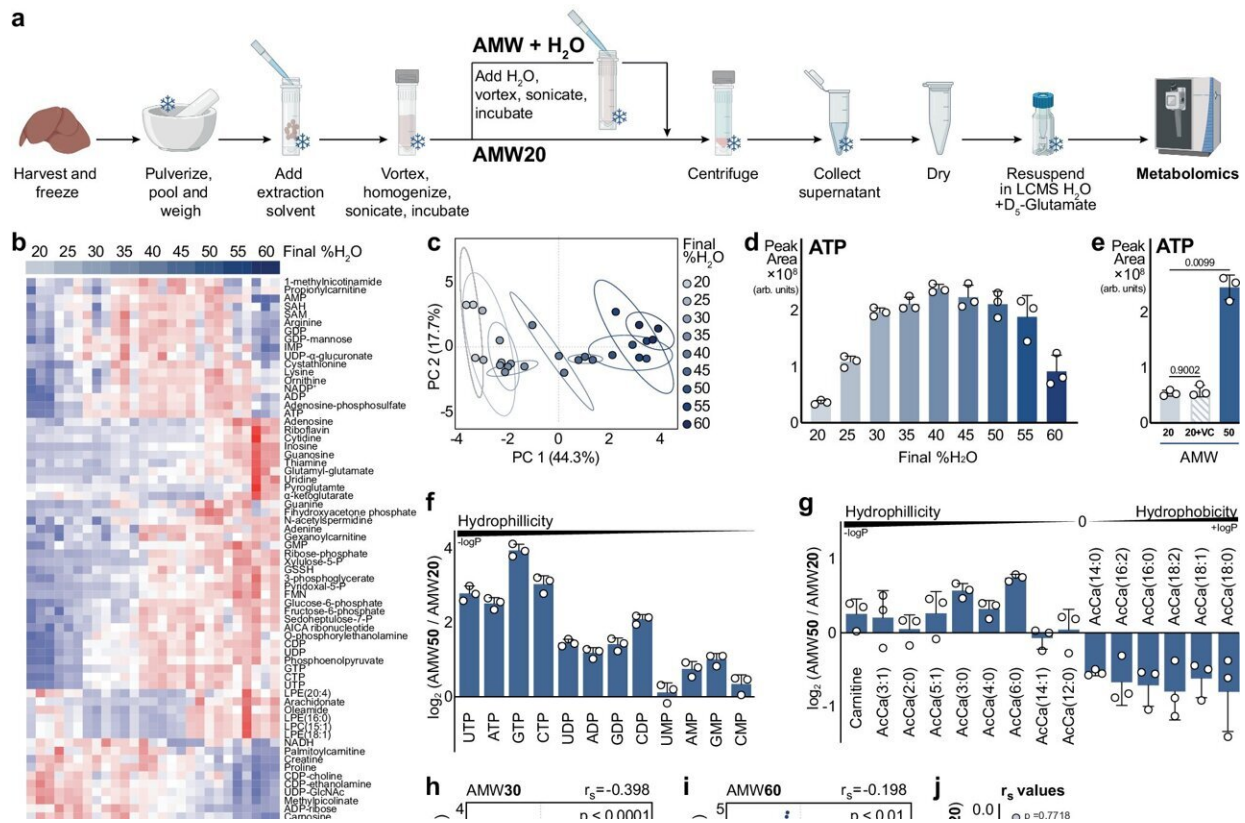


# Study finds persistent proteins may influence metabolomics results

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Metabolomic responses to extraction water content are not fully explained by compound hydrophobicity. Credit: *Nature Communications* (2024). DOI: 10.1038/s41467-024-50128-z

Van Andel Institute scientists have identified more than 1,000 previously undetected proteins in common metabolite samples, which persist

despite extraction methods designed to weed them out.

The findings, [published](#) in *Nature Communications*, give scientists new insights and tools for improving future metabolomics experiments, including a novel protocol for removing these proteins during the extraction process. The study does not invalidate prior results but instead reinforces the importance of appropriate controls and validation in [experimental design](#) and analysis.

"Scientific advances often happen through a combination of chance and keen observation. In this case, we noticed a strange result during an experiment, dug into it and found this vast landscape of proteins that were slipping by standard [metabolite](#) extractions," said Ryan Sheldon, Ph.D., director of VAI's Mass Spectrometry Core and corresponding author of the study.

"These proteins can obscure results and potentially contribute to [false positives](#) and negatives. We hope our findings will raise awareness of these proteomic stowaways and further strengthen the metabolomics field."

It has long been assumed that the chemicals used to extract metabolites destroy proteins present in samples, thus preventing them from interfering with the final analysis. The study demonstrates that some proteins endure, which may shift the desired phenotype of the extracted sample and alter results.

To screen out these potentially problematic proteins, Sheldon and colleagues added a filtration step to their standard [extraction](#) process that removes proteins larger than 3 kilodaltons—a threshold that encompasses most proteins.

"At the end of the day, we can have the best instrumentation in the world

but if there are issues with sample preparation, then the technology can only take us so far," Sheldon said.

"Ensuring that our phenotypes are free of any confounding proteins is critical to attaining accurate results. Our findings help us do just that."

**More information:** Rachel J. House et al, A diverse proteome is present and enzymatically active in metabolite extracts, *Nature Communications* (2024). [DOI: 10.1038/s41467-024-50128-z](https://doi.org/10.1038/s41467-024-50128-z)

Provided by Van Andel Research Institute

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