

Submit a dataset to the Lipid Interactome Repository

This repository is still under construction, please forgive us for incomplete sections as we build features!

We are in the process of building a data submission form here – check back soon for this functionality!

In the meantime, email us at [Contact.Us@LipidInteractome.org](mailto>Contact.Us@LipidInteractome.org) to discuss data handoff and study details.

Study metadata

In addition to the DOI and basic details of the study, we will need additional metadata to describe how the study was performed and how the reported data were collected.

In brief, we will need:

- The lipid probes analyzed, and their structure if novel
- The cell line analyzed
- The mass spectrometry quantification method (i.e., TMT or PSM)
- The details of mass spectrometry data acquisition (Instrument, LC gradient)
- The details of data analysis (e.g., LIMMA analysis, ANOVA testing, etc.)

Mass spectrometry data formatting

The ideal dataset to incorporate into this site will have the following columns:

- **gene_name**
- **LipidProbe** - Which lipid probe was applied in the analysis (especially if there are several)
- **comparison** - The ratiometric comparison reflected by the logFC (i.e. +UV versus -UV)
- **logFC** - the log₂ transformed fold-change between the conditions in the comparison

- **pvalue** - the results of an appropriate statistical test. Ideally share the methods used
- **AveExpr** - the average ion intensity between the two conditions in the reported comparison (for MA plots)
- **hit_annotation** - A statistical representation of the significance of each protein. The standardized nomenclature used in Thomas et al. 2025, Farley et al. 2024, and Farley et al. 2024 has the following:
 - “**no hit**” = unenriched or depleted in the presence of probe
 - “**enriched candidates**” are defined as proteins with a false discovery rate less than 0.2 and a fold change of at least 1.5-fold
 - “**enriched hits**” are defined as proteins with a false discovery rate less than 0.05 and a fold change of at least 2-fold in the +UV over the -UV.
- **FDR** - The false discovery rate of the protein.

If only some of these data are available, reach out to us at Contact.Us@LipidInteractome.org to discuss the best depictions of your data.