

Mass Spectrometry-based Multi-Omics: Combinations of Proteomics, Metabolomics, and/or Lipidomics

This manuscript ([permalink](#)) was automatically generated from [jessegmeyerlab/2022-multi-omics-review@a603d12](#) on December 22, 2021.

Authors

- **Jane Roe**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [janeroe](#)

Department of Something, University of Whatever; Department of Whatever, University of Something

- **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

Abstract

Multi-Omics studies integrate unbiased measurements across at least two omics layers. The number of measurable 'omes' has expanded to include whole genome sequencing (WGS), structural chromatin studies (e.g. ATAC-seq, ChIP-seq), transcriptomics (e.g. RNA-seq or microarrays),

Introduction

Here is where we briefly go over the following:

1. Cover other reviews
2. What is proteomics
3. what is metabolomics
 - polar metabolomics
 - lipidomics
4. what does multi-omic integration mean?

Test adding citation [\[1\]](#)

Test adding citation by PMID [\[2\]](#)

Sample Preparation for Multi-Omic Analysis

Integrative multi-omics analysis is a powerful approach to study complex biological responses and has gained popularity in recent years. To avoid the potential

- 1, Sample preparation for proteomics
- 2, Sample preparation for metabolomics
 - 2.1 non-targeted metabolomics
 - 2.2 targeted metabolomics
 - 2.3 lipidomics
- 3, Integrative sample preparation for multi-omics

In the context of multi-omics analyses, being able to perform multiple measurements on the same sample can also decrease experimental variation.

[\[5\]](#)

[\[6\]](#)

References

1. **Quantitative shotgun proteome analysis by direct infusion**
Jesse G Meyer, Natalie M Niemi, David J Pagliarini, Joshua J Coon
Nature Methods (2020-12) <https://www.nature.com/articles/s41592-020-00999-z>
DOI: [10.1038/s41592-020-00999-z](https://doi.org/10.1038/s41592-020-00999-z)
2. **Charge state coalescence during electrospray ionization improves peptide identification by tandem mass spectrometry.**
Jesse G Meyer, Elizabeth A Komives
Journal of the American Society for Mass Spectrometry (2012-05-18)
<https://www.ncbi.nlm.nih.gov/pubmed/22610994>
DOI: [10.1007/s13361-012-0404-0](https://doi.org/10.1007/s13361-012-0404-0) · PMID: [22610994](https://pubmed.ncbi.nlm.nih.gov/22610994/) · PMCID: [PMC6345509](https://pubmed.ncbi.nlm.nih.gov/PMC6345509/)
3. **Development of a plasma pseudotargeted metabolomics method based on ultra-high-performance liquid chromatography-mass spectrometry**
Fujian Zheng, Xinjie Zhao, Zhongda Zeng, Lichao Wang, Wangjie Lv, Qingqing Wang, Guowang Xu
Nature Protocols (2020-08) <https://www.nature.com/articles/s41596-020-0341-5>
DOI: [10.1038/s41596-020-0341-5](https://doi.org/10.1038/s41596-020-0341-5)
4. **A complete workflow for high-resolution spectral-stitching nanoelectrospray direct-infusion mass-spectrometry-based metabolomics and lipidomics**
Andrew D Southam, Ralf JM Weber, Jasper Engel, Martin R Jones, Mark R Viant
Nature Protocols (2017-02) <https://www.nature.com/articles/nprot.2016.156>
DOI: [10.1038/nprot.2016.156](https://doi.org/10.1038/nprot.2016.156)
5. **Multimic analysis of a dried single-drop plasma sample using an integrated mass spectrometry approach**
Weina Gao, Qiaoyun Zhang, Yiran Su, Peiwu Huang, Xue Lu, Qinyue Gong, Wendong Chen, Ruilian Xu, Ruijun Tian
Analyst (2020-10-12) <https://pubs.rsc.org/en/content/articlelanding/2020/an/d0an01149e>
DOI: [10.1039/d0an01149e](https://doi.org/10.1039/d0an01149e)
6. **MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses**
Ernesto S Nakayasu, Carrie D Nicora, Amy C Sims, Kristin E Burnum-Johnson, Young-Mo Kim, Jennifer E Kyle, Melissa M Matzke, Anil K Shukla, Rosalie K Chu, Athena A Schepmoes, ... Thomas O Metz
mSystems (2016-05-10) <https://journals.asm.org/doi/abs/10.1128/mSystems.00043-16>
DOI: [10.1128/mSystems.00043-16](https://doi.org/10.1128/mSystems.00043-16)