



Answers for Science. Knowledge for Life™

FREE OMICS WORKSHOP



2015 Chemical Proteomics Symposium SWATH™ Workshop

When: 15 July 2015

Time: 1:30pm - 5:00pm (lunch provided from 12:30pm - 1:30pm)

Where: Children's Medical Research Centre, 214 Hawkesbury Road, Westmead, NSW, 2145

Everybody is Talking About SWATH™

First announced at HUPO in 2011 and then released at ASMS in 2012, SWATH™ was the first Data Independent Analysis (DIA) technique that combined the quantitative performance of targeted analysis such as multiple reaction monitoring with the comprehensive coverage of data-dependent discovery LCMS methods. Since then, SWATH™ has moved beyond being just a novel acquisition technique to being an indispensable tool in systems biology research. This is reflected in the rising tide of publications using SWATH™ to unravel complex biological problems. Today, over 30 papers featuring SWATH™ analysis have been published - many in high impact journals (eg. Nature Medicine 21, 407–413 (2015)). In the past year, SWATH™ has also made its way into the literature as a technique for the analysis of small molecules, where it displays distinct advantages over traditional techniques for the identification and quantitation of metabolites and other small molecules in complex samples. This workshop is designed for anyone who has an interest in SWATH™. Concurrent sessions will cater for all levels of experience and understanding. Hear from the experts at SCIEEX as well as those already using SWATH™ in their research. We look forward to seeing you there.

Session 1a - SWATH™ Proteomics for Beginners (presented by Dr Keith Ashman, Senior Field Service Applications Specialist, SCIEEX Oceania)

If you are new to SWATH™ and want to find the best place to start, this session is for you. Here you will find the answers to these questions and more;

- What is SWATH™?
- What are the analytical challenges of proteomics and how does SWATH™ simplify the path from sample to biological insight?
- How do I get started? What hardware and software are required to perform SWATH™ analysis?
- What makes a good SWATH™ method? Simple method setup and optimisation with variable SWATH™ window acquisition.

Session 1b - SWATH™ for ALL Molecules (presented by Chris Hodgkins, Market Development Manager, SCIEEX Oceania)

If you are interested in how SWATH™ can be applied for small molecule analysis, this is the session for you. Learn how SWATH™ provides insights no other technique can access by harnessing the power of dynamic range in high-resolution mass spectrometry. See the latest software workflows from SCIEEX for processing small molecule SWATH™ data, including MasterView™ and XCMSplus.

Session 2 - Next-Generation Proteomics – SWATH™ 2.0 and Beyond

- Evaluation of SWATH quantitation using local and extended libraries – Dr. Xiaomin Song (APAF)
- OneOmics™ in the cloud. See the full-release versions of SCIEEX's BaseSpace apps and the new SWATH™ workflow – Chris Hodgkins (SCIEEX)
- Tips and tricks for SWATH™ library generation – Dr. Ludovic Gillett (ETH, Zurich)

For more details and registration, please email vesna.murdoch@sciex.com or call 1300 62 77 77

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