

PROTEOINFORMATICS OVERVIEW

- PROTEOMICS WORKFLOW
- PEAKLIST PROCESSING
- Search Databases Overview
- Protein Identification
- Protein Validation and Quantification
- **Publication Guidelines**

WHERE ARE THE GUIDELINES?

Recommendations for mass spectrometry data quality metrics for open access data (corollary to the Amsterdam Principles).

Kinsinger CR, Apffel J, Baker M, Bian X, Borchers CH, Bradshaw R, Brusniak MY, Chan DW, Deutsch EW, Domon B, Gorman J, Grimm R, Hancock W, Hermjakob H, Horn D, Hunter C, Kolar P, Kraus HJ, Langen H, Linding R, Moritz RL, Omenn GS, Orlando R, Pandey A, Ping P, Rahbar A, Rivers R, Seymour SL, Simpson RJ, Slotta D, Smith RD, Stein SE, Tabb DL, Tagle D, Yates JR, Rodriguez H.

- *Molecular and Cellular Proteomics. December 2011. PubMed PMID: 22052993*
- *Proteomics. January 2012. PubMed PMID: 22069307*
- *Journal of Proteome Research. February 2012. PubMed PMID: 22053864*

<http://www.mcponline.org/site/misc/MSDataResources.xhtml>

Guidelines remind you to...

- To present a complete methods/results section
 - I. [Search Parameters](#) and Acceptance Criteria
 - VI. [Raw Data Submission](#)
- Follow smart criteria for choosing results to publish
 - II. [Protein and Peptide Identification](#)
 - IV. [Protein Inference](#) from Peptide Assignments
 - V. [Quantification](#)
- To not over-report your results
 - III. [Post-Translational Modifications](#)

MCP Guidelines

The screenshot shows a web browser window with the URL www.mcponline.org/site/misc/MSDataResources.xhtml. The page header features the MCP logo and the text 'MOLECULAR & CELLULAR PROTEOMICS' and 'Institution: University of Minnesota Libraries Sign In'. Below the header is a search bar with fields for Author, Keyword, Year, Vol, and Page, and a 'Go' button. A navigation menu includes links for Home, Current issue, Papers in Press, Archive, Reviews, Editorials, and Special Issues. The main content area is titled 'Resources for Preparing Manuscripts Containing Protein Identification Data' and lists several links: 'Required Manuscript Content and Publication Guidelines', 'Checklist for Publishing Peptide and Protein Identification Data', 'Information on how to provide access to annotated spectra', and 'Tutorial on Complying with the Protein Identification Guidelines'. A sidebar on the right contains a 'Current Issue' section for October 2015, a 'Molecular & Cellular Proteomics' journal cover, and buttons for 'Alert me to new issues', 'Authors', 'Submit', 'Subscribers', and 'About the Journal'.

Resources for Preparing Manuscripts Containing Protein Identification Data

[Required Manuscript Content and Publication Guidelines](#) – Including guidelines for the analysis and documentation of peptide and protein identifications.

[Checklist for Publishing Peptide and Protein Identification Data](#) – A checklist to assist authors in preparing manuscripts that are compliant with the current publication guidelines.

[Information on how to provide access to annotated spectra](#)

[Tutorial on Complying with the Protein Identification Guidelines](#)

For additional information regarding to MCP's guidelines for the publication of articles containing protein identification data, please [contact us](#).

Other information of interest

[Return to Resources for Authors](#)

Current Issue
October 2015, 14 ()

Molecular & Cellular Proteomics

Alert me to new issues
Molecular & Cellular Proteomics

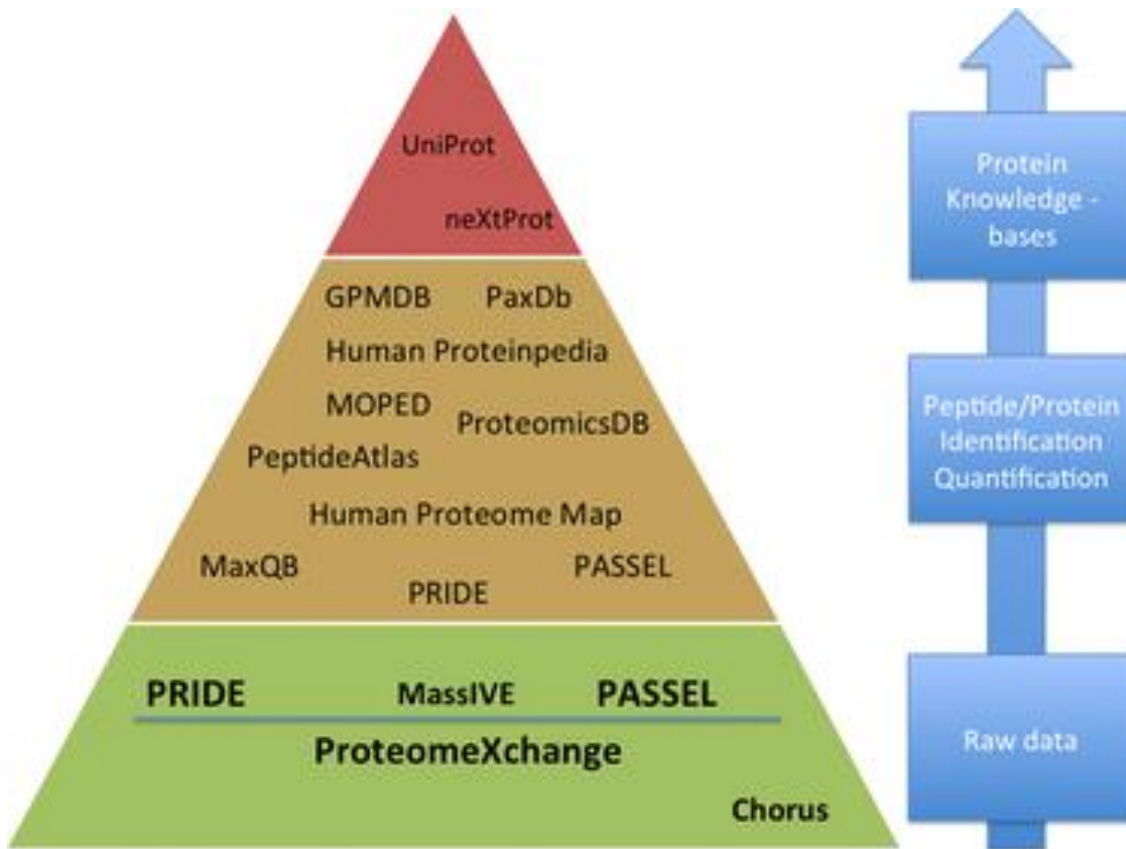
Authors

Submit

Subscribers

About the Journal

Repositories and Databases



Hierarchy of proteomics data repositories and databases according to the different data types stored: raw MS data repositories, resources that store peptide/protein identification and quantification results, and protein knowledge bases. Some resources are duplicated in different levels because they can be included in more than one category.

Perez-Riverol, et al., Proteomics 2015, 15, 930–949

RAW DATA SUBMISSION

[PRIDE](#) > [PRIDE Archive](#)

PRIDE Archive - proteomics data repository

The PRIDE PRoteomics IDentifications database is a centralized, standards compliant, public data repository for proteomics data, including protein and peptide identifications, post-translational modifications and supporting spectral evidence.

Datasets

- o 1398 projects
- o 30470 assays

Submit data

Submit data: we welcome direct submissions of MS/MS proteomics datasets.

ProteomeXchange: accepts both MS/MS proteomics submissions and SRM submissions. PRIDE is the official entry point for MS/MS proteomics submissions.

Access data

Browse: explore all public datasets currently available in our repository.

BioMart: use PRIDE BioMart for custom queries, such as linking PRIDE identifications to REACTOME pathways

FTP: data can be downloaded directly from our FTP site.

Tools

PRIDE Inspector: a desktop application for visualizing and analyzing MS dataset, such as: mzML, mzIdentML, PRIDE XML.

PRIDE Converter: converts common mass spectrometry data formats into PRIDE XML.

News

DEC 04 PXD000478: Tumor model, insights in post-transcriptional gene regulation [link](#) in @GenomeBiology

[link](#)

DEC 03 PXD000578: Whole cell lysate from breast cancer cell line MCF7 spiked w/ 57 protein standards [link](#) [link](#)

[More news](#)

CONCLUDING REMARKS

- **Peaklist processing has an effect on database search results.**
- **Using appropriate search databases is important and closely linked to your experimental strategy.**
- **Using correct parameters ensures optimal identification.**
- **FDR analysis helps you in determining threshold for identifications.**
- **Publication Standards exist to help you.**
- **Researchers are encouraged to submit their data to [ProteomeXChange](#) members such as [PRIDE](#).**