



BEAD-ENABLED, EFFICIENT, AND RAPID MULTI-OMIC SAMPLE PREPARATION FOR MASS SPECTROMETRY ANALYSIS

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WARF: P220205US02

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The Invention

UW-Madison researchers developed a new process for preparing proteins, lipids, and metabolites for MS-based multi-omics. The process is based on a monophasic extraction solvent (e.g., n-butanol) that enables efficient recovery of both metabolites and lipids. The monophasic extraction is paired with immobilizing beads (e.g., unmodified magnetic silica beads) to which the proteins aggregate during a short incubation period. Unbound molecules are removed and the bead-bound proteins are digested with rapid trypsin. After digestion, the protein solution is acidified, desalted, and dried down. The separate metabolite, lipid, and protein solutions are resuspended for MS analysis. All told, the entire sample preparation time is drastically reduced from 1-2 days down to ~3 hours. Practically, when this streamlined preparation technique is paired with an integrated mass spectrometry acquisition method (e.g., multi-omic single-shot technology, MOST) a single lab researcher could process lipids, metabolites, and proteins from a single sample to generate quality multi-omics data.

Additional Information

For More Information About the Inventors

- [Joshua Coon](#)

Tech Fields

- [Analytical Instrumentation, Methods & Materials : Mass spectrometry.](#)

For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854