

# GALAXY-P FOR...?

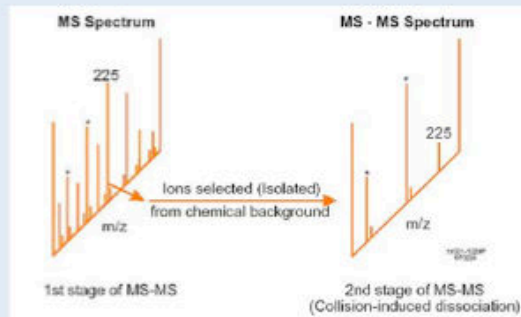
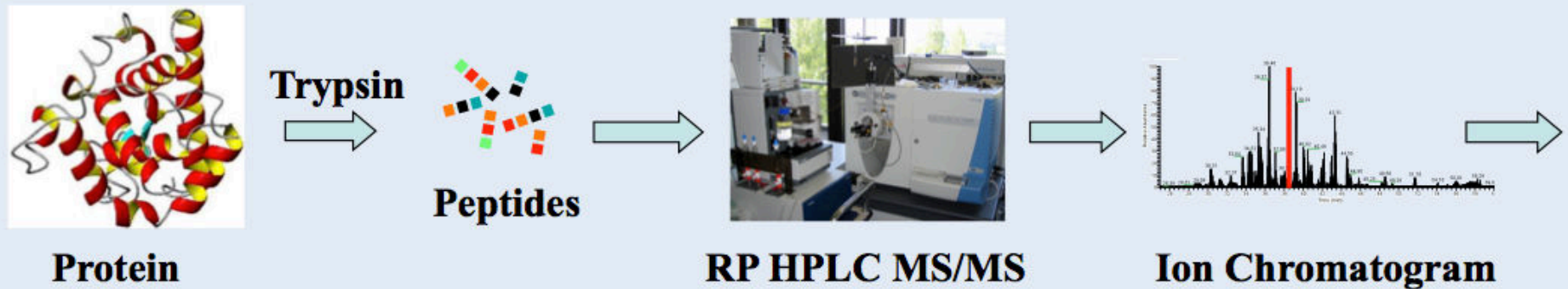
## P for ?

- Possibilities?
- Palaeoanthropology?
  - Padmasana?
  - Pyschology?
    - Psephology?
    - Phrontistery?

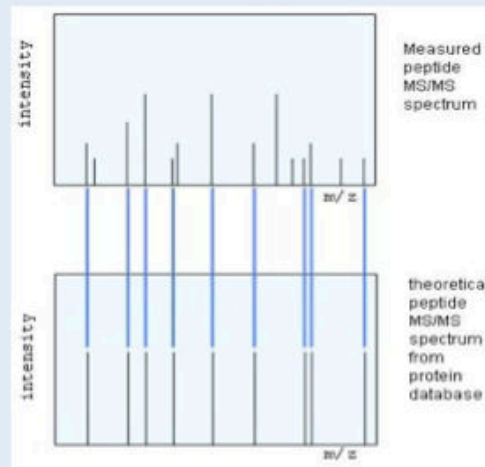
# GALAXY-P FOR PROTEOMICS

<http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=1147079>

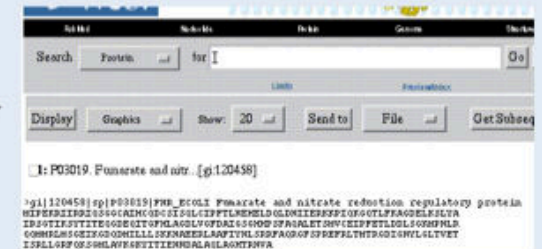
## PROTEOMICS WORKFLOW



**Mass Spectrum And Tandem Mass Spectrum**



**Search Against Database**

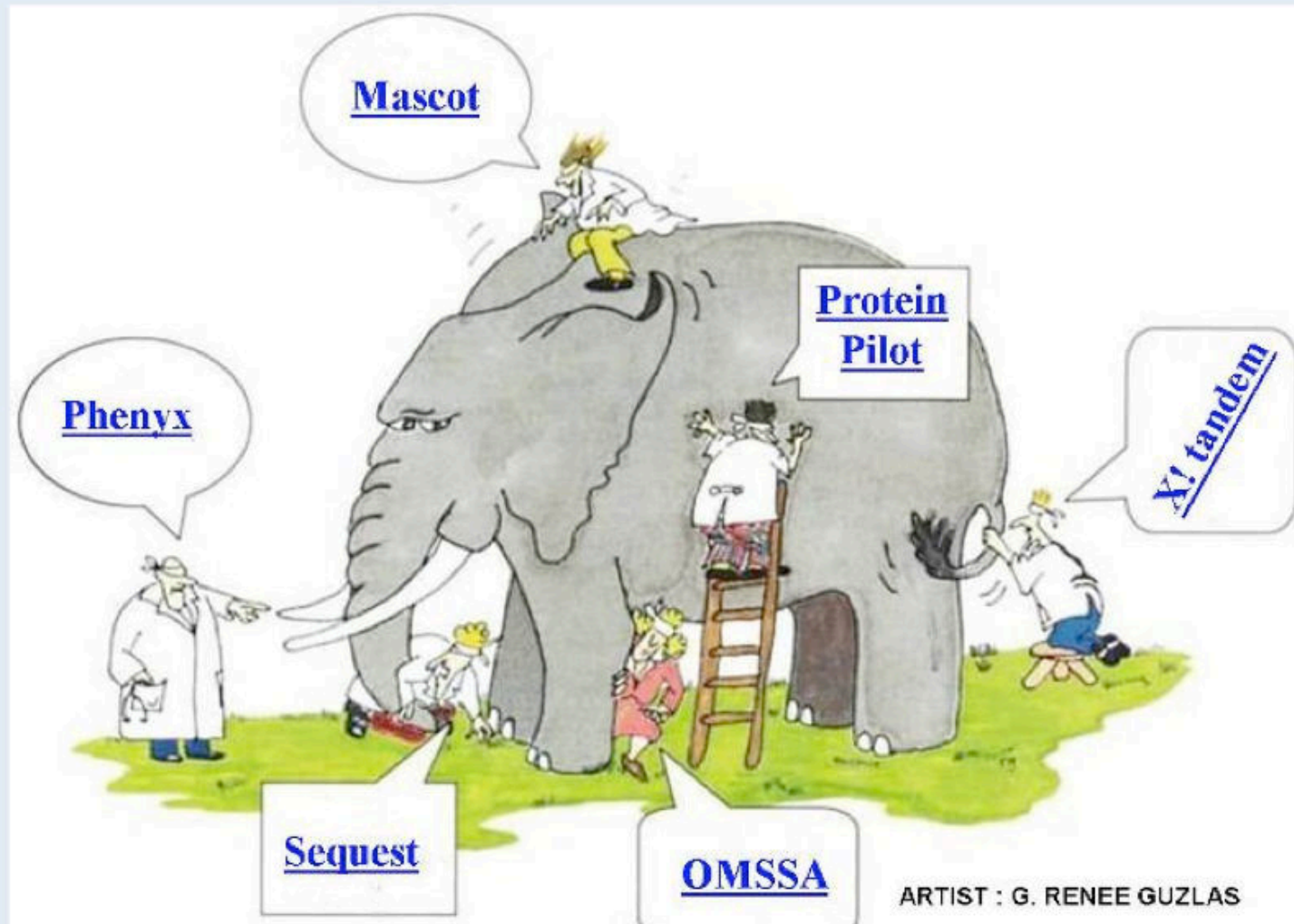


**Protein Identification**

Minnesota Supercomputing Institute



# CHOOSING THE WORKFLOW OUTPUTS TO MAXIMISE IDENTIFICATIONS : HORSES FOR COURSES



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# GALAXY-P

## Challenges

- **Individual preferences for workflows**
  - **Complex workflows**
  - **Windows software**
- **Multiple commercial and open-source tools.**
  - **Software dependencies.**



# **GALAXY-P**

## **Opportunities**

- **Step by step approach for complex workflows**
- **Exploring creative workflows for emerging fields in proteomics**
  - **Integrate command-line Windows software**
  - **Project-based, user-developer team-based approach.**
    - **Visualization**
    - **Cloud computing**

# GALAXY-P FOR...

*(What we are most excited about)*

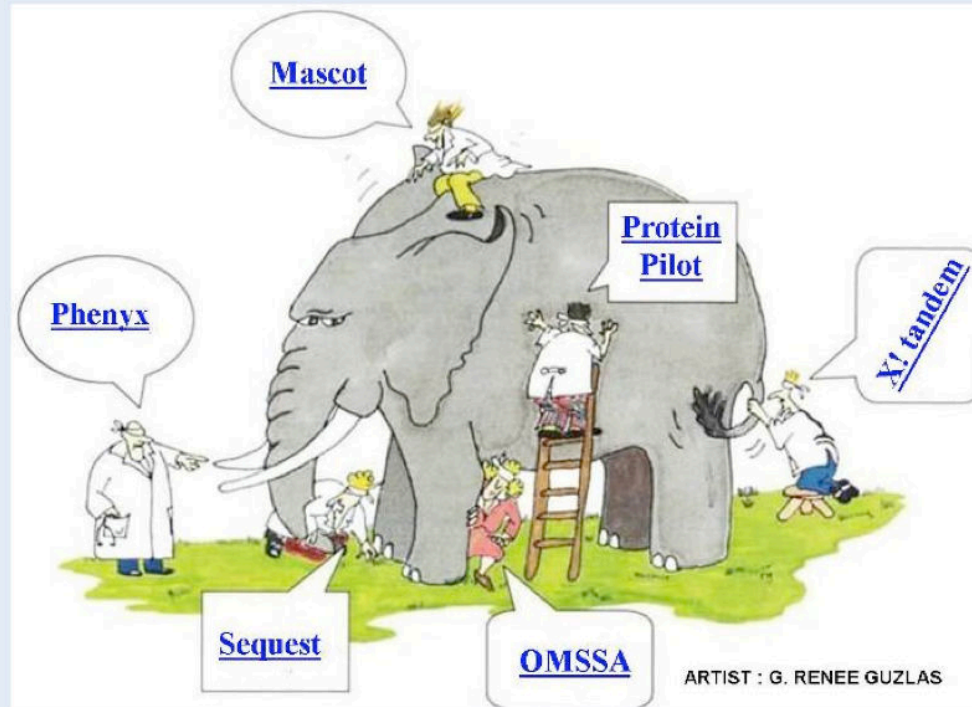
- Its ability to share workflows and not just raw data.
- Developing emerging fields in proteomics such as proteogenomics, spectral library searches, label-free quantitation, metaproteomics, etc.
- Post-identification analysis (Pathway analysis, statistical analysis)...
- Systems Biology : Integration (or combined study) of proteomic data with genomic or transcriptomic datasets...
- Visualizing, accessing and annotating data (mzmine, mzserver, Slice etc.)...
- Magnet for open-source software and workflows...
- Addressing workflows for emerging mass spectrometers...

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# QUESTIONS? / INTEREST?



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