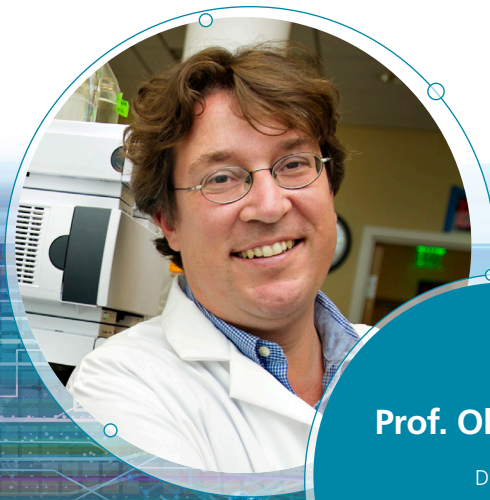




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## Case Study

### Project Goal

To advance tools in analytical chemistry and bioinformatics to generate improved metabolomic data. These tools are used to understand which parts of larger biochemical networks respond to genetic perturbation or environmental strain.

### The Challenges

- Compound identification, to be able to correctly identify all the compounds generated by LC-MS/MS
- Harmonization of data structure, and validation of quantitative and qualitative measurement of metabolites in the metabolomics field, world-wide
- Interpretation of big data sets

### The Solution

Using a selection of powerful LC-MS/MS systems to develop tools and databases freely available to the scientific community for database integrations, genomic data integration, data visualizations, and software for data processing and compound identification.

### The Outcomes

- 15 tools and databases developed to be used for data processing from state of the art LC-MS/MS systems
- Identification of biomarkers for early diagnostics of severe diseases such as diabetes and lung cancer

“Metabolomics is the output of the cell, and you can’t understand what is happening in a cell if you don’t look at the output.”

#### Type of Organization

NIH Regional Resource Core for metabolomics services

#### Goals

To increase the availability of metabolomics services to researchers in diverse fields while concurrently progressing the state-of-the art in metabolomics research.

#### APPLICATIONS

Untargeted metabolomics by LC-MS/MS

#### SCIEX products

- SCIEX QTRAP® 6500 System
- SCIEX QTRAP® 4000 System
- SCIEX TripleTOF® Systems

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