Overview
- We have developed a complete proteogenomic informatics environment that seamlessly combines genomics, transcriptomics and proteomics data.
- We developed new Visualization tools for evaluating and interpreting results.
- Implementation was done on the Galaxy-P framework, an extension of Galaxy. Galaxy is an open, web-based platform for data intensive biomedical research.

Methods
- RNA-Seq data used to generate sample specific protein database of potential novel proteoforms.
- SearchGUI/PeptideShaker match MS/MS data to database to verify presence of variant peptides.
- Multi-Omics Visualization Platform (MVP) used to validate novelty and quality of identified peptides.
- Peptides of interest mapped to the genome and viewed using Integrated Genomics Viewer (IGV) to assess quality of associated RNA-Seq data.

Results
- Complete, flexible and accessible proteogenomic informatics environment geared towards quality assessment and visualization of results.

Introduction
- Proteogenomics enables new insights into complex biological systems, most commonly integrating RNA-Seq and proteomic data.
- Effective proteogenomics requires seamless integration of disparate analysis tools for genomics and proteomics data.
- We present a first-of-its-kind, complete proteogenomics informatics environment implemented in the Galaxy-P platform.
- This environment enables seamless navigation between genomics, transcriptomics & proteomics data and analysis tools, building customizable, easily shared workflows usable by bench researchers.
- It also provides filtering and visualization tools for evaluating and interpreting results.
- Results from a proteogenomic analysis of B-cell development, highlighting the many advantages of this platform.

Conclusion
- Our framework provides a complete, flexible and accessible proteogenomic informatics environment geared towards quality assessment and visualization of results.