

7<sup>th</sup> International Conference and Expo on

# Molecular & Cancer Biomarkers

September 15-16, 2016 Berlin, Germany

## **P-Mart: Interactive statistical resource to enable biomaker discovery from shotgun cancer proteomic datasets**

**Bobbie-Jo M Webb-Robertson, Lisa M Bramer, Jeffrey L Jensen, Markus A Kobold, Jeremiah Rounds, Kelly G Stratton, Mathew Thomas and Amanda M White**  
Pacific Northwest National Laboratory, USA

For the field of clinical proteomics to successfully identify new prognostics or diagnostics of disease or response to therapies requires not only requires high quality data with respect to the instrument, but also high quality statistical analysis of the data. However, one of the major challenges to the discovery of robust cancer biomarker candidates from global shotgun mass spectrometry (MS)-based proteomic experiments is processing these large and complex datasets in a manner that accounts for the underlying statistical hypothesis of interest. P-Mart is a new interactive web-based software environment that enables biomedical and biological scientists to perform in-depth analyses of global proteomics data without requiring knowledge of processing raw mass spectra or complex matrices of peptide abundances. P- Mart offers a series of statistical modules associated with quality assessment, peptide and protein statistics, protein quantification and exploratory data analyses. Currently, P-Mart offers access to multiple cancer proteomic datasets generated through the clinical proteomics tumor analysis consortium (CPTAC) at the peptide, gene and protein levels. Analyses are performed in P-Mart via customized workflows and interactive visualizations. P-Mart is funded through the National Cancer Institute's Informatics Technology for Cancer Research (ITCR) program under grant U01-CA184738-01.

### **Biography**

Bobbie-Jo M Webb-Robertson has a MS in Statistics and Operations Research and PhD in Decision Sciences and done her Engineering Systems from Rensselaer Polytechnic Institute. She leads a research portfolio in statistical and software development for high-throughput proteomic analyses with over 75 peer-reviewed publications in the field. In addition, she is currently the Technical Group Manager of the Applied Statistics and Computational Modeling Group at Pacific Northwest National Laboratory.

bj@pnnl.gov

### **Notes:**