The Lipid Interactome

An interactive and open access platform for exploring cellular lipid-protein interactomes

2025-02-04

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## Summary

### Abstract

Lipid–protein interactions play essential roles in cellular signaling and membrane dynamics, yet their systematic characterization has long been hindered by the inherent biochemical properties of lipids. Recent advances in functionalized lipid probes – equipped with photoactivatable crosslinkers, affinity handles, and photocleavable protecting groups – have enabled proteomics-based identification of lipid interacting proteins with unprecedented specificity and resolution. Despite the growing number of published lipid interactomes, there remains no centralized effort to harmonize, compare, or integrate these datasets.

The Lipid Interactome addresses this gap by providing a structured, interactive site that adheres to FAIR data principles – ensuring that lipid interactome studies are Findable, Accessible, Interoperable, and Reusable. Through standardized data formatting, interactive visualizations, and direct cross-study comparisons, this resource enables researchers to systematically explore the protein-binding partners of diverse bioactive lipids. By consolidating and curating lipid interactome proteomics data from multiple studies, the Lipid Interactome database serves as a critical tool for deciphering the biological functions of lipids in cellular systems.

### Availability

This site can be viewed at [LipidInteractome.org](lipidinteractome.org) all data is available for download. No user information is collected or necessary for data navigation and interaction.

### Data Submission & Contact

If you would like to submit a relevant dataset, see our [Data Submission Page](https://www.lipidinteractome.org/DataSubmission.html) for details, contact info, and instructions. For site feedback and additional questions, please email the site administrators at [Contact.Us@lipidinteractome.org](mailto:Contact.Us@lipidinteractome.org)

### Keywords

Lipid-protein interactions, proteomics, interactomics, database, multifunctionalized lipids

## Introduction

Lipids are more than passive structural components of cellular membranes—they are active participants in signaling pathways, cellular homeostasis, organellar communications, and membrane dynamics. Despite their critical biological roles, lipid–protein interactions have historically been challenging to study. The small size and biophysical properties of lipids make conventional proteomics approaches unsuitable for mapping their interactors. Unlike proteins, which can be readily tagged or immobilized for affinity-based interaction studies, lipids require specialized chemical modifications to enable selective and controlled interaction profiling.

Recent advances in developing multifunctionalized lipid analogs have revolutionized the field, enabling the systematic interrogation of lipid interactomes. These probes incorporate strategically designed functional groups that enable covalent crosslinking, affinity enrichment, and controlled activation. Most commonly, these include: (1) a diazirine ring for photoactivatable crosslinking upon exposure to 355 nm ultraviolet (UV) light, stabilizing lipid–protein interactions; (2) a terminal alkyne, permitting click chemistry-based enrichment; and, in some cases, (3) a coumarin photocage, which shields the lipid probe from premature enzymatic modification until selectively released by 405 nm light. Together, these modifications enable direct proteomic identification of lipid interactors, distinguishing true binding partners from transient or non-specific associations1–3.

Several studies have already employed these lipid probes to elucidate the interactomes of key bioactive lipids, including diacylglycerol, sphingosine, sphinganine, phosphatidic acid, and phosphatidylethanolamine3–6. These studies have followed a comparative proteomics workflow, wherein crosslinked (“+UV”) and non-crosslinked (“-UV”) samples are analyzed side by side to minimize artifacts and confirm specificity1,2. However, despite the growing number of lipid interactome datasets, no centralized resource has existed to compile, compare, and standardize these findings.

To address this gap, we present the Lipid Interactome database – a curated repository designed to facilitate the comparative analysis of lipid–protein interactions from multiple studies. This resource consolidates proteomics data from multifunctional lipid probes, enabling researchers to efficiently explore and contextualize lipid-binding proteins across different lipid species and cellular models. Currently, the repository hosts interactomes derived from trifunctionalized phosphatidic acid, phosphatidylethanolamine, sphingosine, and sphinganine in HeLa and Huh7 cells3,6. Additionally, it includes control datasets from two fatty acid probes to distinguish specific from non-specific lipid-binding proteins5.

By providing a centralized platform for lipid interactome data, the Lipid Interactome significantly lowers the barriers to entry for researchers investigating lipid signaling pathways. This repository represents a necessary step toward systematizing lipid–protein interaction studies, ensuring that bioactive lipids are afforded the same level of proteomic scrutiny as their protein counterparts.

## Description

### Overview

The Lipid Interactome is an interactive discovery platform built using Quarto, designed to centralize and enhance the study of lipid–protein interactions through curated datasets and dynamic visualization tools. Each page seamlessly integrates R-generated figures, embedding scripts directly into the source material to ensure reproducibility and transparency. The repository currently hosts data from five published studies, with an expandable framework that supports the incorporation of future datasets as the field progresses.

At its core, the Lipid Interactome enables the direct comparison of lipid interactomes across studies, providing researchers with invaluable insights into the diverse roles that bioactive lipids play in cellular processes. By leveraging standardized data formatting and interactive visualization—including study-specific analysis pages, lipid probe aggregation, and cross-study comparisons via a Shiny application—the platform facilitates intuitive exploration of protein–lipid interactions. As a living repository, we actively encourage researchers to contribute their findings through our [Data Submission](#Xa39a3ee5e6b4b0d3255bfef95601890afd80709) page, ensuring that this resource continues to evolve alongside advancements in lipidomics research.

### FAIR data principles

The Lipid Interactome database was developed with the FAIR (Findable, Accessible, Interoperable, and Reusable) data principles in mind, ensuring that lipid–protein interaction data can be systematically explored, compared, and reused by the research community. Given the historical inconsistency in proteomics data curation, we have taken deliberate steps to standardize, annotate, and document our datasets for maximum utility.

#### Findable

To address the fragmented nature of lipid interactome studies, we have established a centralized platform where researchers can interact with the results of individual studies or explore aggregated findings across multiple studies on a given lipid. The repository is structured to facilitate intuitive navigation between experimental datasets, offering clear entry points for study-specific and lipid-specific analyses. Because this resource is intended as a living repository, we actively invite researchers to contribute their findings following the submission guidelines detailed on our [Data Submission](https://www.lipidinteractome.org/contactus/datasubmission) page.

#### Accessible

All datasets within the Lipid Interactome are available for download in standardized .csv format, ensuring broad accessibility across different computational environments. To further enhance usability, we provide a [detailed overview of data generation and analysis](https://www.lipidinteractome.org/background/multifunctionallipidprobesoverview), including explicit descriptions of dataset structure, column definitions, and the inherent limitations of multifunctional lipid probes. Only peer-reviewed proteomics datasets are included in this repository to maintain high data quality and reliability.

#### Interoperable

Given the diversity of methodologies employed across lipid interactome studies, we have taken care to harmonize data formats and metadata annotations. While many studies share common analytical pipelines, others employ distinct mass spectrometry workflows. To ensure consistency, we have structured the data to allow parallel comparisons and provided [documentation on methodological differences](https://www.lipidinteractome.org/background/proteomicsusingmultifunctionalprobes). This standardization effort facilitates direct cross-study comparisons without requiring extensive reformatting by the end user.

#### Reusable

To maximize the utility of these datasets, we provide extensive documentation detailing data acquisition, analysis workflows, and potential limitations. Wherever possible, technical jargon has been minimized to ensure accessibility to a broad audience, from lipid biologists to computational scientists. Additionally, we reference key publications that delve deeper into the synthesis of lipid probes and the specifics of each proteomics workflow, allowing researchers to further contextualize and validate their findings.

By adhering to these FAIR principles, the Lipid Interactome database aims to serve as a robust and enduring resource for the lipid biology community, reducing redundancy, improving data transparency, and accelerating the study of lipid-mediated signaling.

### Data Visualization and Download Modules

To facilitate efficient exploration and analysis of lipid–protein interaction data, the Lipid Interactome repository incorporates a suite of interactive visualization and data access tools. These modules are designed to enhance user engagement, provide clear interpretability of experimental findings, and streamline data retrieval for further computational analysis.

#### Study-Specific Data Exploration

Each study contributing to the repository is provided with a dedicated results page, allowing users to examine its findings in detail. These pages include interactive Volcano, Ranked-Order, and MA plots, which enable visualization of differential protein enrichment across experimental conditions. The plots are rendered using the Plotly and htmlwidgetsR packages, ensuring a responsive, client-side experience that supports zooming, hovering, and data filtering [REF: Plotly, htmlwidgets]. For transparency and reproducibility, all datasets associated with a given study are available for direct download.

#### Lipid Probe-Specific Pages

Beyond individual study pages, datasets are further organized by lipid probe, providing a consolidated view of protein interactors detected across multiple experiments. Each lipid-specific page includes study metadata, cell type, and facilitates cross-study comparisons. Future iterations of the repository will extend this functionality by enabling direct comparisons of interactomes obtained from different cell lines treated with the same lipid probe, further refining the contextual understanding of lipid–protein interactions.

#### Comparative Analysis via Shiny Application

Where study design permits, data has been integrated into an interactive Shiny application, allowing users to perform direct probe-to-probe comparisons ([Probe vs Probe Comparisons](https://www.lipidinteractome.org/lipidprobe/enrichedhitscomparison)). This tool enables researchers to explore the similarity of lipid interactomes across experimental conditions via linear regression analysis, highlighting proteins that are significantly enriched in one dataset, both datasets, or neither. By providing an intuitive framework for interactome comparison, this feature aids in the identification of promising targets for further investigation.

These data access and visualization tools are designed to ensure that the Lipid Interactome is not merely a static repository, but rather a dynamic and evolving resource for lipid biologists and bioinformaticians alike.

### Data format

While there are numerous ways to quantify the mass spectrometry (MS) data, the studies included in our repository have utilized the same (or highly similar) quantitative MS pipeline using Tandem Mass Tagging[REF]. These datasets include those reported by Farley et al. (2024), Farley et al. (2024), and Thomas et al. (2025)3,5,6. Correspondingly, the ideal data structure for incorporation into our repository will include the following:

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1: **Example data table for smooth incorporation into Lipid Interactome.** ***Column descriptions:*** *Gene name*: The identifier for genes identified in the dataset (or Accession Number). *Enrichment value*: Fold change of Experimental versus Control fold-change, typically log2-transformed – ideally the product of TMT or other quantitative mass spectrometry methods. *p value*: the results of an ANOVA or LIMMA analysis, corrected for multiple hypothesis testing. *AveExpr*: An averaged value of the m/z ion intensity of the Experimental condition and Control condition used for the enrichment value (used to prepare MA plots for quality control). *FDR*: False-discovery rate of protein identification.   | Gene name | logFC | p value | AveExpr | FDR | | --- | --- | --- | --- | --- | | GeneA | 1.2 | 0.001 | 1.0x1018 | 0.0001 | | GeneB | 0.1 | 0.6 | 1.0x105 | 0.005 | | … | … | … | … | … | |

We are working on providing visualization functionality for studies which utilized Peptide Spectral Matching to report enrichment toward lipid probes.

## Discussion

The advent of functionalized lipid probes has fundamentally transformed lipid biology by enabling the proteomic identification of lipid-binding proteins with unprecedented specificity. However, as the number of published lipid interactome studies grows, the lack of a centralized framework for comparing and integrating these datasets presents a significant challenge. The Lipid Interactome was developed to address this need by providing researchers with a structured platform to explore, cross-reference, and build upon previous findings. By aggregating and standardizing lipid–protein interaction data, this resource facilitates the rapid identification of candidate lipid-binding proteins and supports orthogonal validation efforts.

Designed as a continuously expanding repository, the Lipid Interactome will evolve alongside advances in lipid probe technologies and interactomics. Future iterations will incorporate validation studies for each lipid probe, offering researchers a dedicated space to compare findings across experimental contexts. This functionality will not only reduce redundancy in experimental design but also strengthen the reproducibility and biological interpretation of lipid interactome research. To support this vision, we invite researchers to contribute their datasets via our [Data Submission page](https://www.lipidinteractome.org/DataSubmission.html), fostering a collaborative and transparent approach to lipid biology.

## Abbreviations

UV

*U*ltra *V*iolet

MS

*M*ass *S*pectrometry

LIMMA

*Li*near *M*odels for *M*icro*a*rray and RNA-Seq Data

ANOVA

*An*alysis *o*f *Va*riance

## Contributions

GG designed, implemented, and wrote the majority of the LipidInteractome site and manuscript. FS wrote the data analysis section of the site, provided significant intellectual contribution to the site design, and edited the manuscript. AN provided substantial editing of the site and manuscript. CS and FT provided significant intellectual contribution and text editing of the site and manuscript, and oversaw the site development.

## Conflicts of Interest

The authors have no conflicts of interest to declare.

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