruker Corporation** (Nasdaq: BRKR) today announced that Melvin A. Park and Oliver Raether were awarded the **HUPO Science and Technology Award** for the commercialization of Trapped Ion Mobility Spectrometry (TIMS) and the Parallel Accumulation Serial Fragmentation (PASEF®) method. This award recognizes innovation that changes the way scientists do proteomics, validating the role the timSTOF Pro has on enabling short gradients for large cohort deep 4D-Proteomics translational studies. Bruker also takes the opportunity to recognize the contributions of PASEF co-inventor **Professor Matthias Mann**.

This press release features multimedia. View the full release here:

<https://www.businesswire.com/news/home/20201019005249/en/>

Figure 1: Real-time PaSER can monitor 4D-Proteomics data acquisition (Photo: Business Wire)

A. Real-Time Database searching with PaSER™ for

“Run and Done’ 4D-Proteomics

Bruker further announced the release of **PaSER**, a complete GPU-based device enabling proteomics database search in ‘real time’, building on the recently announced acquisition of **IP2** software. The term ‘PaSER’ was coined

by **Professor John Yates III** and **Dr. Robin Park** from The Scripps Research Institute and stands for **Parallel Database Search Engine in Real-time**. The unique **PaSER** architecture uses a parallelized, multi-threaded search engine running on GPUs to search proteomics results in real time at or faster than the data acquisition. This result is 'Run and Done' high-throughput 4D-Proteomics where scientists have identified peptides and protein groups as soon as the experiment is complete.

Professor Yates will present on "The Synergies of Mass Spectrometry and Informatics" in Bruker's Virtual Industry Seminar (hyperlinks to HUPO talks and events mentioned in this news release are included below), and Dr. Robin Park will discuss IP2 and PaSER at Bruker's virtual proteomics user's meeting.

Dr. Gary Kruppa, Vice President of Proteomics at Bruker Daltonics, commented: "The timsTOF Pro enables 4D-Proteomics with the large-scale measurement of ion mobility yielding collision cross sections (CCS) for every measured peptide. Combined with the timsTOF Pro speed this means that the bottleneck in proteomics has moved from measurement to processing large amounts of data. The speed of IP2 and the PaSER GPU-based search are an ideal match for the timsTOF Pro, and we are thrilled to have Robin Park join us to continue the development of IP2 and PaSER for TIMS/PASEF methods."

B. Ultra-high Sensitivity and True Single Cell 4D-Proteomics

The groups of **Prof. Matthias Mann** at the Max Planck Institute in Martinsried, Germany, and at the Medical School of the University of Copenhagen, with collaborators at Evosep and Bruker, have made significant advances in high sensitivity and true single cell proteomics. A modified timsTOF Pro allows robust measurements of proteomes from low sample amounts and even from single cells. Matthias Mann will present his work in "Deep Visual Proteomics for Systems Biology" in the HUPO Connect 2020 program, while his Ph.D. student Andreas Brunner will present at Bruker's virtual user's meeting on "Ultra-high sensitivity MS on a timsTOF enables proteomics analysis of single cells – one by one".

Matthias Mann stated: "Making meaningful measurements of protein expression at the true single cell level is extremely challenging both from a sample handling and measurement perspective. We are delighted to have Evosep and Bruker as collaborative partners to help us implement, prove and ultimately bring to the clinic our ideas so that true single cell proteomics can be made available to all researchers in the near future."

C. Targeted Quantitative 4D-Proteomics and prm-PASEF

Bruker's prm-PASEF workflow for quantitative proteomics enables the most highly multiplexed targeted proteomics methods available. The additional dimension of separation provided by TIMS also reduces interferences in MS2 quantitation. Taking advantage of the speed and additional TIMS separation of the underlying PASEF method, prm-

PASEF can now target more than a dozen precursors in each 100 msec TIMS separation. **Professor Gunnar Dittmar** of the Luxembourg Institute of Health and Professor of Proteomics at the University of Luxembourg will present on “New prm-PASEF Method for Highly Multiplexed Targeted Quantitative Proteomics for Clinical Research” at Bruker’s Virtual Industry Seminar at HUPO Connect 2020.

D. caps-PASEF Crosslinking for Structural 4D-Proteomics and the PhoX Crosslinker

Bruker is pleased to announce licensing PhoX cross-linking technology (IMAC-enrichable) as result of the collaboration with **Albert Heck** and **Richard Scheltema** at Utrecht University. The advantage the timsTOF Pro provides for cross-linking aided by PhoX and the novel caps-PASEF method is described in the paper “Benefits of Collisional Cross Section Assisted Precursor Selection for Cross-linking Mass Spectrometry”, published in Molecular and Cellular Proteomics. The PhoX cross-linking reagent from Bruker will be available in early 2021.

E. Software Developments for Analysis of 4D-Proteomics Data

The third-party software ecosystem around the timsTOF Pro continues to grow as the community takes advantage of Bruker’s unique, open data file format. New developments include support for dia-PASEF from Bioinformatics Solutions Inc.’s PEAKS Studio and PEAKS Online software packages. In particular, PEAKS Online provides an enhanced, cloud-based solution for processing of large datasets from large sample cohorts, including further improvements for LFQ quantitation and new workflows like SILAC. MaxQuant will soon support dia-PASEF processing capabilities.

Biognosys announced rapid processing of timsTOF Pro 4D PASEF data with SpectroMine, their software solution for multiplexed and label-free quantitative DDA proteomics, built around the powerful Pulsar search engine. **Dr. Lukas Reiter**, Chief Technology Officer of Biognosys commented: “It has been a priority for us to optimize support for timsTOF Pro in our software, resulting in fast processing of 4D PASEF data with deep proteome coverage. SpectroMine 2 can now be used for isobaric labeling, as well as for label-free quantification (LFQ) workflows with timsTOF Pro data.”

Links to Bruker events at HUPO 2020 can be found here: <https://www.bruker.com/events-records/2020/hupo-connect-2020.html>.

About Bruker Corporation (Nasdaq: BRKR)

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