

A Practical Beginner's Guide to Proteomics

This manuscript ([permalink](#)) was automatically generated from [jessegmeyerlab/proteomics-tutorial@dcd1119](#) on January 16, 2022.

Authors

- **Jesse G. Meyer**

 [0000-0003-2753-3926](#) ·  [jessegmeyerlab](#) ·  [j_my_sci](#)

Department of Biochemistry, Medical College of Wisconsin · Funded by Grant R21 AG074234; Grant R35 GM142502

- **Dina Schuster**

 [0000-0001-6611-8237](#) ·  [dschust-r](#) ·  [dina_sch](#)

Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Zurich 8093, Switzerland; Department of Biology, Institute of Molecular Biology and Biophysics, ETH Zurich, Zurich 8093, Switzerland; Laboratory of Biomolecular Research, Division of Biology and Chemistry, Paul Scherrer Institute, Villigen 5232, Switzerland

Abstract

Proteomics is the large scale study of protein structure and function from biological systems. "Shotgun proteomics" or "bottom-up proteomics" is the prevailing strategy, in which proteins are hydrolyzed into peptide that are analyzed by mass spectrometry. Proteomics studies can be applied to diverse studies ranging from simple protein identification to studies of protein-protein interactions, post-translational modifications, and protein stability. To enable this range of different experiments, there are diverse strategies for proteome analysis. The nuances of how proteomic workflows differ may be difficult to understand for new practitioners. Here, we provide a comprehensive tutorial of different proteomics methods. Our tutorial covers all necessary steps starting from protein extraction and ending with biological interpretation. We expect that this work will serve as a basic resource for new practitioners of the field of shotgun or bottom-up proteomics.

Introduction

[paragraph about what proteomics means today]

[history of proteomics? how we got here]

[paragraph about what proteomics can do] A wide range of questions are addressable with proteomics experiments, which translates to a wide range of variations of proteomics workflows. Sometimes identifying what proteins are present is desired, and sometimes the quantities of as many proteins as possible are desired.

Types of Experiments

[List of common types of experiments and brief description]

- Protein abundance changes
- Phosphoproteomics
- Glycoproteomics
- Structural techniques (XL-MS, HDX-MS, FPOP, protein-painting, LiP-MS, ...)
- Protein stability measurements (Thermal denaturation)
- PPIs: AP-MS, APEX, BioID
- ...

Protein Extraction

Discussion of methods for protein extraction and solubilization.

1. Choice of Lysis buffer

- Urea can cause chemical modifications

2. chemicals to avoid

3. removal of contaminations, Protein Precipitation

4. protein alkylation

- choices of reduction and alkylation reagents, TCEP/DTT/2BME, Chloroacetamide/iodoacetamide, n-ethyl maleimide

Proteolysis

1. discussion of protein sequence coverage is determined by the choice of proteolysis
2. why trypsin is the most common choice (charge and length character)
3. theoretical studies of proteolysis and enzyme [\[1\]](#)
4. Challenges associated with alternative enzyme choices (non-specific and semi-specific enzymes)
5. Alternative enzyme choices (one paragraph each?) - LysC
6. GluC
7. AspN
8. Alpha-lytic protease [\[2\]](#) and how it enables mapping human SUMO sites [\[3\]](#).
9. others?

Peptide and Protein Labeling

Discussion of methods to isotopically label peptides or proteins that enable quantification

1. SILAC/SILAM
2. iTRAQ
3. TMT
4. dimethyl labeling

Peptide or Protein Enrichment

Protein enrichment (e.g. for protein protein interactions)

- coIP
- APEX
- bioID
- bioplex

Peptide enrichment

- antibody enrichments of modifications, e.g. lysine acetylation [\[4\]](#).
- TiO₂ and Fe enrichment of phosphorylation
- Glycosylation
- SISCAPA

Methods for Peptide Purification

1. Reverse phase including tips and cartridges
2. stage tips
3. in stage tip (iST)
4. SP2, SP3
5. s traps

Types of Mass Spectrometers used for Proteomics

1. QQQ
2. Q-TOF
3. Q-Orbitrap
4. LTQ-Orbitrap
5. TOF/TOF
6. FT-ICR
7. types of ion mobility

- SLIM
- FAIMS
- traveling wave
- tims

Peptide Ionization

The 2002 Nobel Prize in Chemistry was awarded to partially to John Fenn and Koichi Tanaka “for their development of soft desorption ionisation methods for mass spectrometric analyses of biological macromolecules” [[5/](#)].

MALDI

Electrospray Ionization

Data Acquisition

Data acquisition strategies for proteomics fall generally within targeted or untargeted, and they can depend on the data (data dependent acquisition or DDA) or be data independent (data-independent acquisition or DIA).

DDA

Targeted DDA

Untargeted DIA

DIA

Targeted DIA

Untargeted DIA

Analysis of Raw Data

The goal of basic data analysis is to convert raw spectral data into identities and quantities of peptides and proteins that can be used for biologically-focused analysis. This step may often include measures of quality control, cross-run data normalization, quantification on different levels (precursor, peptide, protein), protein inference, PTM (post translational modification) localization and also first steps of data analysis, such as statistical hypothesis tests.

In typical bottom-up proteomics experiments, proteins are digested into peptides and further analyzed with LC-MS/MS systems. Peptides can have different PTMs and ionize differently depending on their length and amino acid distributions. Therefore, mass spectrometers often record different charge and modification states of one single peptide. The entity that is recorded on a mass spectrometer is usually referred to as a precursor ion (peptide with its modification and charge state). This precursor ion is fragmented and the precursor or peptide sequences are obtained through spectral matching. The quantity of a precursor is estimated with various methods. The measured precursor quantities are combined to generate a peptide quantity. Peptides are also often combined into a protein group through protein inference, which combines multiple peptide identifications into a single protein identification [6] [7]. Protein inference is still a challenge in bottom-up proteomics.

Due to the inherent differences in the data structures of DDA and DIA measurements, there exist different types of software that can facilitate the steps mentioned above. The existing software for DDA and DIA analysis can be further divided into freeware and non-freeware:

DDA freeware: - MaxQuant [8/] - MSFragger [9/] - Mascot (for smaller data sets) [10/] [11] - MS-GF+ [12]

DIA freeware: - MaxDIA (within MaxQuant) [8/] - Skyline [13] - DIA-NN [14] Targeted proteomics freeware: - Skyline [13]

DDA non-freeware: - ProteomeDiscoverer[15] - Mascot (for larger data sets) [10/] - Spectromine [16/?gclid=Cj0KCQiAoY-PBhCNARIsABcz770mjUz6iavBr9Ql7RPudMvaHu9RYgPNrEfZco1wExEeoFwnQXuCHscaAlgBEALw_wcB] - PEAKS [17/]

DIA non-freeware: - Spectronaut [18/?gclid=Cj0KCQiAoY-PBhCNARIsABcz770nuaU2SgIriS-ZJJGsC6CtzXc9AC8b9K3w5FIFDsDfGtnuUjlhankaAvegEALw_wcB] - PEAKS [17/]

Analysis of DDA data

Strategies for analysis of DIA data

Targeted proteomics data analysis

Quality control

Statistical hypothesis testing

Biological Interpretation

1. term enrichment analysis (KEGG, GO)
2. network analysis methods
3. structure analysis
4. isoform analysis
5. follow-up experiments

Experiment Design

This section should discuss trade offs and balancing them to design an experiment. 1. constraints: Each experiment will have different constraints, which may include the number of samples needed for analysis, or desire to quantify a specific subset of proteins within a sample. 2. sample size 3. statistics 4. costs

References

1. **<i>In Silico</i> Proteome Cleavage Reveals Iterative Digestion Strategy for High Sequence Coverage**
Jesse G Meyer
ISRN Computational Biology (2014-04-22) <https://doi.org/gb6s2r>
DOI: <https://doi.org/10.1155/2014/960902>
2. **Expanding Proteome Coverage with Orthogonal-specificity α -Lytic Proteases**
Jesse G Meyer, Sangtae Kim, David A Maltby, Majid Ghassemian, Nuno Bandeira, Elizabeth A Komives
Molecular & Cellular Proteomics (2014-03) <https://doi.org/f5vgcg>
DOI: <https://doi.org/10.1074/mcp.m113.034710>
3. **Site-specific identification and quantitation of endogenous SUMO modifications under native conditions.**
Ryan J Lumpkin, Hongbo Gu, Yiyang Zhu, Marilyn Leonard, Alla S Ahmad, Karl R Clauser, Jesse G Meyer, Eric J Bennett, Elizabeth A Komives
Nature communications (2017-10-27) <https://www.ncbi.nlm.nih.gov/pubmed/29079793>
DOI: [10.1038/s41467-017-01271-3](https://doi.org/10.1038/s41467-017-01271-3) · PMID: [29079793](https://pubmed.ncbi.nlm.nih.gov/29079793/) · PMCID: [PMC5660086](https://pubmed.ncbi.nlm.nih.gov/PMC5660086/)
4. **Simultaneous Quantification of the Acetylome and Succinylome by 'One-Pot' Affinity Enrichment**
Nathan Basisty, Jesse G Meyer, Lei Wei, Bradford W Gibson, Birgit Schilling
PROTEOMICS (2018-08-19) <https://doi.org/gn4cmb>
DOI: [10.1002/pmic.201800123](https://doi.org/10.1002/pmic.201800123) · PMID: [30035354](https://pubmed.ncbi.nlm.nih.gov/30035354/) · PMCID: [PMC6175148](https://pubmed.ncbi.nlm.nih.gov/PMC6175148/)
5. **The Nobel Prize in Chemistry 2002**
NobelPrize.org
<https://www.nobelprize.org/prizes/chemistry/2002/summary/>
6. **Interpretation of Shotgun Proteomic Data**
Alexey I Nesvizhskii, Ruedi Aebersold
Molecular & Cellular Proteomics (2005-10) <https://doi.org/cm99cj>
DOI: <https://doi.org/10.1074/mcp.r500012-mcp200>
7. **In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics**
Enrique Audain, Julian Uszkoreit, Timo Sachsenberg, Julianus Pfeuffer, Xiao Liang, Henning Hermjakob, Aniel Sanchez, Martin Eisenacher, Knut Reinert, David L Tabb, ... Yasset Perez-Riverol
Journal of Proteomics (2017-01) <https://doi.org/f9r8r6>
DOI: [10.1016/j.jprot.2016.08.002](https://doi.org/10.1016/j.jprot.2016.08.002) · PMID: [27498275](https://pubmed.ncbi.nlm.nih.gov/27498275/)
8. **MaxQuant** <https://www.maxquant.org/>
9. **MSFragger**
MSFragger
<https://msfragger.nesvilab.org/>
10. **Mascot search engine | Protein identification software for mass spec data**
<https://www.matrixscience.com/>

11. **Probability-based protein identification by searching sequence databases using mass spectrometry data.**
DN Perkins, DJ Pappin, DM Creasy, JS Cottrell
Electrophoresis (1999-12) <https://www.ncbi.nlm.nih.gov/pubmed/10612281>
DOI: [10.1002/\(sici\)1522-2683\(19991201\)20:18<3551::aid-elps3551>3.0.co;2-2](https://doi.org/10.1002/(sici)1522-2683(19991201)20:18<3551::aid-elps3551>3.0.co;2-2) · PMID: [10612281](https://pubmed.ncbi.nlm.nih.gov/10612281/)
12. **MS-GF+ makes progress towards a universal database search tool for proteomics**
Sangtae Kim, Pavel A Pevzner
Nature Communications (2014-12) <https://doi.org/ggkdq8>
DOI: <https://doi.org/10.1038/ncomms6277>
13. **Start Page: /home/software/Skyline**
<https://skyline.ms/project/home/software/Skyline/begin.view>
14. **DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput**
Vadim Demichev, Christoph B Messner, Spyros I Vernardis, Kathryn S Lilley, Markus Ralser
Nature Methods (2020-01) <https://doi.org/gj9xgj>
DOI: <https://doi.org/10.1038/s41592-019-0638-x>
15. **Proteome Discoverer Software - US** [//www.thermofisher.com/us/en/home/industrial/mass-spectrometry/liquid-chromatography-mass-spectrometry-lc-ms/lc-ms-software/multi-omics-data-analysis/proteome-discoverer-software.html](https://www.thermofisher.com/us/en/home/industrial/mass-spectrometry/liquid-chromatography-mass-spectrometry-lc-ms/lc-ms-software/multi-omics-data-analysis/proteome-discoverer-software.html)
16. **Proteomics Analysis Software | Shotgun Proteomics | DDA Proteomics**
Biognosys
<https://biognosys.com/software/spectromine/>
17. **Protein Identification & Quantification Software, PTM & Variant Search**
Bioinformatics Solutions Inc.
<https://www.bioinfor.com/peaks-studio/>
18. **Proteomics Software | DIA Proteomics | Discovery Proteomics**
Biognosys
<https://biognosys.com/software/spectronaut/>