

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

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## Abstract

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Studies that integrate unbiased measurements across at least two omics layers are often referred to as “multiomics”. Measurable “omes” include the genome, transcriptome, proteome, and metabolome. Any combination of omic measures can be referred to as multiomics; for the scope of this review we focus on research combining proteomics and metabolomics. Mass spectrometry is the leading technique for analysis of the proteome and the metabolome. Due to improvements in sample preparation and data collection, more studies are incorporating both mass spectrometry-based proteomics and metabolomics. In this review, we discuss the perceived value of multiomics, advances in sample preparation and data collection, the current state of multiomic data integration, and clinical examples of multiomic analysis. Finally, we explore major barriers preventing democratization of mass spectrometry based multiomics to the same level as nucleic acid analysis, and we suggest solutions to break these barriers.

# Introduction

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Topics:

1. concept of multiomics
2. What is proteomics
3. what is metabolomics
  - polar metabolomics
  - lipidomics
4. what does multi-omic integration mean?
5. Other reviews

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## Sample Preparation for Multi-Omic Analysis

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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  
[\[3\]](#)
  - 2.2 targeted metabolomics
  - 2.3 lipidomics  
[\[4\]](#)

- 3, Integrative sample prepatation 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.

[\[5\]](#)

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## References

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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)
7. [10.3389/fgene.2021.635971](https://doi.org/10.3389/fgene.2021.635971)
8. <https://doi.org/10.1074/mcp.M115.053702>