

# Enhancing the Proteomics Core Facility Operation through Use of Cloud Computing

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**PAR-19-301:** NIGMS to support mission relevant resources with economy of scale to provide access to state-of-the-art services for national/regional user base

**Goal:** Provide unmatched and most cost effective access to state-of-the-art quantitative proteomics platforms and skilled bioinformaticians, which will increase the capacity of IDeA states to perform cutting-edge research

**Specific Aim 1. Provide state-of-the-art quantitative proteomics services to the IDeA network.**

- Access to state-of-the art instrumentation, cutting-edge proteomics services, and associated bioinformatics
- Increase efficiency of operation and leverage economy of scale to minimize recharge

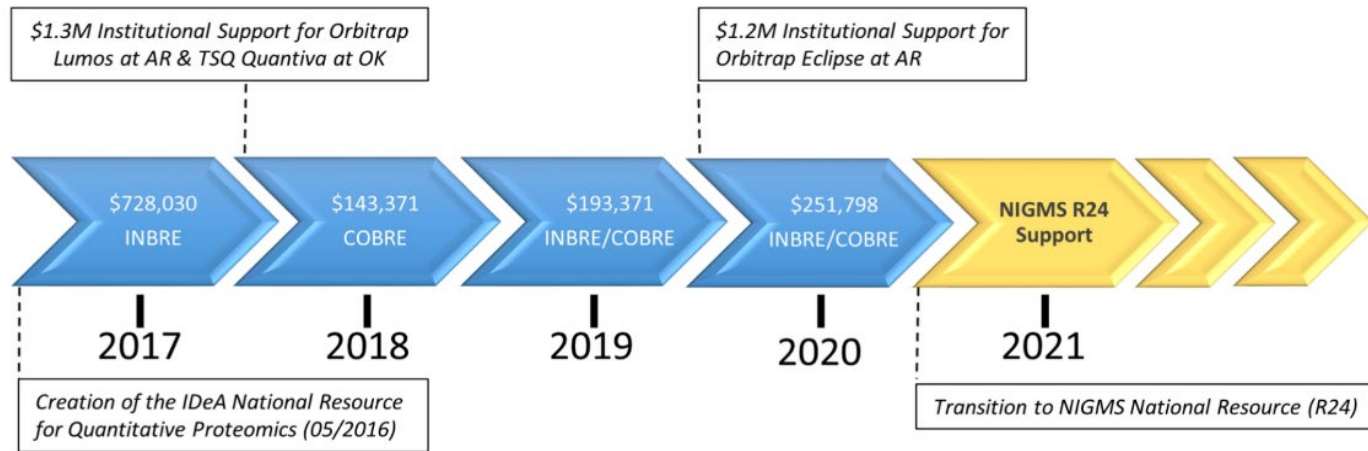
**Specific Aim 2. Provide outreach opportunities for quantitative proteomics to the IDeA network.**

- Voucher program
- Internship

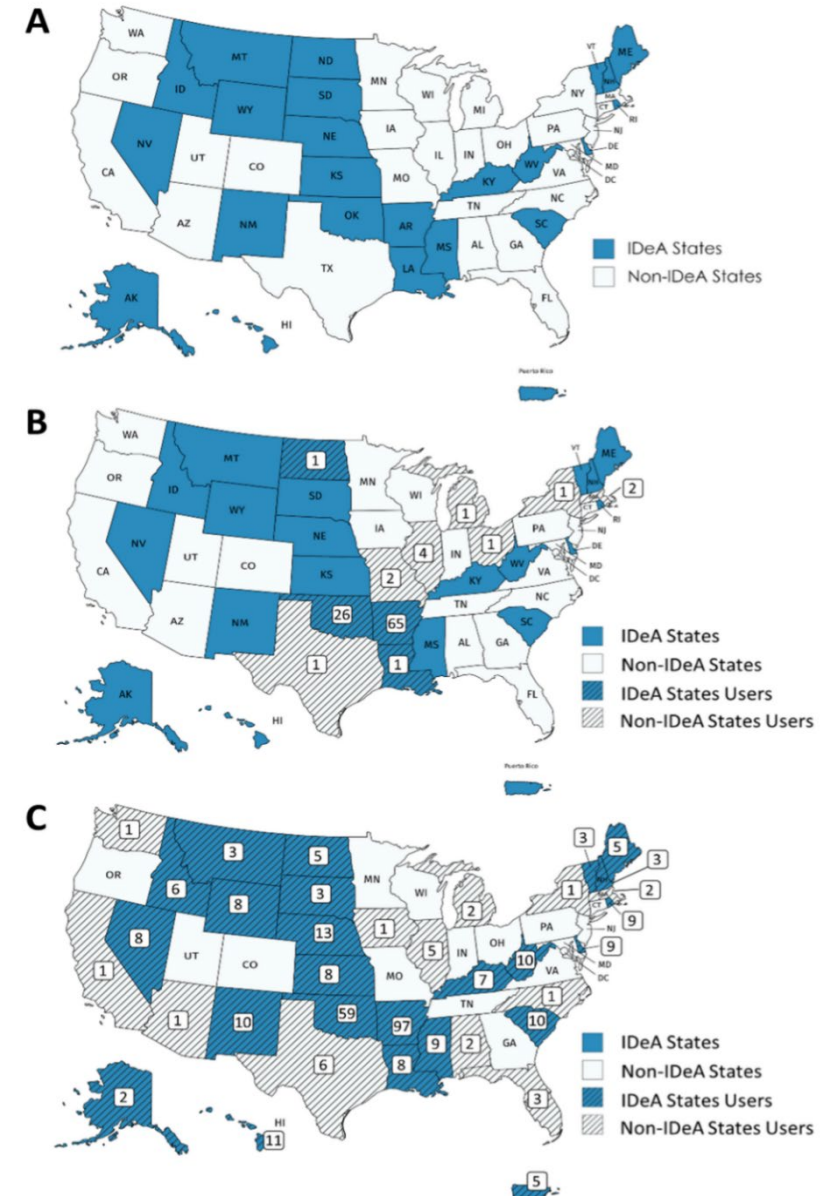
**Specific Aim 3. Provide educational opportunities for quantitative proteomics to the IDeA network.**

- Workshops
- Symposia
- Web Resources

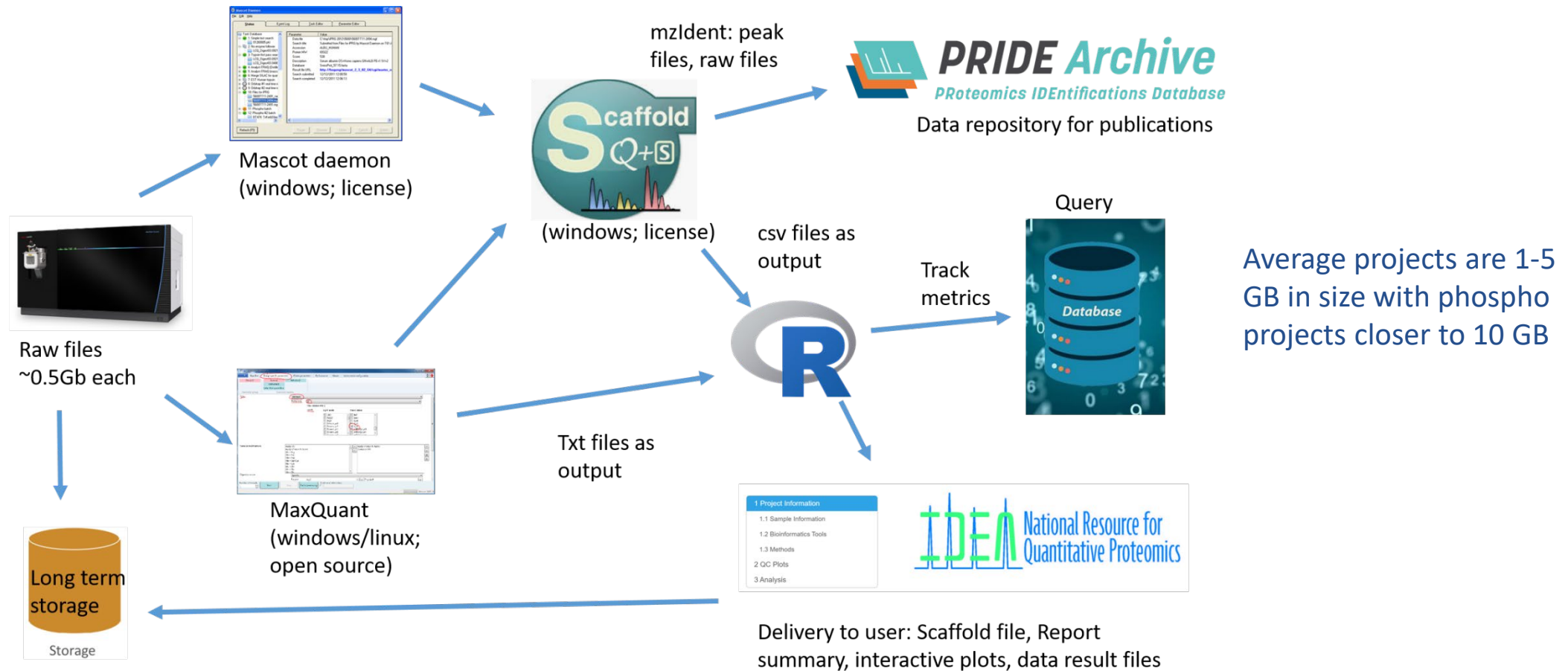
# Historical User Base



**IDeA National Resource for Quantitative Proteomics serves the entire IDeA network.** A) Twenty-three states and Puerto Rico make up the IDeA network. B) IDeA state investigators using our services three years prior to resource (FY14-16). C) IDeA state investigators using our services since establishing the resource (FY17-19). Boxed numbers indicate total investigators using services in the 3-year windows.



# Bioinformatics Workflow – lift and shift

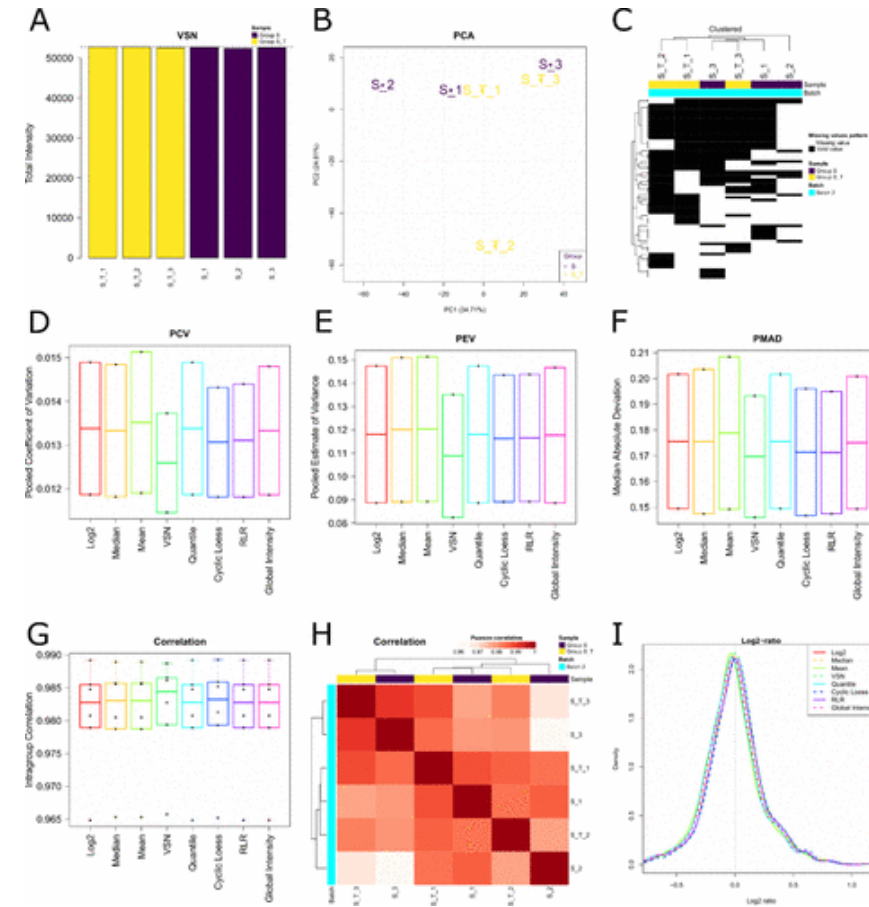
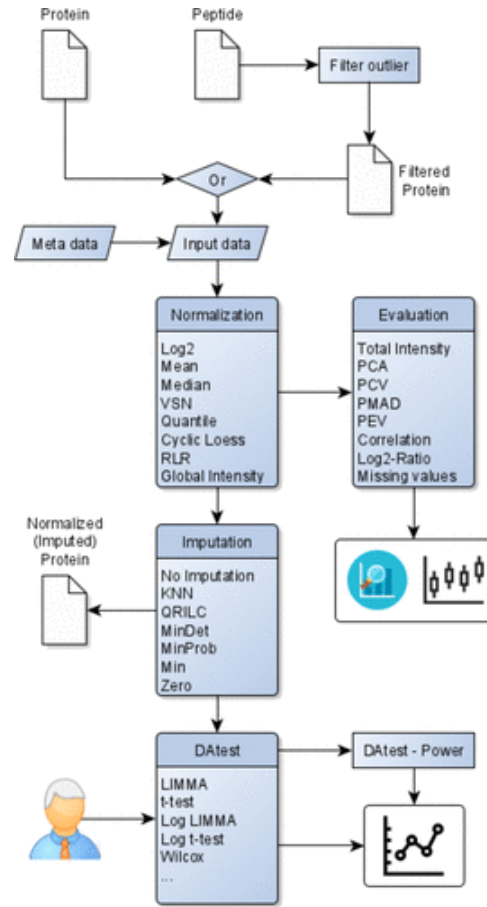


# proteiNorm – A User-Friendly Tool for Normalization and Analysis of TMT and Label-Free Protein Quantification

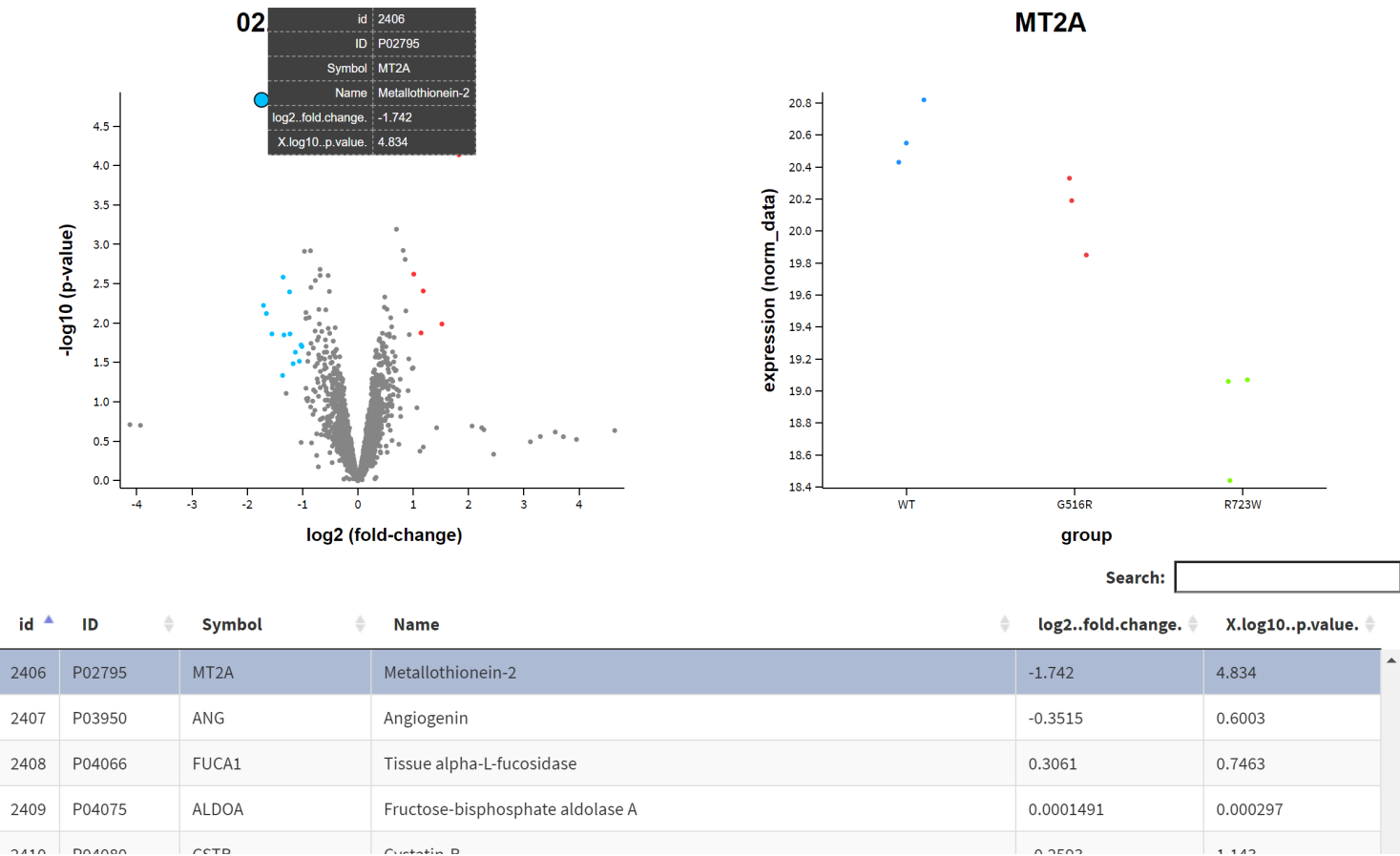
Stefan Graw, Jillian Tang, Maroof K Zafar, Alicia K Byrd, Chris Bolden, Eric C. Peterson, and Stephanie D Byrum\*

R Shiny App to check data QC and best normalization.

Currently runs on local computer so anyone that wants to use it must download the R scripts from Github and install all R package dependencies



# R: Glimma interactive plots can be opened in a web browser



Name

css

js

01\_G516R\_vs\_WT\_volcano.noadj.plot.html

01\_G516R\_vs\_WT\_volcano.plot.html

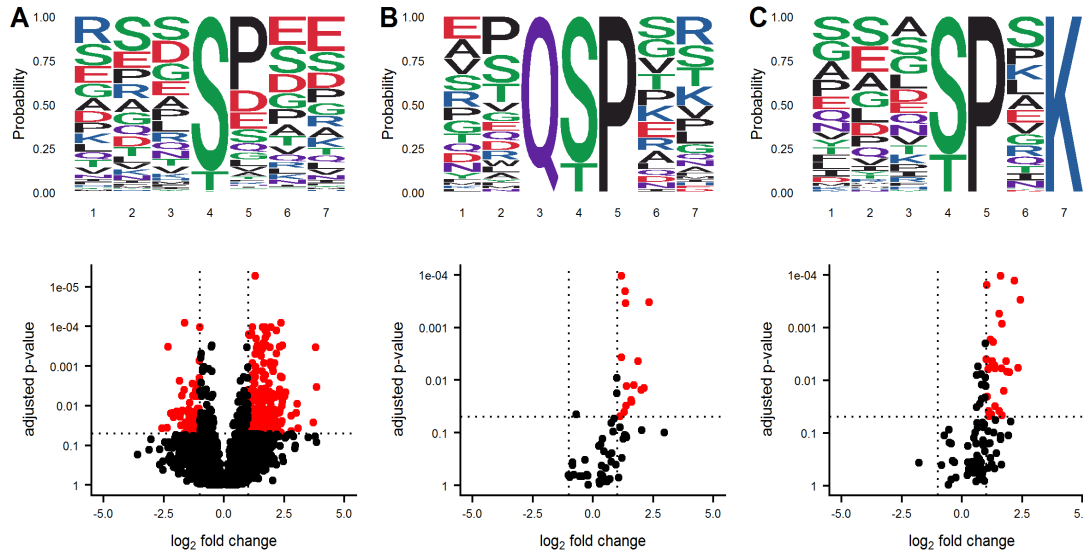
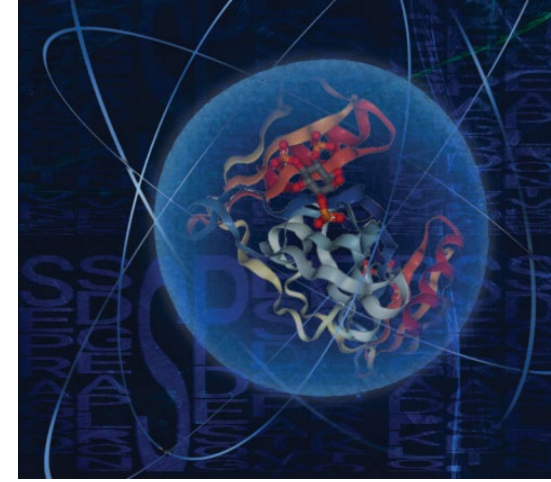
02\_R723W\_vs\_WT\_volcano.noadj.plot.html

02\_R723W\_vs\_WT\_volcano.plot.html

Currently the user must  
download all files to run  
locally on their own computer

# ProteoViz: a tool for the analysis and interactive visualization of phosphoproteomics data†

Aaron J. Storey,<sup>a</sup> Kevin S. Naceanceno,<sup>a</sup> Renny S. Lan,<sup>a</sup> Charity L. Washam,<sup>ab</sup> Lisa M. Orr,<sup>a</sup> Samuel G. Mackintosh,<sup>a</sup> Alan J. Tackett,<sup>ab</sup> Rick D. Edmondson,<sup>c</sup> Zhengyu Wang,<sup>d</sup> Hong-yu Li,<sup>d</sup> Brendan Frett,<sup>id</sup><sup>d</sup> Samantha Kendrick<sup>\*a</sup> and Stephanie D. Byrum<sup>id</sup><sup>\*ab</sup>



R Shiny App for phosphoproteomics analysis.

Currently runs on local computer so anyone that wants to use it must download the R scripts from Github and install all R package dependencies

Limited number of projects hosted on R shinyapps.io – runs out of memory for large projects

# Project Team



**Kyle O'Connell**  
Bioinformatics Consultant



**Thad Carlson**  
Senior Consultant  
GCP Engineer



**Ben Kopchick**  
Consultant - Data Science and  
Medical Physics



**David Belardo**  
Cloud Customer Engineer



**Grant Sorbo**  
Cloud Consultant

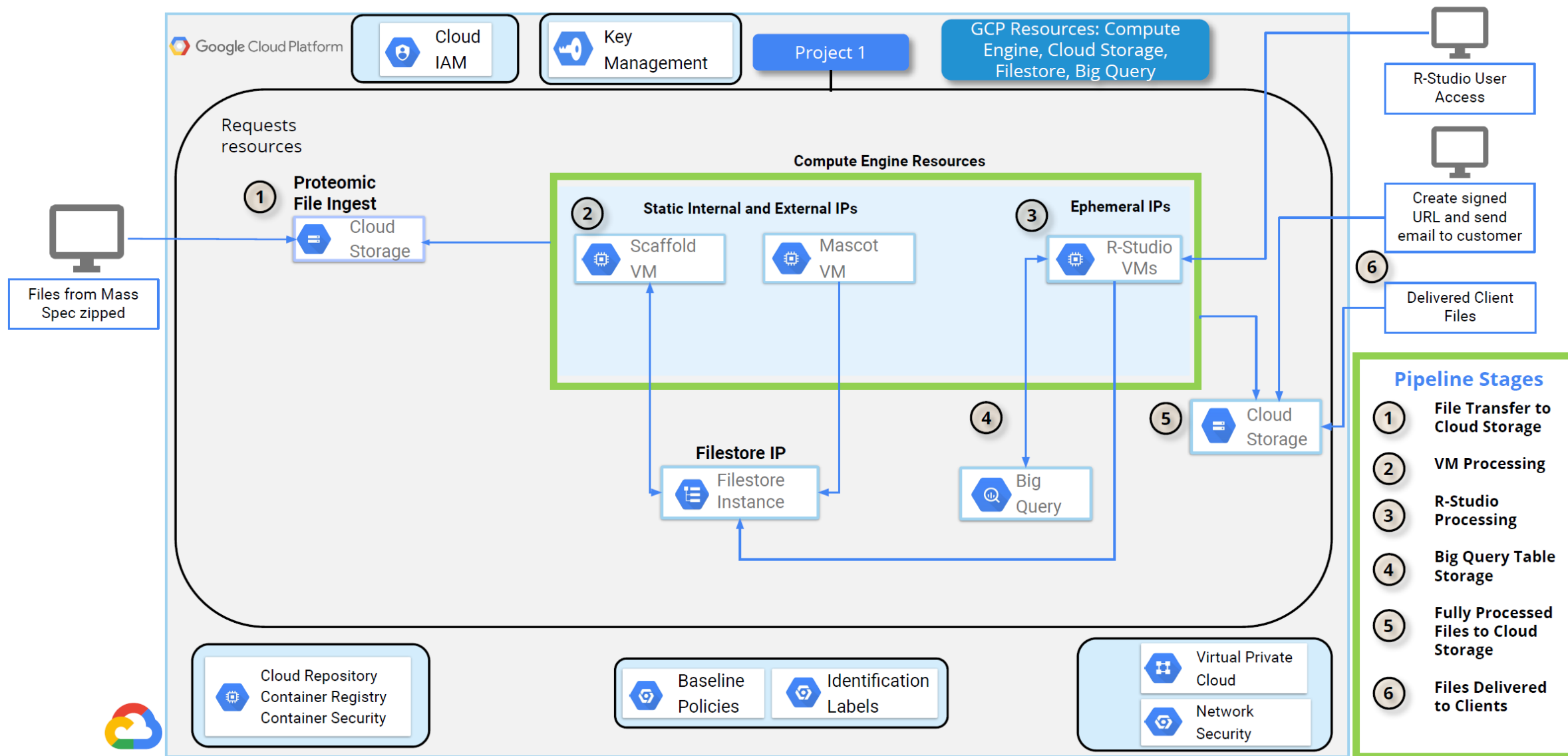


**Phatty Arbuckle**  
Cloud Program Manager



**Sam Russ**  
Cloud Program Manager

# Proteomics Workflow on GCP



# Demonstration of Training Module

# Summary

- IDeA National Resource for Quantitative Proteomics
  - Provide high quality proteomics for large user base
  - Provide education opportunities
- Google cloud platform
  - Provides computational resources to provide high throughput proteomics analysis
  - Flexible and allows implementation of new methods
  - Ability to transfer large file sizes to external researchers