

Mass Spectrometry Resource University at Albany

MS Technologies Series

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10:00 am

D'Ambra Auditorium, Life Sciences Research Building
1400 Washington Avenue, Albany, NY 12222

Gary Kruppa, PhD

Vice President, Global Omics Solutions, Bruker Daltonics

Digging Deeper into the Proteome by using TimsTOF Pro with PASEF

Abstract: Proteomics researchers require mass spectrometers with increased speed and sensitivity to address the complex mixture of peptides eluting from nano-flow LC columns in data dependent shotgun proteomics workflows. The previously introduced “Parallel Accumulation Serial Fragmentation” method (PASEF, Meier et al., JPR 2015, PMID: 26538118) for trapped ion mobility spectrometry (TIMS) quadrupole time of flight (QTOF) instruments, enabled five to ten times faster data dependent acquisition of fragment ion spectra. The potential demonstrated in 2015 has now been achieved, along with even more impressive gains in sensitivity due to the 100% duty cycle, and focusing of the ions in time and space, provided by the PASEF method.

In this talk the principles of TIMS and the PASEF method, and how they enable a simultaneous gain in speed and sensitivity, at the same time, will be explained. The speed of the PASEF method is only compatible with a very fast scanning instrument such as QTOFs, and it will be shown how this combination results in full sensitivity resolution (FSR) with resolving power of 50,000 FWHM (at m/z 1222) for both MS and MS/MS data, with low ppm mass accuracy and true isotopic patterns (TIP) all at MS/MS acquisition rates in excess of 100 Hz. The benefits of the PASEF method for identifying more proteins in less time and with less sample in data-dependent shotgun proteomics experiments will be demonstrated.

Host: Prof. Dan Fabris, MS Resource, University at Albany, fabris@albany.edu,

For additional information, please contact Dr. Kasia Janota at kasia.janota@bruker.com

