

# Development of High Throughput Proteomics and Metabolomics Assays

CID NL0033729d, WBS# 2.5.3.700d

Jon Magnuson\*, Kristin Burnum-Johnson, Chris Petzold, Corey Hudson, Alex Apffel

## Project Type

- **DFO, Agile BioFoundry**
- **Goal of DFO-FOA:** To accelerate innovation and adoption of new biomanufacturing approaches that will foster growth of the bioeconomy, the DOE's Agile BioFoundry ([www.agilebiofoundry.org](http://www.agilebiofoundry.org)) is overseeing a directed funding opportunity for participating national labs and industry partners to **utilize the ABF to develop novel microbial hosts and bioproducts or to develop new capabilities and approaches that will advance all aspects of the Design-Build-Test-Learn biomanufacturing cycle.**

## Management Approach

- PNNL (Kristin Burnum-Johnson & Jon Magnuson) LBNL (Chris Petzold) and SNL (Corey Hudson) partners
- Coordination of the efforts of Agilent (Dr. Alex Apffel) and the three national labs will benefit from an existing close working relationship with Agilent
- Kick off meeting with all participants and BETO
- Monthly project meetings via phone conferencing
- Quarterly written and verbal reporting to BETO
- Internal and External Reviews
- Milestones to gauge progress



## Timeline

- *Project Start Date: 3/7/19, (final signatures expected)*
- *Project End Date: 2/28/21*
- *Percent Completed: 0%*

## Technical Approach

- We will couple two powerful mass spectrometry (MS) platforms; (1) PNNL's **Drift Tube Ion Mobility Spectrometry (DTIMS)** with **Time of Flight MS (TOF-MS)** and (2) PNNL's and LBNL's **triple quadrupole (QQQ) MS with Agilent's prototype system** to process hundreds of metabolomic and proteomic samples per day via **automated analytical workflows (AAW)** and Ultra-High Performance Liquid Chromatography (UHPLC).
- **Outcome:** The success of this project will fulfill a need for high-throughput analytical workflows that reduce time and resource needs, thus increasing the number of samples analyzed for a fixed resource allocation
- **Learn** approaches employing variations of deep learning benefit from large data sets.
- Thus, this ability to increase sample numbers and throughput will directly benefit **Learn** and therefore increase the value of each turn of the DBTL cycle, as well as accelerating that cycle.

## Milestones

- (LBNL/PNNL) Implement the Agilent high-throughput (<1.5 minute gradient) metabolomics methods on a UHPLC-QQQ and UHPLC-DTIMS platforms.
- Perform concentration based calibration curves on a mixture of small molecule standards to understand the sensitivity and linearity of the platforms.
- (LBNL/SNL) Implement AAW software for UHPLC-QQQ method selection, data acquisition and data processing. Interface the AAW software inputs and outputs with ABF-EDD software.
- (PNNL) Perform high-throughput UHPLC-QQQ & UHPLC-DTIMS analyses on over 100 ABF strains in 3 minutes per sample for metabolomic extracts of 2-3 ABF hosts with detection of over 50 metabolites. (Go/No-Go)
- (SNL) Expand AMS (Automated Method Selector) software to include additional physical/chemical properties and demonstrate model predictions.
- (PNNL, LBNL, and SNL) implement AMS software to detect >50 metabolites in rapid analyses acquired through LBNL UHPLC-QQQ and PNNL UHPLC-DTIMS platforms

	Total Funding Pre-FY17*	FY 17 Funding	FY 18 Funding	Total Planned Funding (FY 19-Project End Date)
DOE Funded			800K (forward funded)	800 K
Project Cost Share (if applicable)				20%

Partners: If multiple DOE recipients are involved in the project, please list level of involvement, expressed as percentages of project funding from FY 17-18. [(i.e. PNNL (50%); SNL(19%); LBNL (31%)]

## Team

- Alex Apffel
- Jon Magnuson
- Kristin Burnum-Johnson
- Chris Petzold
- Corey Hudson
- John Gladden