



Ben Schulz

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Biochemistry

Case Study

Project Goal

Use proteomic approaches to study the bioprocess of beer production and the proteomic changes occurring that can impact flavour. This can be used to inform process optimisation, product development and quality control, or to confirm product authenticity.

The Solution

- **SWATH® Acquisition on TripleTOF®** for quantitative protein profiling. SWATH allows for consideration of unusual proteolysis products and PTMs that are formed during bioprocessing.
- **ProteinPilot™** software for library generation, allowing proteolysis sites and a multitude of potential modifications to be identified and incorporated into an ion library.

Biggest Challenges Right Now

- Working with unfamiliar and/or unavailable proteomic and genomic databases.
- Identification of novel modifications that can arise as a result of bioprocessing.

Outcomes of research

- SWATH® Acquisition allows for retrospective data analysis using a variety of bespoke data analysis approaches.
- Development of novel experimental approaches for identification and quantitative profiling challenging post translational modifications using SWATH® Acquisition.

“Remining data is the major advantages of SWATH® Acquisition, to take advantage of recent gene annotations for example.”

Type of Organization

School of Chemistry and Molecular Biosciences
University of Queensland.
Use of molecular-based approaches to create understanding and lead to discovery.

Goals

To use novel proteomics approaches to detect, quantify and understand post translational modification of proteins.

SCIEX PRODUCTS/ APPLICATIONS

- TripleTOF® 5600+
- 5500 QTRAP®
- SWATH® Acquisition

“We apply a variety of bespoke analytics, but the beauty of SWATH® Acquisition is that the data is all in there.”

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