

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

This manuscript ([permalink](#)) was automatically generated from [jessegmeyerlab/2022-multi-omics-review@3ee6e9b](#) on December 20, 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

Introduction

Here is where we briefly go over the following:

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

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

Sample Preparation for Multi-Omic Analysis

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/22610994/)