

# THE GALAXY FRAMEWORK AS A BIOINFORMATICS SOLUTION FOR PROTEOMICS AND MULTI-OMICS STUDIES.

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# ‘OMICS’ RESEARCH

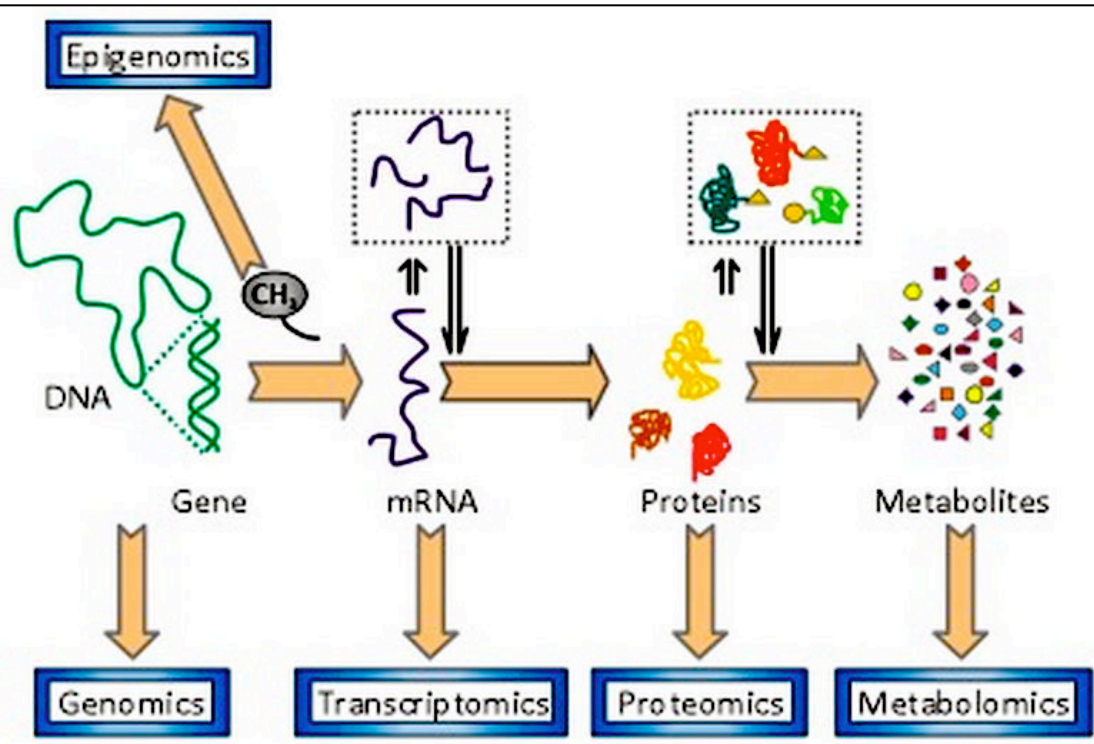


Image Source: Goodacre, J. Exp. Bot 2005.

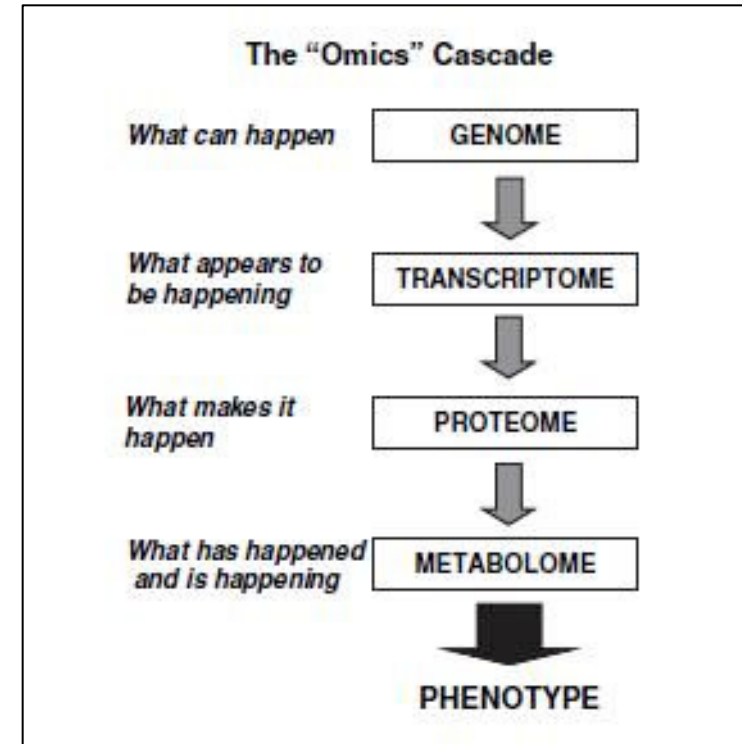
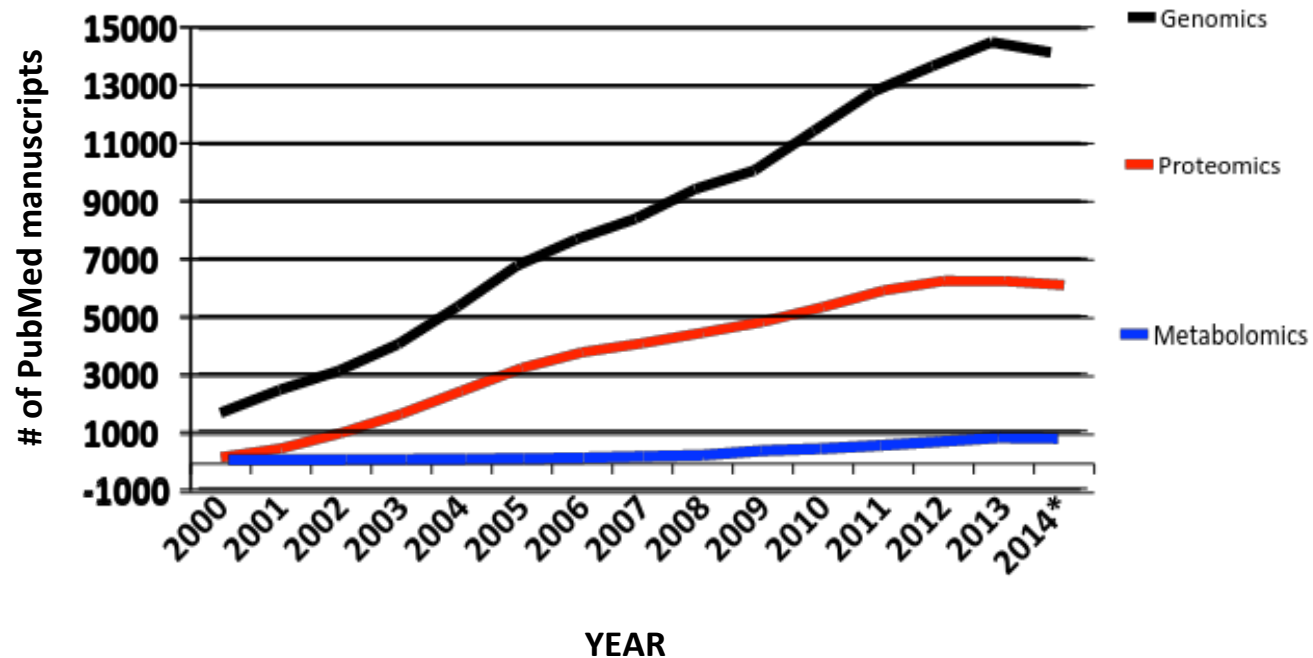


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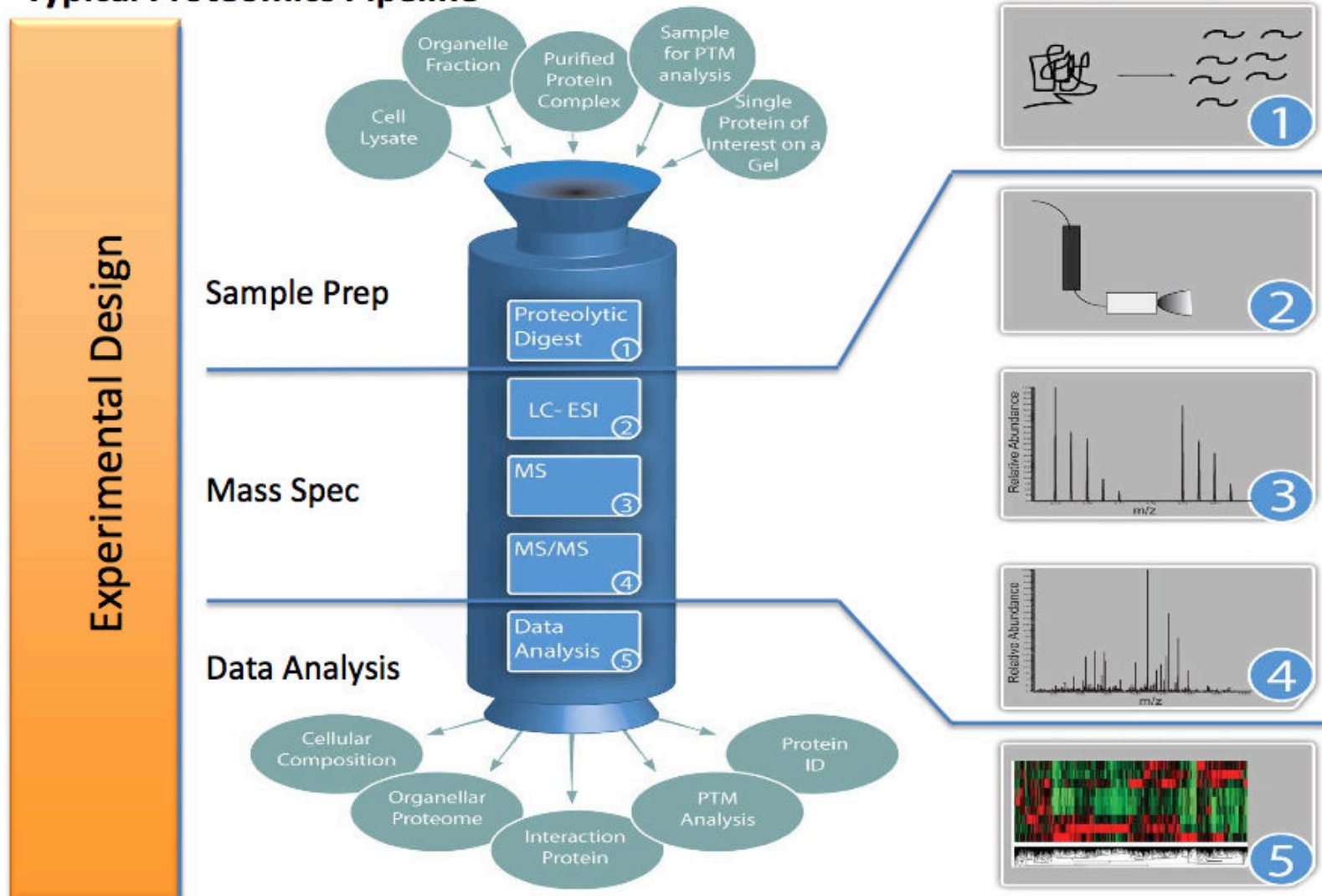
# TRENDS IN OMICS RESEARCH



- **Genomics: Established Technology.**
- **Proteomics: Standard Technology.**
- **Metabolomics: Emerging Technology.**

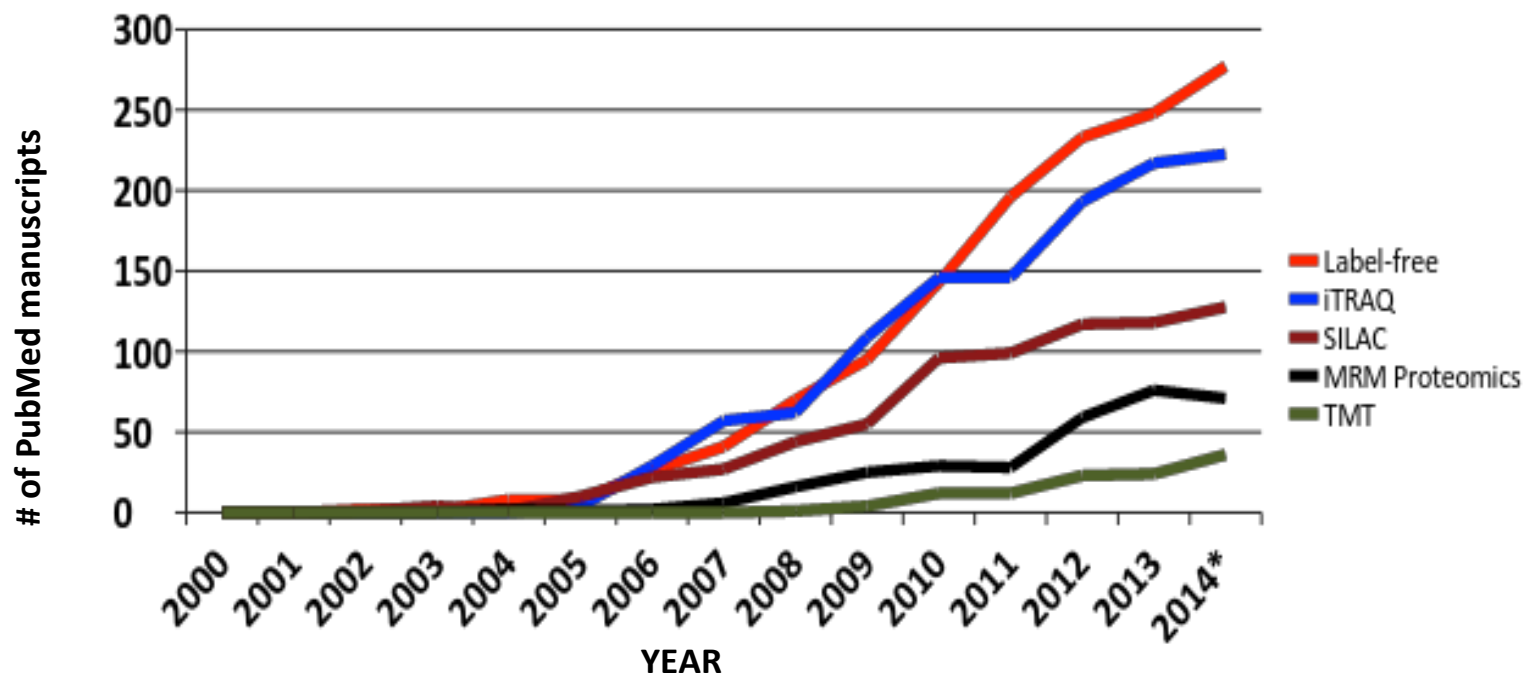
# PROTEOMICS WORKFLOW

## Typical Proteomics Pipeline



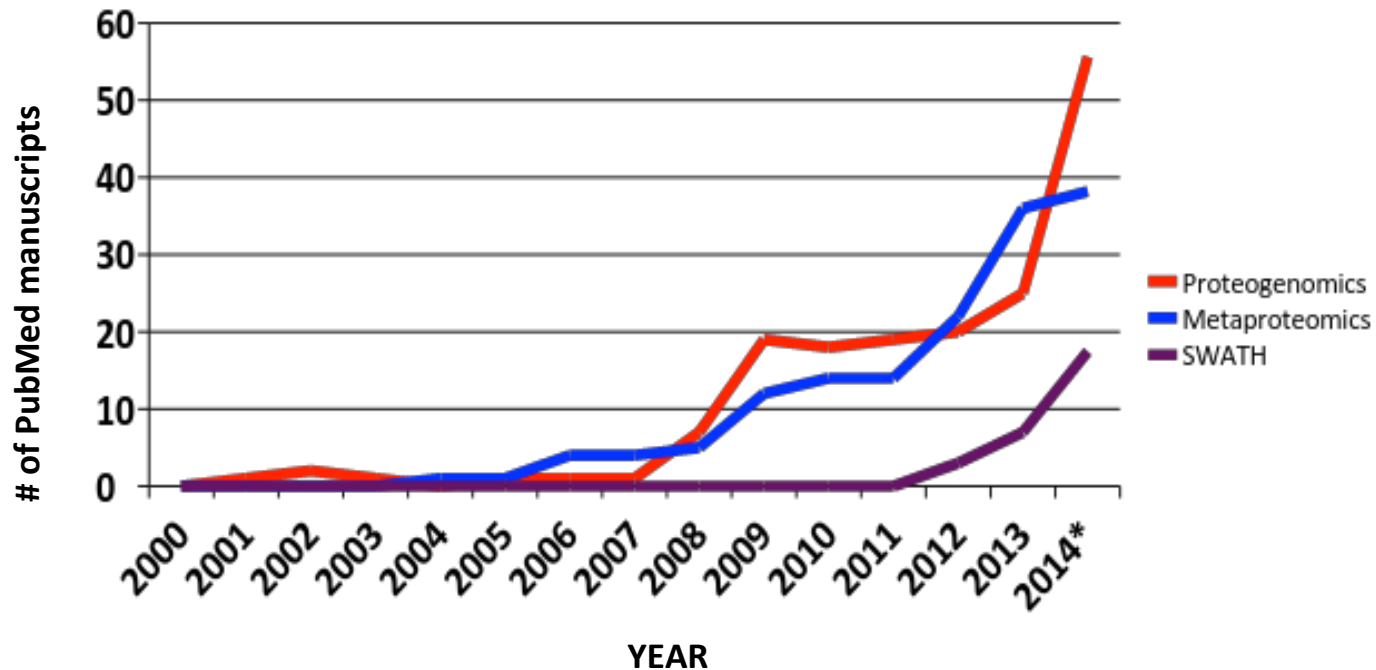
Adapted from Walther T, Mann M. JCB 2010;190:491-500

# QUANTITATIVE PROTEOMICS



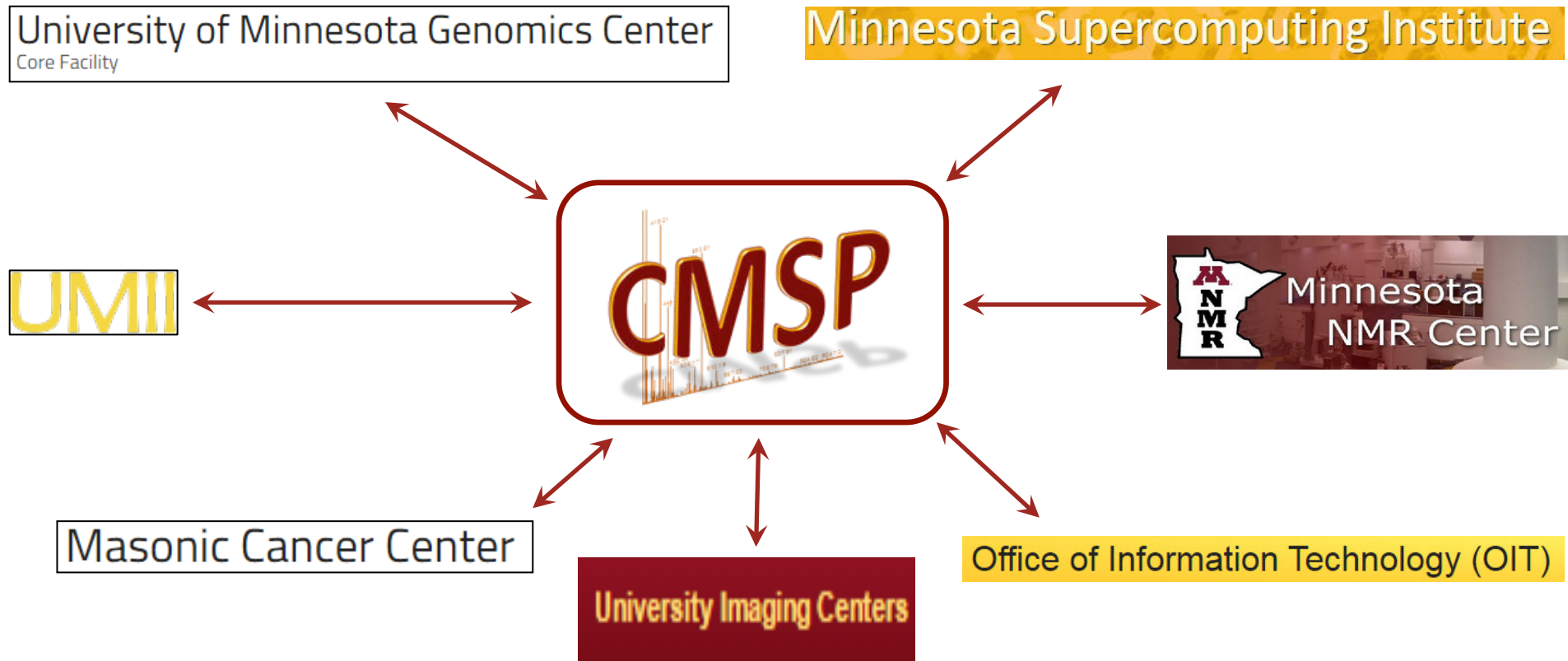
- **Label-free quantitation. (AUC for MS1)**
- **iTRAQ (MS/MS reporter ion)**
- **SILAC (precursor MS ion)**
- **TMT (MS/MS reporter ion)**
- **MRM (Targeted Proteomics)**

# EMERGING FIELDS IN PROTEOMICS RESEARCH



- **Next Generation Proteomics.**
  - Proteogenomics (Uses data from RNASeq data)
  - Metaproteomics (uses metagenomics data)
  - Data-independent acquisition (For example SWATH)

# PARTNERSHIP WITH UNIVERSITY OF MINNESOTA RESEARCH UNITS



# **GALAXY-P : IMPLEMENTATION OF PROTEOMICS TOOLS WITHIN GALAXY ENVIRONMENT.**



**Galaxy-P: A new community-based informatics paradigm for MS-based proteomics**

- Funded via the NSF Advances in Biological Informatics program
- 3 years of funding; effective July 15, 2012-June 30, 2015

## **Grant objective in a nutshell:**

We propose to extend the Galaxy framework for genomics by deploying and integrating a series of key software programs for MS-based proteomics data analysis, thus creating Galaxy Tool Modules for Proteomics which we refer to as Galaxy-P

Project-based strategy for Galaxy-P development:

Collaborate with biological researchers with “real” projects to guide developments.

# GALAXY-P : IMPLEMENTATION OF PROTEOMICS TOOLS WITHIN GALAXY ENVIRONMENT.

Galaxy / GalaxyP

Analyze Data Workflow Shared Data Visualization Help User

Using 1.3 TB

Tools

search tools

CORE TOOLS

Get Data

Send Data

Lift-Over

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

Extract Features

Statistics

Graph/Display Data

FASTA manipulation

PROTEOMICS

MS Data Conversion

Sequence Database Tools

Protein/Peptide Search Algorithms

Data Conversion Tools

Visualizers

Quantification

BLAST-P

Proteogenomics

GENOMICS

Fetch Sequences

Fetch Alignments

NGS: Mapping

NGS: RNA Analysis

NGS: SAM Tools

NGS: Variant

EMBOSS

Blast

Picard

MISC

Misc

Workflows

795 NS WS For Rudney datasets : Workflow for paired metaproteomics comparison studies.


MP1: Workflow for paired metaproteomics comparison studies - HOMD db search, (imported from uploaded file)

All workflows

✓ Welcome to GalaxyP

GalaxyP is a multiple 'omics' data analysis platform with particular emphasis on mass spectrometry based proteomics. GalaxyP is developed at the University of Minnesota, deployed at the Minnesota Supercomputing Institute, and is an extension of the popular Galaxy project. The GalaxyP project is supported by a grant from [NSF](#).

This public Galaxy instance is meant for testing with small-scale data sets, and sharing workflows and tools. Users with larger data analysis needs are encouraged to [install a local instance](#) of Galaxy and access GalaxyP tools via the [Tool Shed](#).



Updates


February 13, 2015

All Galaxy Tools running nominally

February 12, 2015


All Galaxy Tools running nominally

Tweets

 The GalaxyP Project @usegalaxy 6 Feb

Multi-omic data analysis using #usegalaxy z.umn.edu/multomicsnbt #proteomics #metabolomics #interactomics #proteogenomics #metaproteomics

Expand

 John Chilton @jmchilton 30 Oct

Pair of good #proteogenomics articles in Nature Methods including excellent shoutout to GalaxyP in one. nature.com/nmeth/journal/... #usegalaxy

Retweeted by The GalaxyP Project

Tweet to @usegalaxy

Links

[Large-scale multi-omic data integration and analysis: challenges and opportunities](#)

[Metaproteomics: an opportunity-rich complement to metagenomics](#)

[The Galaxy framework as a unifying bioinformatics solution for 'omics' core facilities](#)

History

search datasets

NS Peptide Summary to Input for MEGAN5 analysis. 32 shown

519.7 MB

32: MEGAN5 Output for NS

31: blastp on db nr current

30: blastp-short on db nr current

29: Filter sequences by length on data 27

105 sequences

format: fasta, database: 2

>APAAIGPYVQAVDLGNLVLTSQGIPVNPATC  
APAAIGPYVQAVDLGNLVLTSQGIPVNPATGE  
>APAAIGPYVQAVDLGNLVLTSQGIPVNPATC  
APAAIGPYVQAVDLGNLVLTSQGIPVNPATGE  
>QVPSGQLPSAVGVVQNTGTAAAIYEAVVNC  
QVPSGQLPSAVGVVQNTGTAAAIYEAVVNC

28: Filter sequences by length on data 27

4,241 sequences

format: fasta, database: 2

>TQDATHGNSLSHR1 length=13  
TQDATHGNSLSHR  
>NNVANSLLVTGAILGVNWHIFSPK2 length=13  
NNVANSLLVTGAILGVNWHIFSPK  
>VDGLLVGVVANAQGLLMNYPEYR3 length=13  
VDGLLVGVVANAQGLLMNYPEYR

27: Regex Find And Replace on data 26

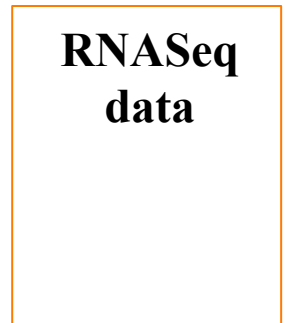
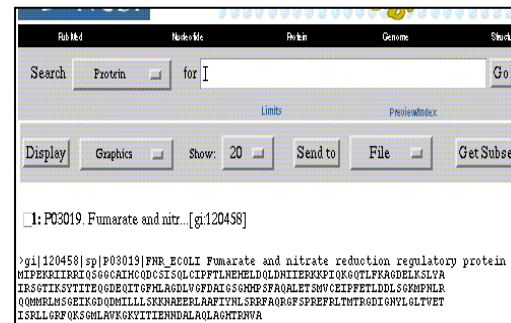
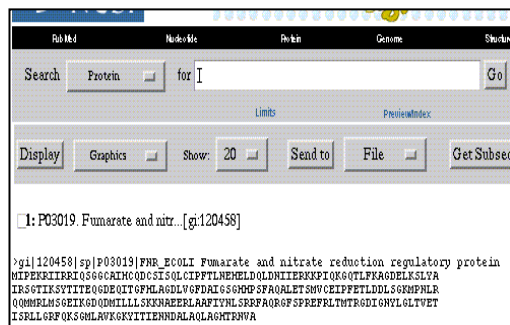
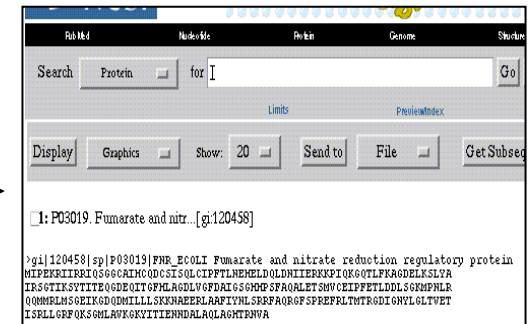
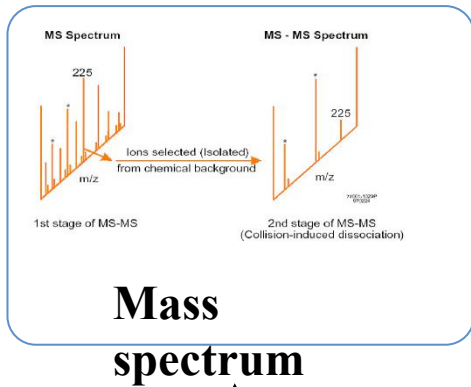
26: Tabular-to-FASTA on data 25

25: Cut on data 24

24: Merge Columns on data 23

23: Add column on data 22

# PROTEOGENOMICS AND METAPROTEOMICS



# PROTEOGENOMICS: STEPS INVOLVED

~ 2 million proteins

Database Generation\*

Peaklist generation

~ 10,000 proteins

Database search

~ 5,000 proteins

First-step

Two-step

Identifying peptides from  
translated nucleotide db

~ 1,000 peptides

Automated BLAST-P search\*

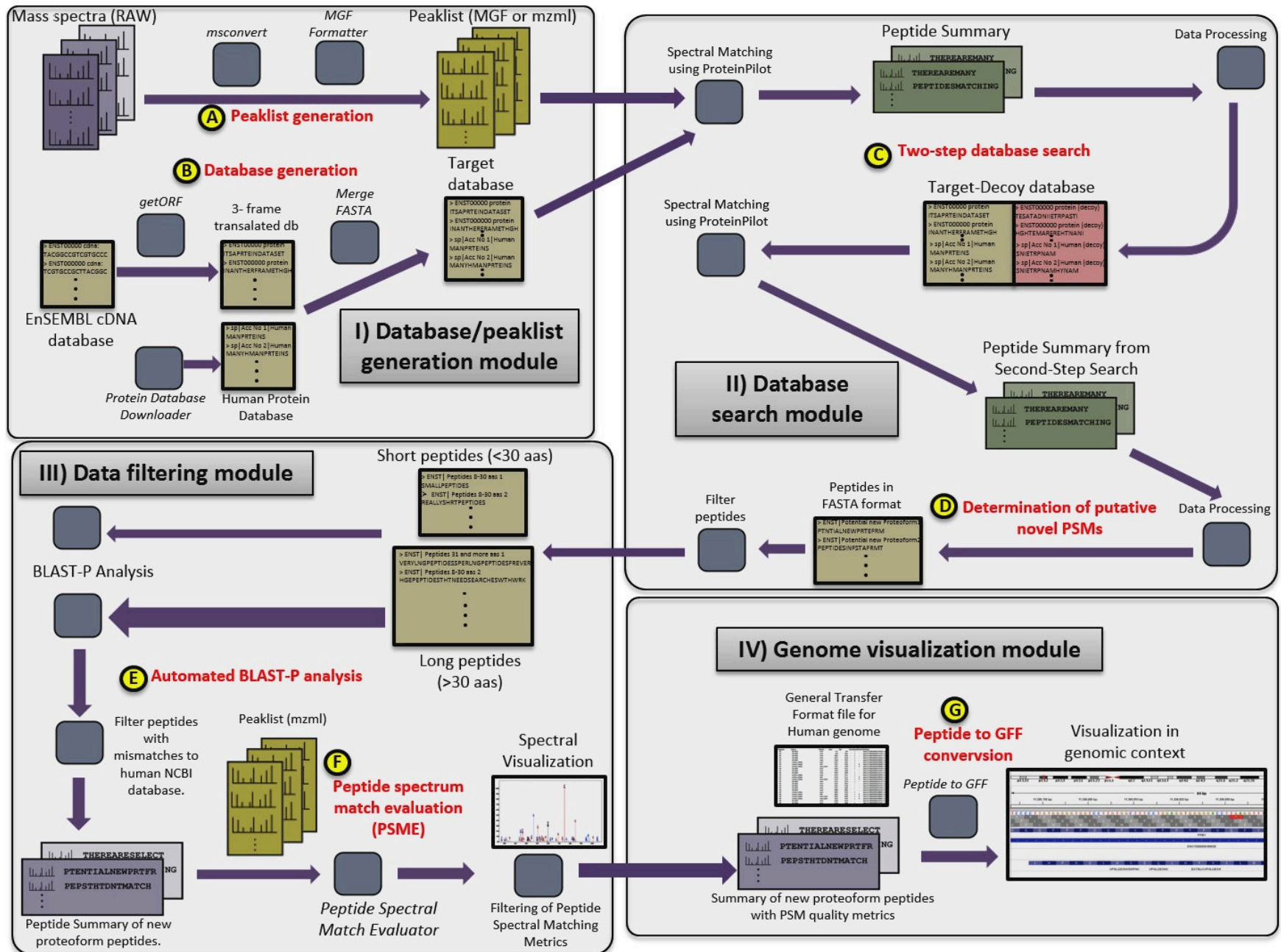
~ 100 peptides

Peptide-Spectral-Match Evaluation

~ 50 peptides

Genomic context analysis\*

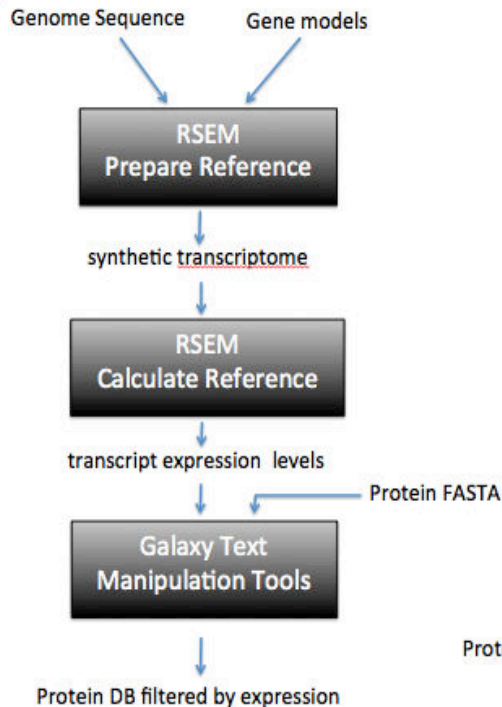
# PROTEOGENOMICS WORKFLOW



# RNASeq DERIVED PROTEOMIC DATABASES

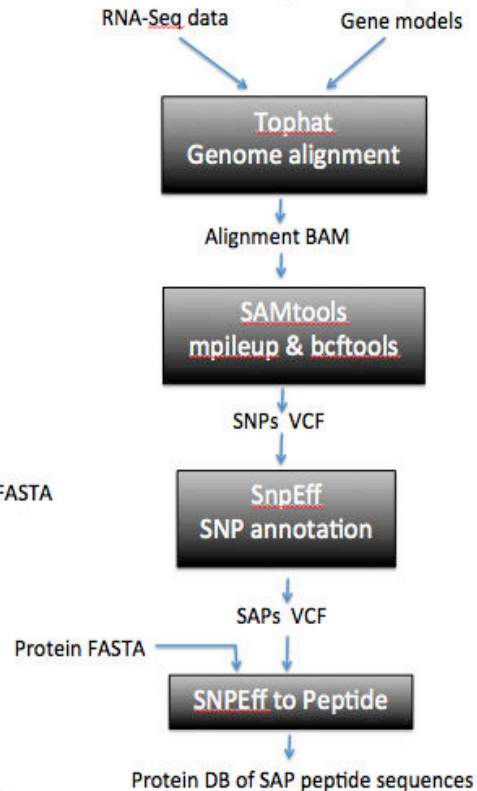
## Reduced Database

RSEM determines the RNA-Seq transcripts expressed at detectable levels. Proteins from transcripts that are not expressed are filtered out.



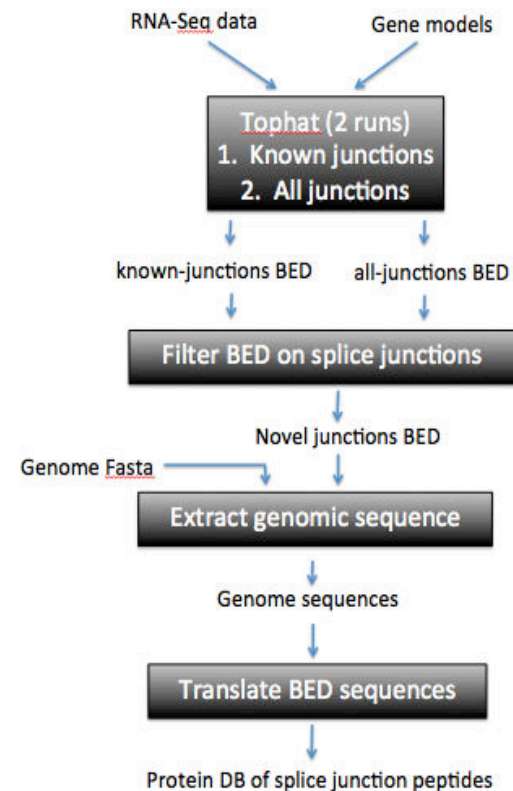
## SAP Database

RNA-Seq reads are aligned to the reference genome with tophat. SAMtools identifies variant DNA bases. SnpEff annotates the variants with effects to genes and proteins.



## Splice Database

Tophat alignments are used to find evidence of novel splice variant transcripts. The novel splice junctions are translated into a protein database.



**“Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations.”**  
*Sheynkman G et al BMC Genomics. doi: 10.1186/1471-2164-15-703.*



Gloria Sheynkman



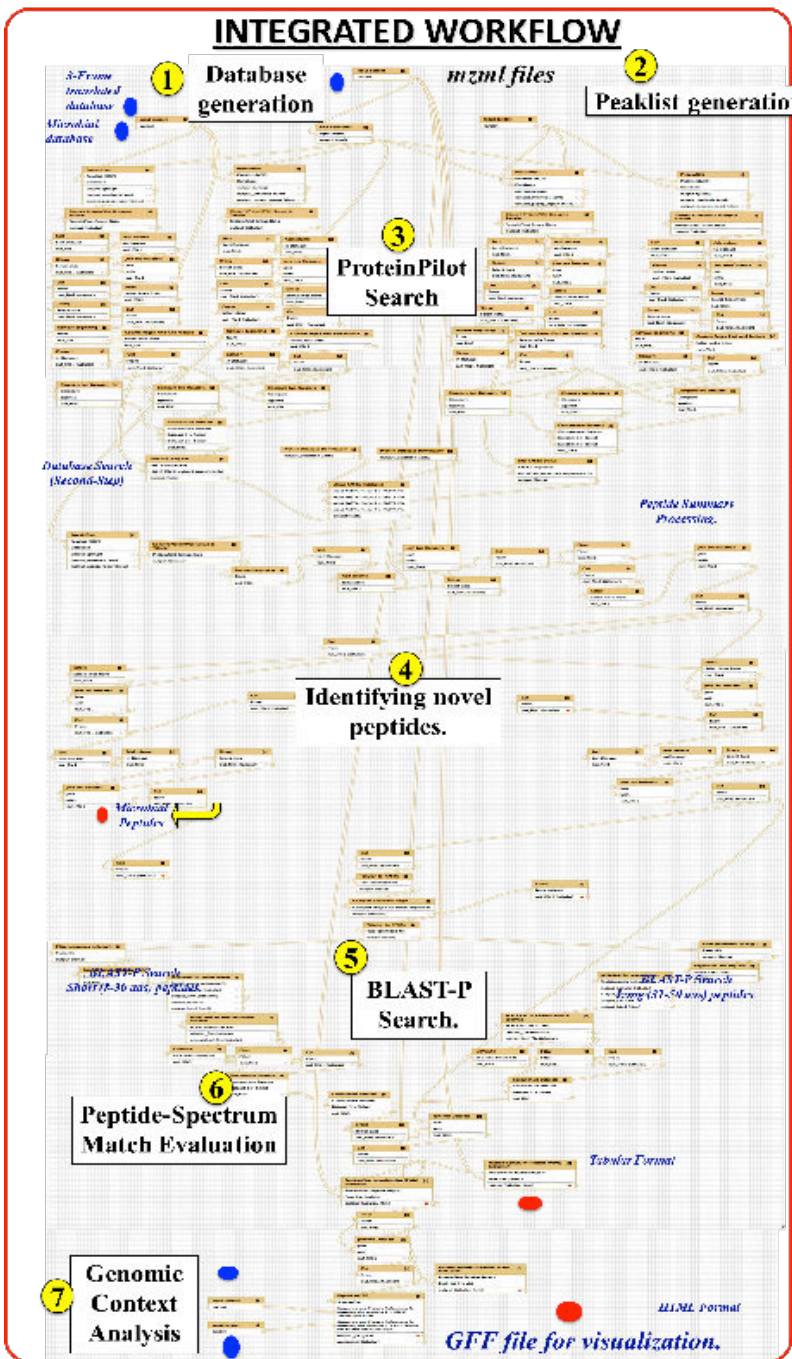
James Johnson

# PROTEOGENOMICS WORKFLOW

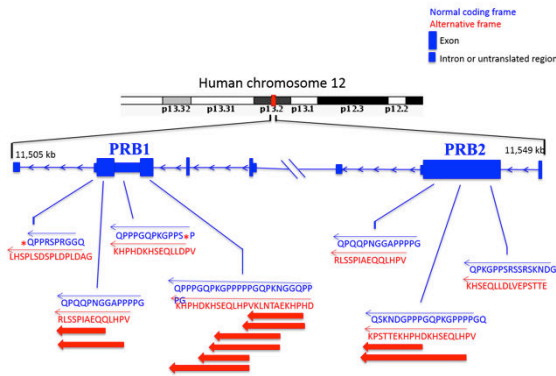
**Galaxy-P provides an integrated platform for every step of proteogenomic analysis.**

- **Build target database – download and translate EST databases or perform gene prediction with Augustus.**
- **Numerous tools for identification and text manipulation.**
- **Workflow utilizing BLAST to identify novel peptides.**
- **Tool to assess peptide-spectrum matches and visualize spectra.**
- **Visualize identified peptides on the genome.**
- **140 steps: Seamless, integrated proteogenomic workflow.**

**Flexible and accessible workflows for improved proteogenomic analysis using Galaxy framework.**  
J. Proteome Res. (2014) DOI: 10.1021/pr500812t  
Link: [z.umn.edu/pgfirstlook](http://z.umn.edu/pgfirstlook)

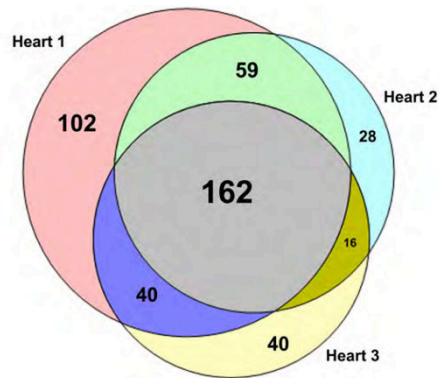


# PROTEOGENOMIC INSIGHTS USING GALAXYP



## SALIVARY PROTEOGENOMICS

- **52 novel proteoforms were identified in a 3D-fractionated salivary dataset.**
- **Alternate frame translation was identified in PRB1 and PRB2 (12p13) region of human genome.**
- **PRB proteins are cleaved and secrete peptides and are known to have implications in synovial sarcoma and gastric acid secretion.**



## NON-MODEL ORGANISM PROTEOGENOMICS

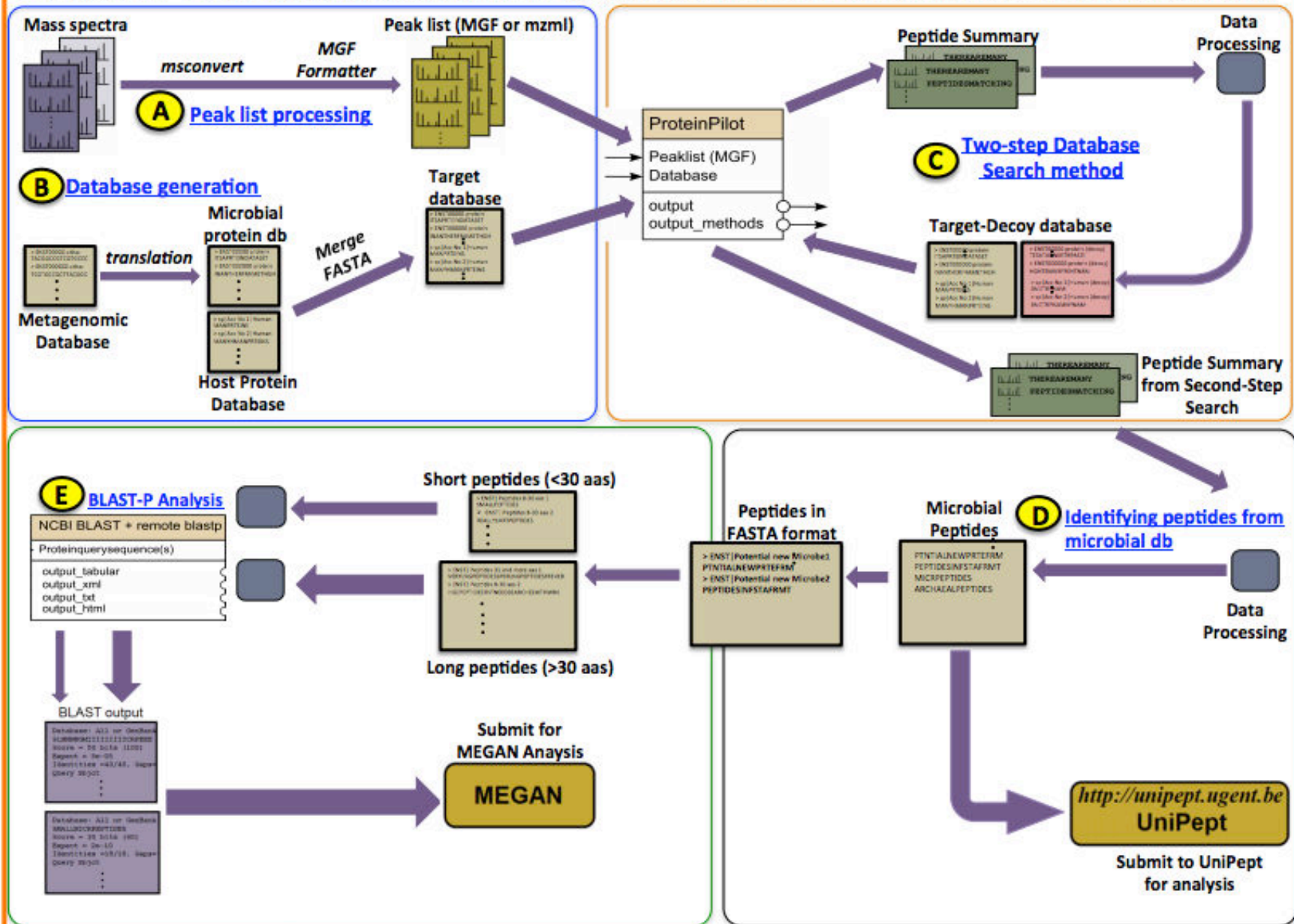
- **Hibernation proteogenomics in 13-lined ground squirrel.**
- **Identified multiple novel proteoforms across three replicates.**
- **Plans for improving on genome annotation; correlation of RNASeq quantitative data with proteomic quantitative data and identification of the role of both known and novel proteoforms in hibernation.**



**Katie Vermillion**

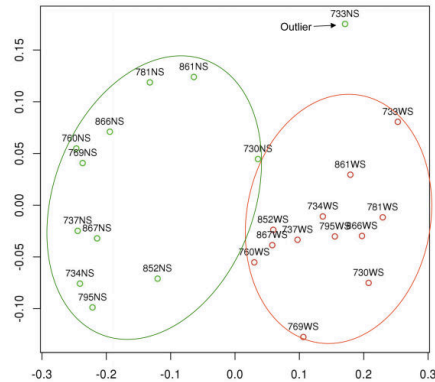
# METAPROTEOMICS: STEPS INVOLVED

## OVERVIEW OF MODULES AND ANALYTICAL WORKFLOWS FOR METAPROTEOMIC ANALYSIS.



# METAPROTEOMICS : BIOLOGICAL INSIGHTS

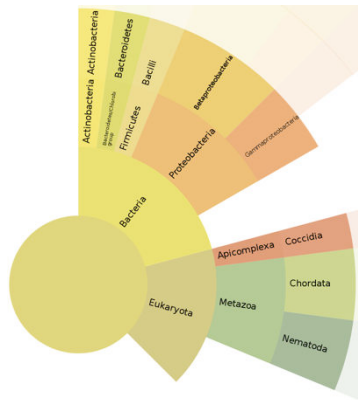
## METAPROTEOMICS OF CHILDHOOD CARIES



- *In vitro* investigation of sucrose-induced changes in the metaproteomes of children with caries.
- Major shifts in taxonomy and function in paired microcosm oral biofilms grown without and with sucrose respectively.
- Twelve replicates currently being analyzed. Targeted proteomics on certain candidates



Prof. Joel Rudney



## LUNG CANCER METAPROTEOMICS

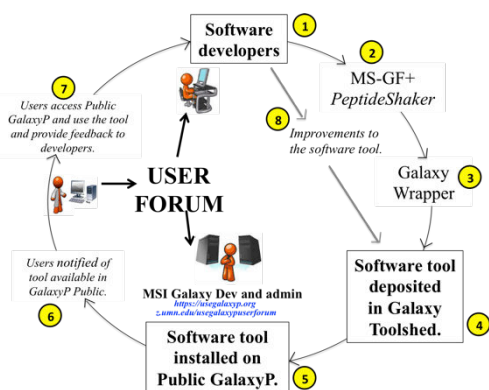
- Human lung cancer associated dataset subjected to proteogenomic & metaproteomic analysis.
- Lung-infection causing species from *Achromobacter*, *Actinomyces*, *Stenotrophomonas* and *Streptococcus* genera were identified.
- Data from 16s rRNA will be used to generate databases for further analysis.



Brian Sandri

# GALAXYP : ONGOING PROJECTS

## COMMUNITY BASED SOFTWARE DEVELOPMENT



- Community-based software development model is proving effective for implementation, testing and continued improvement of command-line driven software tools.
- We have added tools such as SearchGUI and PeptideShaker in Galaxy, along with opportunities for integration with other software tools such as OpenSWATH via use of workflows.

## REPertoire OF WORKFLOWS

	WORKFLOW	INPUT	TOOLS	OUTPUT
1	<a href="#">Peaklist Generation</a>	RAW File.	msconvert, MGF Formatter	mzml and MGF files
2	<a href="#">Database Generation</a>	cDNA database, Protein FASTA files.	getORF, get data, merge FASTA	Merged Protein FASTA file
3	<a href="#">Database Search by Two-Step Method</a>	MGF Files, Search database.	ProteinPilot, Text processing tools	.group file, peptide summary and PSPEP FDR report.
4	<a href="#">Identifying peptides from translated nucleotide database.</a>	Peptide Summary.	Text processing tools	Peptide List with accession numbers within cDNA database.
5	<a href="#">BLAST-P Analysis</a>	Peptide List with accession numbers within cDNA database.	BLAST-P and short BLAST-P; Text processing tools	List of peptides that do not match with current human proteome.
6	<a href="#">Peptide Spectral Match Evaluation</a>	Peptide Summary, mzml files.	PSM Evaluator, Text processing tools	PSM Evaluation metric and HTML Links.
7	<a href="#">Peptide to GTF conversion</a>	Peptide Summary, cDNA database, GTF file.	Peptides to GTF	GTF file.

- Sharing of analytical workflows that can be reused, shared and creatively modified for multiple studies.
- Multiple workflows for metaproteomics, quantitative proteomics, proteogenomics, RNASeq workflows, are being developed, shared and used.

# CONCLUDING REMARKS

- **Galaxy offers an excellent resource for reproducible workflows that can be shared with users.**
- **We have developed workflows for proteogenomics and metaproteomics analysis that can be creatively modified by users for their projects.**
- **We are also working on improving on our published blueprint workflows for proteogenomics and metaproteomics workflows by adding visualization capabilities, etc.**
- **We are working on adding new tools and workflows for emerging fields in proteomics (such as data independent acquisition / SWATH analysis).**



Biochemistry, Molecular Biology  
& Biophysics

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Candace Guerrero

Kevin Murray



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**COMMUNITY BASED  
SOFTWARE DEVELOPMENT**

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