

# Guiding the choice of informatics software and tools for lipidomics research applications

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Progress in mass spectrometry lipidomics has led to a rapid proliferation of studies across biology and biomedicine. These generate extremely large raw datasets requiring sophisticated solutions to support automated data processing. To address this, numerous software tools have been developed and tailored for specific tasks. However, for researchers, deciding which approach best suits their application relies on ad hoc testing, which is inefficient and time consuming. Here we first review the data processing pipeline, summarizing the scope of available tools. Next, to support researchers, LIPID MAPS provides an interactive online portal listing open-access tools with a graphical user interface. This guides users towards appropriate solutions within major areas in data processing, including (1) lipid-oriented databases, (2) mass spectrometry data repositories, (3) analysis of targeted lipidomics datasets, (4) lipid identification and (5) quantification from untargeted lipidomics datasets, (6) statistical analysis and visualization, and (7) data integration solutions. Detailed descriptions of functions and requirements are provided to guide customized data analysis workflows.

Lipidomics is a rapidly growing sub-area of metabolomics, reporting on the generation and metabolism of lipid species in relation to health and disease<sup>1–5</sup>. There is increasing interest in the use of lipidomics to identify biomarkers and new targets for intervention in disease progression, as well as to delineate underpinning mechanisms<sup>6–8</sup>. Over the last 10 years, there has been an explosion in the establishment and

application of lipidomics mass spectrometry (MS) approaches for biomedical research. Newer generation MS instruments, particularly high-resolution time-of-flight and orbitrap configurations, enable the generation of large 'omics'-type datasets that can report on literally thousands of lipids in a single analytical run. With the current drive in the field being to analyze large numbers of samples (for example, blood

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plasmas and tissue extracts), the amount of data generated experimentally is increasing exponentially. This has led to challenges in both data processing and downstream storage for later (open access) reuse that requires smart computational solutions.

Researchers have responded strongly to the emerging challenges of data analytics in lipidomics through developing new algorithms and tools that enable effective computational processing of data. These tools have already begun to enable the application of new lipidomics methods to the characterization of diverse biological processes, in many cases leading to notable discoveries, and some examples are listed here. Several tools have been applied to the profiling of plasma lipidomes, for example LipidXplorer, LipidFinder, and Lipid Data Analyser (LDA)<sup>9,10</sup>. LDA has also contributed to a diverse range of biochemical studies, including adipocyte-derived extracellular vesicle characterization<sup>11</sup>, determining the role of phosphatidylserine in autophagy<sup>12</sup>, analysis of the role of lipids in flavivirus replication<sup>13</sup>, and how the lipid bilayer stabilizes the serotonin receptor<sup>14</sup>. Meanwhile, LipidFinder performed an extended clean-up of high-resolution MS data for the first report of the SARS-CoV2 envelope composition<sup>15</sup>. As further examples, the Lipid Ontology enrichment web tool, LION/web<sup>16</sup> enabled the investigation of the role of lipids in bone marrow neutrophils during aging<sup>17</sup> and the effect of sex and genetics on the metabolic response to calorie restriction<sup>18</sup>. Several of the tools described in this review, including LION/Web and XCMS have enabled the investigation of cellular metabolic states<sup>19,20</sup>. Furthermore, XCMS elucidated a role for sphingolipids in neuropathic pain to be identified<sup>21</sup>. Although this is only a small illustrative list of studies using existing tools, the number and diversity of biological applications for lipidomics tools is increasing as more and more researchers enter the field. LIPID MAPS has around 72,000 users globally, with the LIPID MAPS Structure Database downloaded >4,600 times and viewed ~380,000 times in 2021, along with ~2,500 citations in publications during 2020–2021 (Google Scholar, Google Analytics data).

When it comes to the choice of data analysis approaches to use, researchers need to consider the underlying data structure and the research questions being asked. They also need to understand the underlying approaches used by algorithms to determine whether they will perform as expected for their particular data. However, making decisions on the most appropriate software is currently based on ad hoc processes, such as manual searching of the literature and testing packages individually. This is time consuming and inefficient since implementing tools requires extensive training and familiarization. Furthermore, the inappropriate use of software can lead to significant errors, for example, incorrect annotation of lipid identifications or erroneous interpretation of noise as peaks to suggest the presence of lipids in samples.

To address these issues and to support researchers with identification and testing of appropriate computational solutions for lipidomics, LIPID MAPS has generated a Lipidomics Tools Guide ([https://www.lipidmaps.org/resources/tools?page=flow\\_chart](https://www.lipidmaps.org/resources/tools?page=flow_chart)), accessible through our home page. This comprises an interactive display that guides researchers towards appropriate solutions and provides detailed descriptions of key features and performance of individual tools, enabling informed decision making on processing pipelines (Fig. 1). To accompany the tool, in this review, we provide full details on the Lipidomics Tools Guide and listed software, together with practical advice from the individual developers relating to the primary and secondary applications of each tool. Additionally, two tutorials provided in the Supplementary Note illustrate the interoperability of different tools, exemplified for targeted and untargeted lipidomics experiments.

On the LIPID MAPS website, the tools are represented in the form of an interactive flow chart ([https://www.lipidmaps.org/resources/tools?page=flow\\_chart](https://www.lipidmaps.org/resources/tools?page=flow_chart)), which covers available, open-access solutions supported by a graphical user interface (GUI) for different types of lipidomics-derived datasets. This is integrated into LIPID MAPS with

links, descriptions, video tutorials, and contact details for software developers. The new tool comprehensively covers the seven major areas in lipidomics data processing, as follows: (1) lipid-oriented databases; (2) MS data repositories; (3) analysis of targeted lipidomics datasets; (4) lipid identification and (5) quantification from untargeted lipidomics datasets; (6) statistical analysis and visualization; and (7) data integration solutions (Fig. 2). To support informed decision making by lipidomics analysts, for each software, a short description is provided, highlighting the main functionalities and the areas of applications, followed by the specific features listed under ‘Technical information’ and ‘Task specific information’ tabs (Figs. 3 and 4). Additionally, users can review simplified, tabular representations of the available functions for each tool in a given section by using the ‘Tools Overview’ tab.

In the ‘Technical information’ section, users can view the type of the license under which the tool is distributed, the availability of desktop and/or web-based interfaces, data input/output formats, and compatibility with different operating systems (for example, Windows, Linux, macOS). There is also information accessible via clickable links, which allow the downloading of the tool together with related documentation, user guides, and training datasets. Additional fields list how to use the tool through the command line or via API interfaces for advanced users wishing to construct their own customized pipelines. ‘Task specific information’ tabs navigate users to pages describing functionalities of the software for particular tasks covering the seven areas outlined above (Figs. 1 and 2). Some comprehensive tools have multiple functions integrated into one combined package and can be configured for a wide range of workflows. These tools are assigned to each task with associated descriptions accordingly, and the list of tools is shown in Table 1. In the next section, we provide more details about each area and its associated software and tools.

## The categories of lipidomics tools

### Lipid-oriented databases

Databases that curate individual lipid structures, both from historical and new publications into organized repositories are essential for researchers who aim to identify the specific molecules present in their biological samples. Databases also serve as a foundation for many data analysis pipelines as well as key knowledge bases for lipid research. Over the last 5–10 years, the size of lipidomics research datasets generated using MS and tandem MS (MS/MS) has increased massively, and their routine analysis requires automated programmatic approaches to enable database searching. To support the selection of the databases suitable for a particular application, the ‘Task specific information’ tabs within ‘Lipid Oriented Databases’ section provide an overview of the database functionalities, including the number of included lipid structures, structural ontology, covered lipid (sub) classes, levels of curation and annotation. Automated approaches to support data searchability and utility are described, including used identifiers, structural representation, availability of spectral libraries, and calculated physicochemical properties when available.

The most widely used lipid-specific databases are provided by LIPID MAPS and SwissLipids. LIPID MAPS hosts several databases in which lipid structures are cataloged according to the LIPID MAPS nomenclature and classification<sup>22–24</sup>. Specific databases provide utility for different use-cases as follows. LIPID MAPS Structure Database (LMSD)<sup>22</sup> contains over 47,000 lipids (August 2022) obtained from sources that include experimental work performed by the LIPID MAPS consortium, from other lipid databases, from the scientific literature, and also some that are computationally generated on the basis of commonly occurring fatty acid chains in mammalian lipids. LMSD can return either bulk (lipid species) annotations for MS data, on the basis of the shorthand nomenclature described by Liebisch et al.<sup>24</sup>, or fully annotated names (structure-defined lipids), where users already have additional structural information, for example, from MS/MS

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## Lipidomics Tools Guide

MS Analysis	Structure Drawing	Statistical Analysis
Nomenclature	LIPID MAPS® Software	Lipidomics Tools Guide

MS based lipidomics data acquisition

Targeted MS datasets

Untargeted MS datasets

1 Lipid oriented DBs

3 Method design and quantification

4 Identification

2 Data deposition (lipid IDs, relative and absolute quantification)

5 Quantification

6 Stats analysis and visualization

7.1 Lipid ID converters

7.2 Ontology enrichment analysis

7.3 Pathway and network solutions

View All Tools

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W welcome

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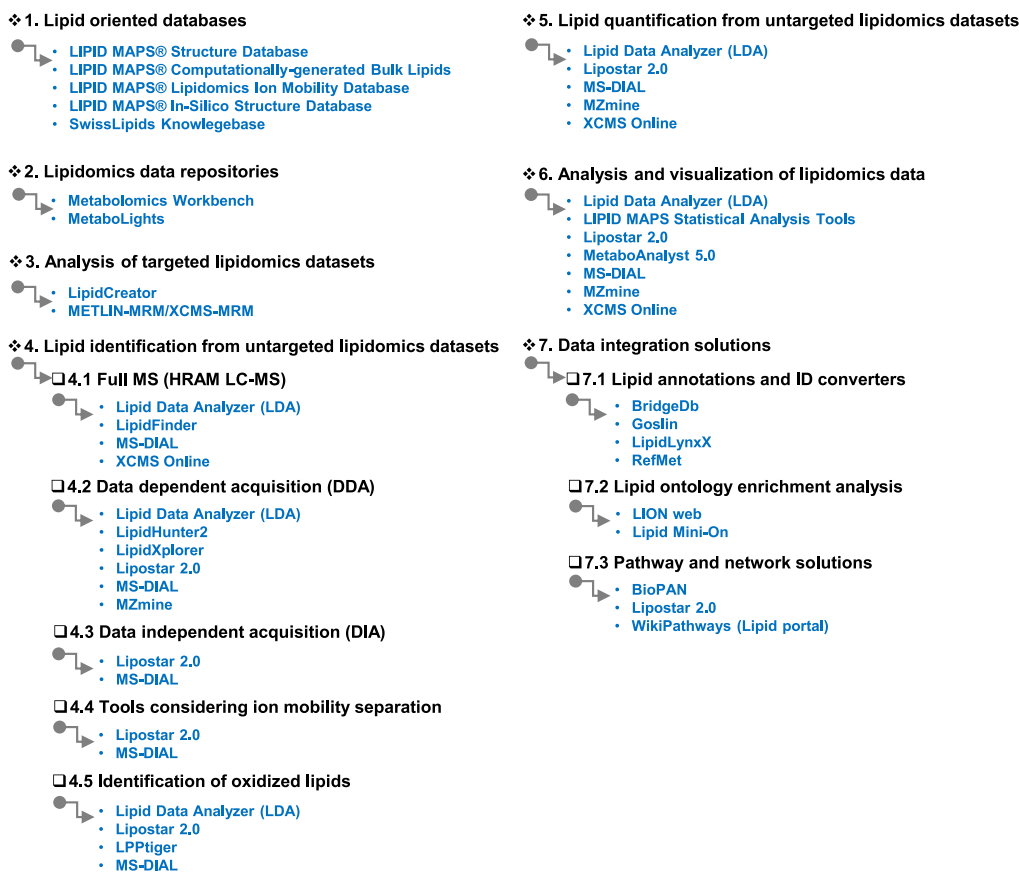
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**Fig. 1** A screenshot of Lipidomics Tools Guide guiding the choice of the tools organized by the major tasks for lipidomics data processing. Each task is marked by a clickable button to redirect the user to the list of corresponding tools and their descriptions.

experiments. LMSD has recently implemented a display of reaction data to link together lipid species by biochemical transformations. This was initially obtained from Rhea<sup>25</sup>, WikiPathways<sup>26</sup>, Reactome<sup>27</sup>, and other sources and is now in place for many generic lipids. This is in the process of being cascaded down to individual lipid species. In the case of (high-resolution) MS experiments, the user may only have information on the  $m/z$  value of detected lipid ions. In this case, searching databases will provide information on elemental compositions and, using this, generate putative matches. It is recommended to use the BULK search tool on LIPID MAPS to perform this operation since this returns shorthand nomenclature as a first step. Putative matches on the basis of MS indicate the number of carbons in fatty acyl chains and double bonds or rings present, but not how these are distributed between or within acyl chains in the molecule. For some users, the LIPID MAPS Computationally Generated Bulk Lipids (COMP\_DB)<sup>22</sup> may be a more suitable resource to query. This database contains over 59,000 lipid species in shorthand format (in the major classes such as fatty

acyls, glycerol- and glycerophospholipids, sterols, and sphingolipids), computationally generated from a list of commonly occurring acyl and alkyl chains. Most entries in this database represent hierarchical structures that could map to many different specific annotations. The LIPID MAPS In Silico Structure Database (LMISSD)<sup>22</sup> contains over 1,100,000 entries derived from the computational expansion of headgroups and chains for common lipid classes. These are provided as specific structural annotations but can also be provided as a hierarchy of sum composition and chain composition. Lastly, the Lipidomic Ion Mobility Database<sup>22</sup> was developed using data from the McLean and Griffin labs<sup>28–30</sup> to provide collisional cross section measurements for drift tube MS experiments.

The SwissLipids knowledgebase<sup>31</sup> was developed to aid lipidomics researchers in interpreting experimental datasets and integrating them with prior biological knowledge, allowing also for data exploration and hypothesis generation. In SwissLipids, experimentally characterized lipids are curated from peer-reviewed literature using the



**Fig. 2 | List of tools represented within LIPID MAPS Lipidomics Tools Guide assigned for each of the seven data processing categories.** These include (1) lipid-oriented databases, (2) MS data repositories, (3) analysis of targeted

lipidomics datasets, (4) lipid identification, and (5) quantification from untargeted lipidomics datasets, (6) statistical analysis and visualization, and (7) data integration solutions.

ChEBI<sup>32</sup> ontology (<https://www.ebi.ac.uk/chebi/>). Lipid metabolism is described using the Rhea knowledgebase<sup>25</sup> for biochemical and transport reactions (<https://www.rhea-db.org>), which is itself based on ChEBI, while enzymes, transporters, and interacting proteins are described using the UniProt Knowledgebase UniProtKB<sup>33</sup> (<https://www.uniprot.org>), for which Rhea is the reference vocabulary for such annotation<sup>34</sup>. As the number of experimentally characterized lipid structures represents only a small fraction of the possible structures that may exist in nature, expert-curated knowledge of lipid structures and metabolism in ChEBI, Rhea, and UniProt is used to design and create a library of all theoretically feasible lipid structures in silico, which is fully mapped to these three resources. The current version of the SwissLipids library contains almost 600,000 lipid structures from over 550 lipid classes, organized into two distinct hierarchical lipid classifications—one that parallels the structural classification of LIPID MAPS<sup>35</sup> and one that is based on the shorthand notation for MS data<sup>36</sup> that links lipid identifications from MS-based experiments to structures and biological knowledge.

### MS data repositories

Raw and/or processed data deposition using free repositories services, although a standard task before publication of the results in the field of proteomics for many years, is only now finding its way into the lipidomics community<sup>37</sup>. MS data repositories increase data transparency and reproducibility, allow reanalysis for new discoveries and data-driven hypothesis generation, as well as benchmarking of new software tools<sup>38</sup>. Although numerous platforms for upload of raw MS datasets exist (for example, MassIVE (<https://massive.ucsd.edu/>), ProteomeXchange (<http://www.proteomexchange.org/>)), specific

functionalities to support metadata, sample preparation protocols, and data matrices are necessary to improve the reusability of the deposited datasets following FAIR principles<sup>39</sup>. To select the optimal solution for data upload or download, users would need to be informed about the types of stored raw, processed, and metadata, curation strategy, total number of available datasets, and species coverage.

Repositories tuned for metabolomics and lipidomics data, such as Metabolomics Workbench<sup>40</sup> and MetaboLights<sup>41</sup> have the functionality to associate deposited data with compound query results to enhance the reusability of the datasets, allowing further interrogation. Each dataset is assigned a unique project accession ID, sufficient space to host the raw and/or processed data, supported by detailed information, including study design, associated metadata, details on sample preparation, and analysis protocols. Datasets can be browsed and searched by specific keywords, organisms of origin and reported compounds, and are usually associated with a source publication. MetaboLights has unique fields for data transformation and metabolite identification and provides an online viewer to review lipid identifiers, quantities, and corresponding structures, while Metabolomics Workbench is bundled with the RefMet<sup>42</sup> data resource (containing over 160,000 annotated metabolite species, including a large collection of lipids) and a suite of online data analysis tools. MetaboLights and Metabolomics Workbench are accepted by mainstream journals as data repositories for publications of lipidomics datasets.

### Analysis of targeted lipidomics datasets

Lipidomics data acquisition strategies can be generally subdivided into targeted and untargeted workflows. In targeted lipidomics, a pre-defined set of lipids with a known mass-to-charge ratio (*m/z*) of the

The screenshot shows the LIPID MAPS Structure Database (LMSD) website. At the top, there is a navigation bar with 'Home', 'Updates', 'Resources', and 'About' links, along with a search box. The main header features the LIPID MAPS logo and the title 'LIPID MAPS® Structure Database (LMSD)' with the subtitle 'Relational database of biologically-relevant lipids'. Below this is a 'Description' section explaining the database's scope and sources. A 'Technical Information' section is divided into two columns. The left column lists various features like URL, web search, browse by class, API access, and export formats. The right column, titled '- 1) Lipid oriented databases', provides detailed technical specifications such as the number of structures (47313), structural ontology, covered sub-classes, and various identifiers and properties.

**URL:**  
<https://lipidmaps.org/resources/databases/index.php?tab=lmsd>

**Web search:**  
 Yes

**Browse by class:**  
 Yes

**API Access:**  
[Yes](#)

**Full DB download:**  
 Yes

**Export formats:**  
 MOL, [SDF](#), CSV, TSV

**- 1) Lipid oriented databases**

**Number of lipid structures:** [47313](#)

**Structural ontology:**  
 Based on LIPID MAPS® Lipid Classification System

**Covered lipid sub classes:**  
 All lipid categories and classes are included (mainly mammalian but has been expanded to include some lipids from other sources including plants).

**Has curated lipids:** [Yes](#)

**Has computationally generated lipids:** [Yes](#)

**Level of annotations:** Species level, Structure defined level

**Main identifier:** LMID

**Other identifiers:** InChIKey, SwissLipids, PubChem, LipidBank, HMDB, ChEBI

**Structure representations:** SMILES, InChI, 2D-image

**Spectra library:** [MoNA MS spectra](#)

**Other fields:** Classification, Exact mass, Formula, Synonyms, Systematic name, Common name

**Calculated physicochemical properties:** Molar refractivity, LogP, Hydrogen bond acceptors, Hydrogen bond donors, Surface area, Topological polar, Molecular volume, Van der Waals, Rotatable bonds, Aromatic rings, Rings, Heavy atoms

**Searchable by properties:** Structure, Formula, m/z, Exact mass

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**Fig. 3 | A screenshot example of individual tool details pages from LIPID MAPS Structure Database.** Each tool has three sections: a 'Description' section for the brief introduction of the tool, a 'Technical Information' section listing all essential technical information from links to compatible file formats, and

a 'Task specific information' section containing detailed features tailored to the corresponding task. Hovering on the underlined text field displays further features for the section.

precursor and fragment/product ion(s) need to be provided by the user before data acquisition. Moreover, optimization of ionization and MS parameters for each pair of precursor–product ions (so-called 'transition') must be performed to optimize the sensitivity of the method. Targeted analysis using single or multiple reaction monitoring (SRM, MRM) on triple quadrupole instruments and, more recently, parallel reaction monitoring (PRM) on orbitrap and quadrupole time-of-flight instruments are successfully applied to the quantification of selected sets of lipids as well as hundreds of lipids in large sample cohorts (for example, over 600 lipid species in one liquid chromatography (LC)–MS/MS analysis<sup>43</sup>). However, to quantify a large number of lipids in a correspondingly large sample cohort, targeted lipidomics workflows should be quick to establish, and obtained results should be easy to inspect and validate. This process can be extremely time consuming and most often is not accessible to non-experts. Thus, specialized tools can be used to facilitate both method design and data processing steps. For software-assisted method design, the user should define the type of the targeted acquisition method planned (SRM/MRM or PRM) and lipid (sub)classes/species aimed to be covered. The selection of transitions can be done among experimentally validated or computationally optimized or can be even predicted on-the-fly on the basis of common knowledge of lipid subclass-specific gas phase fragmentation

chemistry. The set of fragment ions and their yield will strongly depend on class, the number of double bonds and fatty acyl length and even the type of instrument on which data were acquired. For instance, with LipidCreator<sup>44</sup> the targeted assay can be generated in three steps. In brief, during step 1 the user would select the lipid category and class to work with and define fatty acyl, double bond, hydroxyl group, and adduct constraints (precursor selection) as well as the polarity mode to analyze lipids of interest. In step 2 the monitored fragments at the MS/MS level can be defined. In step 3 the designed molecules can be added to the target list, reviewed, and transferred to the MS instrument for data acquisition. METLIN-MRM<sup>45</sup> is another data-rich resource where users can choose from experimentally and/or computationally optimized transitions or even public repository transitions with links to corresponding DOIs.

Although method design requires careful optimization and is time consuming, post-acquisition data processing of targeted lipidomics datasets is relatively straightforward and follows general rules of LC–MS/MS-based targeted quantification accepted in both the proteomics and metabolomics communities. Indeed, several open-access tools originally developed for targeted analysis of peptides (Skyline) or metabolites (XCMS-MRM) have been adapted for lipidomics applications. Thus, LipidCreator is fully integrated with

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**LipidLynx**  
A data transfer hub to support integration of large scale lipidomics datasets

### Description

LipidLynx was developed to provide efficient and accurate data transfer between analytical lipidomics datasets and data integration tools. It consists of three main modules supporting the conversion of diverse lipid annotations deriving from experimental lipidomics to unified identifier of user choice (Converter), cross-matching and equalizing lipid identifications obtained at different levels of structural confirmation (Equalizer), and mapping of annotated lipids to identifiers in a collection of databases and knowledge bases such as LIPID MAPS, SwissLipids, KEGG, Rhea, UniprotKB etc. that can be connected to ontology, pathway and network analysis workflows (Linker). LipidLynx has built-in support to read and generate abbreviation of lipids while keeping the information e.g. modifications types and positions to perform hierarchical comparison. Based on this, LipidLynx can reduce the over reporting of lipid identifiers and obtain associated identifiers from multiple databases. LipidLynx provides a high-throughput solution to format large-scale lipidomics identifiers and assist data integration workflows.

### Technical Information

**License:**  
GPL

**GUI:**  
Yes

**CLI:**  
Yes

**Desktop client:**  
No

**Web platform:**  
[Yes](#)

**Input formats:**  
REST service, Excel, CSV, [Text](#)

**Output formats:**  
Excel, CSV, HTML

**Platforms:**  
MacOS, Linux, Windows

**Programming languages:**  
JavaScript, Python

**Source code repository:**  
[Yes](#)

**Download / Web-service link:**  
[LIPID MAPS](#), [Github](#)

**Documentation and user guide:**  
[Yes](#)

**Reference:**  
[Yes](#)

**- 7.1) Lipid annotations and ID converters**

**Supported lipid classes:** 5 out of 8 LIPID MAPS classes

**Nomenclature:**  
LIPID MAPS classification, Nomenclature, and Shorthand notation (PMID: 33037133)

**Supported levels of structural annotations:**  
Structure defined levels, Molecular species, Species

**Input annotations or ids:** Common name, Shorthand notation (according to PMID: 33037133), MZmine2, MS-DIAL, MetFrag, LPPtiger, LIQUID, Lipostar, LipidSearch, LipidPro, LipidMatch, LipidHunter, LipidFrag, LipiDex, LipidCreator, LipidBlast, LDA 2, Greazy, ALEX123 lipid calculator, SwissLipids, RefMet, LipidHome, LIPID MAPS COMP\_DB, LIPID MAPS LMSD, HMDB

**Output annotations or ids:** LipidLynx, BioPAN, Shorthand notation (according to PMID: 33037133)

**Link to the external databases:** Uniprot KB, Rhea, KEGG, PubChem, ChEBI, LION/Web, HMDB, SwissLipids, LIPID MAPS LMSD

**Other features:**  
Linker: cross link lipid identifiers to the identifiers from a collection of databases and knowledge bases used by ontology, pathway and network analysis tools.,  
Equalizer: cross-match and equalize lipid identifications obtained from various sources at different levels of structural confirmation.

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**Fig. 4 | A screenshot example of individual tool details pages LipidLynx.**

Each tool has three sections: a 'Description' section for the brief introduction of the tool, a 'Technical Information' section listing all essential technical information from links to compatible file formats, and a 'Task specific

information' section containing detailed features tailored to the corresponding task. Hovering on the underlined text field displays further features for the section.

Skyline<sup>46</sup> for small molecules, making it a vendor-independent software. METLIN-MRM-assisted method development can be directly extended to post-acquisition data processing using the XCMS-MRM<sup>45</sup> platform. Both Skyline and XCMS-MRM tools provide automated solutions for peak integration, relative and absolute quantification, and data quality control.

### Lipid identification from untargeted lipidomics datasets

A second analytical strategy commonly used in lipidomics relates to untargeted workflows on the basis of data-dependent (DDA) or data-independent acquisition (DIA). Here users perform MS analysis of a lipidome in so-called 'discovery' mode without prior knowledge of the exact set of lipids to be analyzed in the sample. Generally, the main aim of untargeted lipidomics is to analyze and ideally identify as many lipid species as possible (ultimately all ionizable constituents extracted from the sample). Both DDA and DIA experiments rely on the iteration of instrument cycles that include MS1 survey scans (usually acquired at high resolution to define the elemental composition of the lipid ions)

and a number of MS/MS spectra in which lipid ions, selected on the basis of their abundance (DDA) or within a given  $m/z$  range (DIA), undergo collision-induced dissociation (CID). MS/MS information is then used to assign lipids to particular molecular species on the basis of their known gas phase fragmentation patterns. Thus, untargeted lipidomics experiments can support lipid identification at different levels of structural assignment with high-resolution MS spectra providing only elemental composition and thus the putative bulk composition of the lipid (for example, PC 36:4), but with additional MS/MS information supporting the identification of lipids at molecular species levels (for example, PC 16:0\_20:4). Although this is possible by manually checking MS and corresponding MS/MS spectra, lipid identification requires automated solutions to support analysis throughput, as within commonly used LC-MS/MS DDA setups, thousands of individual MS/MS spectra are generated within a single analysis.

Owing to the high demand and popularity of untargeted lipidomics workflows, numerous tools have been developed to support this area. Thus, the section of the interactive chart for untargeted

**Table 1 | The list of tools covered by the interactive LIPID MAP Lipidomics Tools Guide assigned with the corresponding task**

Task	Tool	URL	Video tutorial	Reference
1	LIPID MAPS Structure Database	<a href="https://lipidmaps.org/resources/databases/index.php?tab=lmsd">https://lipidmaps.org/resources/databases/index.php?tab=lmsd</a>	<a href="https://youtu.be/WNxsatndc2E">https://youtu.be/WNxsatndc2E</a>	22
1	LIPID MAPS Computationally generated Bulk Lipids (COMP_DB)	<a href="https://lipidmaps.org/resources/databases/index.php?tab=comp_db">https://lipidmaps.org/resources/databases/index.php?tab=comp_db</a>	<a href="https://youtu.be/WNxsatndc2E">https://youtu.be/WNxsatndc2E</a>	22
1	LIPID MAPS Lipidomic Ion Mobility Database	<a href="https://lipidmaps.org/resources/databases/index.php?tab=ion_mobility">https://lipidmaps.org/resources/databases/index.php?tab=ion_mobility</a>	<a href="https://youtu.be/WNxsatndc2E">https://youtu.be/WNxsatndc2E</a>	22
1	LIPID MAPS In-Silico Structure Database (LMISSD)	<a href="https://lipidmaps.org/resources/databases/index.php?tab=lmissd&amp;intro=full">https://lipidmaps.org/resources/databases/index.php?tab=lmissd&amp;intro=full</a>	<a href="https://youtu.be/WNxsatndc2E">https://youtu.be/WNxsatndc2E</a>	22
1	SwissLipids Knowledgebase	<a href="http://www.swisslipids.org/">http://www.swisslipids.org/</a>		31
2	Metabolomics Workbench	<a href="https://metabolomicsworkbench.org">https://metabolomicsworkbench.org</a>		40
2	MetaboLights	<a href="https://www.ebi.ac.uk/metabolights/">https://www.ebi.ac.uk/metabolights/</a>		41
3	LipidCreator	<a href="https://lifs-tools.org/lipidcreator.html">https://lifs-tools.org/lipidcreator.html</a>	<a href="https://youtu.be/1QjcFTah1YI">https://youtu.be/1QjcFTah1YI</a>	44
3	METLIN-MRM/XCMS-MRM	<a href="http://metlin.scripps.edu/">http://metlin.scripps.edu/</a>		45
4.1, 4.2, 4.5, 5 and 6	Lipid Data Analyzer (LDA)	<a href="http://genome.tugraz.at/lda2/lda_description.shtml">http://genome.tugraz.at/lda2/lda_description.shtml</a>	<a href="https://youtu.be/GiKM-urfNIg">https://youtu.be/GiKM-urfNIg</a>	51
4.1	LipidFinder	<a href="https://lipidmaps.org/resources/tools/lipidfinder/">https://lipidmaps.org/resources/tools/lipidfinder/</a>	<a href="https://youtu.be/UHLht5FKo1IE">https://youtu.be/UHLht5FKo1IE</a>	48
4.1, 4.2, 4.3, 4.5, 5 and 6	MS-DIAL	<a href="http://prime.psc.riken.jp/compms/msdial/main.html">http://prime.psc.riken.jp/compms/msdial/main.html</a>	<a href="https://youtu.be/ozowb75vHXc">https://youtu.be/ozowb75vHXc</a>	49
4.1, 5 and 6	XCMS_online	<a href="https://xcmsonline.scripps.edu/">https://xcmsonline.scripps.edu/</a>	<a href="https://youtu.be/D9vBMw78_qI">https://youtu.be/D9vBMw78_qI</a>	50
4.2	LipidHunter2	<a href="https://github.com/SysMedOs/lipidhunter/releases">https://github.com/SysMedOs/lipidhunter/releases</a>		53
4.2	LipidXplorer	<a href="https://lifs-tools.org/lipidxplorer">https://lifs-tools.org/lipidxplorer</a>	<a href="https://cloud.mpi-cbg.de/index.php/s/cAOv62Gwy2YXvHw">https://cloud.mpi-cbg.de/index.php/s/cAOv62Gwy2YXvHw</a>	54
4.2, 4.3, 4.4, 4.5, 5, 6 and 7.3	Lipostar2.0	<a href="https://www.moldiscovery.com/software/lipostar/">https://www.moldiscovery.com/software/lipostar/</a>		55
4.2, 5 and 6	MZmine	<a href="http://www.mzmine.org">www.mzmine.org</a>	<a href="https://youtu.be/vRSh4GmnrH8">https://youtu.be/vRSh4GmnrH8</a>	56
4.5	LPptiger	<a href="https://github.com/SysMedOs/lpptiger/releases/">https://github.com/SysMedOs/lpptiger/releases/</a>	<a href="https://youtu.be/OeRkO9RzT3c">https://youtu.be/OeRkO9RzT3c</a>	60
6	LIPID MAPS Statistical Analysis Tools	<a href="https://lipidmaps.org/data/stats/">https://lipidmaps.org/data/stats/</a>		77
6	MetaboAnalyst 5.0	<a href="https://www.metaboanalyst.ca">https://www.metaboanalyst.ca</a>		78
7.1	BridgeDb	<a href="https://bridgedb.github.io/">https://bridgedb.github.io/</a>		82
7.1	Goslin	<a href="https://lifs-tools.org/goslin.html">https://lifs-tools.org/goslin.html</a>		80
7.1	LipidLynxX	<a href="http://www.lipidmaps.org/lipidlynxx/">http://www.lipidmaps.org/lipidlynxx/</a>	<a href="https://youtu.be/6WBzzgiAyLc">https://youtu.be/6WBzzgiAyLc</a>	81
7.1	RefMet	<a href="https://www.metabolomicsworkbench.org/databases/refmet/">https://www.metabolomicsworkbench.org/databases/refmet/</a>		42
7.2	LION/web	<a href="http://www.lipidontology.com/">http://www.lipidontology.com/</a>	<a href="https://youtu.be/KkO5mUJu-8g">https://youtu.be/KkO5mUJu-8g</a>	16
7.2	Lipid Mini-On	<a href="https://omicstools.pnnl.gov/shiny/lipid-mini-on/">https://omicstools.pnnl.gov/shiny/lipid-mini-on/</a>		83
7.3	BioPAN	<a href="https://lipidmaps.org/biopan">https://lipidmaps.org/biopan</a>	<a href="https://youtu.be/3OrjRzbCB04">https://youtu.be/3OrjRzbCB04</a>	84
7.3	WikiPathways (lipid portal)	<a href="https://www.wikipathways.org/index.php/Portal:Lipids">https://www.wikipathways.org/index.php/Portal:Lipids</a>	<a href="https://www.youtube.com/playlist?list=PL-Z5Z7-ljMwb2wBi3yL5wvB3nG7-ewYK-">https://www.youtube.com/playlist?list=PL-Z5Z7-ljMwb2wBi3yL5wvB3nG7-ewYK-</a>	26

URL, links to video tutorials (when available) and reference are provided for each tool.

lipidomics is represented by nine software tools with open access for academic users. By clicking on the corresponding ‘Task specific information’ tabs, users can get familiar with the tools which support specific acquisition strategies only versus other tools which cover larger application areas. To support the selection of the optimal identification tool, the user can select between high-resolution MS applications (Lipid Data Analyzer (LDA)<sup>47</sup>, LipidFinder<sup>48</sup>, MS-DIAL<sup>49</sup>, XCMS online<sup>50</sup>), DDA (LDA<sup>51,52</sup>, MS-DIAL, LipidHunter2<sup>53</sup>, LipidXplorer<sup>54</sup>, Lipostar2<sup>55</sup>, and MZmine<sup>56–58</sup>), DIA (MS-DIAL and Lipostar2), and even datasets acquired using ion mobility methods, which provide orthogonal to LC–MS/

MS separation (MS-DIAL, MZmine, Lipostar2). Furthermore, analysis of epilipidomics datasets focusing on the identification of oxidized lipids can be supported by LDA<sup>59</sup>, Lipostar2, LPptiger<sup>60</sup>, and MS-DIAL tools. For each particular application listed above, the ‘Task specific information’ tab provides information about the main principles of operation and scoring, and accuracy measures.

### Lipid quantification from untargeted lipidomics datasets

The quantification of lipids provides their abundance (relative or absolute) in a biological sample, enabling comparison with other samples.

Quantified values aid harmonization across lipidomics datasets. Quantitative analysis can be performed using data acquired from targeted and untargeted approaches regardless of whether they were acquired using Full-MS, DDA, or DIA modes. Untargeted lipidomics quantification can be subdivided into relative (for example, fold change between condition 1 and condition 2) and semi-absolute (for example, expressed in pmol  $\mu\text{g}^{-1}$  of proteins). Owing to the extremely large diversity of lipid structures in natural lipidomes and relatively limited numbers of commercially available lipid standards, it is not feasible to perform absolute quantification at a true lipidome level<sup>61,62</sup>. On the other hand, owing to the close similarity in ionization and MS behavior of lipids from the same subclass, the use of one or a small number of internal standards per subclass is currently considered as a compromise. Isotopic correction algorithms can be used during data processing to minimize the effect of structural differences between internal standards and individual lipid molecular species<sup>63</sup>. Lipids present a particular challenge for accurate identification since there will be several hundreds of lipids distributed over a relatively narrow  $m/z$  range (for example, from 400 to 900  $m/z$ ), as well as a high number of isobaric and even isomeric species. Additionally, lipids are detected over a large dynamic range of concentrations in natural lipidomes. These issues result in significant challenges for accurate peak assignment and integration and downstream accurate quantification<sup>62</sup>. Tools for processing quantitative lipidomics datasets have benefited from previously developed software solutions designed for quantitative proteomics and metabolomics. However, owing to the special properties of lipids as outlined above, additional optimizations are necessary to ensure the accuracy of lipidomics data processing. For instance, data normalization using a preconfigured set of internal standards (for example, Lipostar2 and MS-DIAL) is introduced to simplify the normalization process and reduce the post-processing of the data matrix. Additionally, robust peak picking and peak boundary selection algorithms are critical for obtaining accurate peak areas for quantitative analysis. Though several robust peak picking algorithms are available, manual adjustment and re-integration is often required because of the high number of isobaric and isomeric species. Additional features integrated within data processing tools such as peak alignment and deconvolution are important to handle lipid species with multiple adducts types and to process DIA datasets. Current available quantification tools such as LDA, Lipostar2, MS-DIAL, MZmine, and XCMS online generally provide integrated pipelines from lipid identification up to quantification including essential normalization functions. For each tool, the 'Task specific information' section within the LIPID MAPS Lipidomics Tools Guide displays multiple features to guide the choice of the tool on the basis of user requirements, including details on quantification methods and accuracy measures.

### Statistical analysis and visualization of lipidomics datasets

Lipidomics research generates large datasets, and the complexity of experimental design is also increasing. Therefore, a critical bottleneck in lipidomics data processing is often the statistical analysis, which requires extensive use of tailored approaches that take into account the specific characteristics of lipid data. Different methods are available for the analysis of lipidomics data, each one with its own advantages and pitfalls. The choice of statistical methods to be applied should be first guided by the aim of the lipidomic study. When testing for statistical significance between predefined groups is desired (for example, health versus disease), differences between groups of samples are usually evaluated by applying parametric (for example,  $t$ -test, ANOVA) or non-parametric (for example, Wilcoxon signed-rank test, Kruskal–Wallis) statistical hypothesis tests<sup>64</sup>. With thousands of lipids being considered in some lipidomics experiments, the high number of variables increases the chance to find spurious correlated variables (false positives). Therefore, correction for multiple comparison testing is required. In addition, in lipidomics, variables (lipids) are usually not

all truly independent (for example, one lipid can be represented by several ions or adducts), meaning that corrections commonly applied for genomics/transcriptomics, such as Bonferroni or Benjamini–Hochberg can significantly overcorrect. Here, softer corrections, such as sequential goodness of fit, represent an alternative that may be more appropriate<sup>65</sup>.

Another consideration is that detected features might not always follow a normal distribution<sup>66</sup>. Thus, multivariate statistical approaches, in which all the variables are considered simultaneously, often by assuming they are correlated and not fully independent, are extensively applied in lipidomics. For explorative purposes, principal component analysis (PCA)<sup>67</sup> represents the most widely used approach in omics, including lipidomics<sup>68</sup>. Using PCA, the original dataset is represented in a lower-dimensional subspace that maintains most of the relevant information (variance). Being an unsupervised method, PCA does not require a priori knowledge of the dataset and can be used not only to explore clusters of samples eventually formed but also for interpretation without imposing any information on classification or cluster association. Hierarchical or non-hierarchical clustering methods aim at grouping samples by similarity, which is measured utilizing statistical distances or similarities between samples<sup>69</sup>. Supervised regression algorithms for dimensionality reduction, such as linear discriminant analysis<sup>70,71</sup> or partial least squares discriminant analysis<sup>72,73</sup>, are also available to evaluate and classify sample identity. In addition to partial least squares methods, other machine learning approaches have been also used in lipidomics applications. Among them, supervised methods like support vector machine<sup>74</sup> and random forest<sup>75</sup> were used for classification purposes and can also be used for feature selection. Despite the wide availability of statistical tools applied to lipidomics, several potential issues need to be considered. For example, in large studies, the so-called 'batch effect' can hamper statistical analysis, and correction with internal standards and/or quality controls must be made before the application of statistical tools. Also, missing data, which are the result of molecule concentrations below detection limits and very common in lipidomics, can be detrimental in model generation and interpretation, with some tools more sensitive than others<sup>68</sup>. Nevertheless, several strategies for missing data imputation have been proposed<sup>76</sup>.

Generally, the multi-functional tools described above for quantitative lipidomics all provide integrated platforms for statistical analysis and data visualization (LDA, Lipostar2, MS-DIAL, MZmine, and XCMS online). Additionally, several tools were specifically developed to support chemometrics analysis and result visualization of metabolomics and lipidomics data (LIPID MAPS Statistical Analysis Tools<sup>77</sup> and MetaboAnalyst 5.0<sup>78</sup>). Integrated statistical analysis and visualization functions provide easy access to most common functions, including univariate (parametric and non-parametric testing) as well as multivariate (non-supervised and supervised) solutions with a close interactive connection to the corresponding lipid quantification data matrix and often bundled with data pretreatments including normalization, scaling, and visualization of filtered data subset. Dedicated tools (LIPID MAPS Statistical Analysis Tools and MetaboAnalyst 5.0) might require researchers to transform the quantification data according to specific templates for dataset import but can provide a more extensive set of statistical and visualization functions with detailed customizable configurations. MetaboAnalyst 5.0, for instance, has a dedicated utility for batch-effect correction, which contains nine methods well established in the field of metabolomics as well as eight methods for missing value imputation<sup>79</sup>.

### Data integration solutions

The ultimate aim of many lipidomics studies is to investigate biological relevance and mechanisms behind lipidome remodeling driven by the specific biological conditions. Considering the nature of 'big data' produced by lipidomics experiments, manual evaluation of the biological



significance of obtained results would be extremely time consuming and require extensive knowledge in diverse areas of biochemistry and cell biology. Such advanced data integration goes well beyond single lipidomics data matrices and extends into related multiomics approaches using curated pathways or network analysis strategies. The combination and utilization of multiomics data from different sources require sophisticated data pretreatments, including manual curation and advanced bioinformatics solutions. This type of workflow can be generally divided into three steps: conversion of lipid annotations to their corresponding IDs within knowledge and ontology databases, lipid ontology enrichment, and advanced pathway/network analysis.

Tools that are capable of bridging lipid annotations supported by purely lipidomics software with the structural or functional IDs in data integration tools provide the first critical step towards systems biology integration of lipidomics datasets. To reduce the complexity of ID cross-validation and database queries, several tools are available to assist this conversion (Goslin<sup>80</sup>, LipidLynxX<sup>81</sup>, and RefMet<sup>42</sup>) and to link lipid identifiers to various databases (BridgeDb<sup>82</sup>, Goslin, LipidLynxX, and RefMet). For example, BridgeDb has mappings to other databases for almost 19,000 LIPID MAPS identifiers (<https://doi.org/10.6084/m9.figshare.13550384.v1>).

Biological interpretation of lipidomics data is often driven by the focus on individual lipids. Although this approach is useful in biomarker discovery, it obscures the possible effects of shared properties of molecules related to the biological phenomenon. A way to circumvent this is to manually curate lipid groups that share specific properties (for example, lipid class, level of unsaturation) and report aggregate statistics. However, the manual construction of these groups is often laborious owing to the ambiguity in lipid nomenclature and introduces a risk of cherry-picking. Ontologies, formalizations of concepts, and their relations have been successful in other omics fields to provide frameworks for constructing groups of molecules with shared biological properties. For lipidomics data, several ontologies, such as lipid ontology (LION/Web)<sup>16</sup> and Lipid Mini-On<sup>83</sup>, are useful in aiding in the biological interpretation. Currently, LION links over 50,000 lipids to chemical (for example, LIPID MAPS classification and fatty acid associations), physicochemical (for example, membrane fluidity and intrinsic curvature), and cell biological (for example, predominant subcellular localization) properties and Lipid Mini-On uses a text mining strategy to attribute Lipid Ontology structural terms to lipids.

Typically, ontology-derived groups of molecules ('terms') are analyzed using enrichment analysis approaches. In these analyses, a given term is enriched if the molecules belonging to the term are overrepresented in a target list or are higher ranked in a list of molecules ordered by a statistic (for example, fold change and *P* value) than expected by chance. Both LION/web and Lipid Mini-On are freely available online tools that perform ontology-term enrichment analysis of user-provided lipidomics data. LION/web allows specific LION-term categories to be included for analysis. After submission, LION/web reports descriptive matching statistics and enrichment analysis, as well as publication-ready figures. Traditionally, enrichment analyses compare two groups of samples. To analyze datasets with more sample groups, LION/web was recently expanded with the PCA-LION heat map module. This module generates a heat map showing the most dynamic LION-terms for all samples on the basis of the enrichment analysis of a given number of principle components. Lipid IDs of significantly enriched terms can be further mapped to available pathways and networks to investigate the changes at the systems level. Lipid Mini-On enables to generate a variety of visualization of lipid enrichment by structural characteristics. Lipids and their associated lipid ontology terms can be visualized as a network to hierarchize interpretations of the enrichment performed.

Several tools are available to support pathway and network analysis of lipidomics datasets, including integrated pathway graph analysis modules in Lipostar2 and stand-alone web application BioPAN<sup>84</sup>,

which allows the visualization of quantitative lipidomics data in the context of known biosynthetic pathways, as well as the central hub of community-driven pathways represented by the Lipid Portal on WikiPathways<sup>26</sup>, in collaboration with LIPID MAPS. Though more advanced analysis can be performed with highly customized programs and scripts by experienced bioinformaticians, these tools provide simple interfaces for researchers to begin to map lipidomics data to obtain essential lipid centric analysis results from predefined pathways and networks in, for example, PathVisio<sup>85</sup> and Cytoscape<sup>86</sup>. Furthermore, the pathways from WikiPathways can be easily converted to a network through the WikiPathways App<sup>87</sup>, after which these networks can be extended with additional knowledge such as micro RNAs, transcription factors, or drugs through the CyTargetLinker<sup>88</sup> app.

## Conclusion

Lipidomics is a fast-growing field that is increasingly supporting the analysis of ever larger datasets of high complexity. To assist with high-throughput data processing, many new software tools have been developed by academic researchers and are now openly available on developers' websites. To guide the user and provide a point of contact for finding these tools, in this review, we provide detailed specifications on the most widely used software packages for lipidomics along with a complementary interactive Lipidomics Tools Guide available on LIPID MAPS. Two tutorials are provided as Supplementary Notes to exemplify the interoperability of the Guide and how to combine different tools for targeted and untargeted lipidomics experiments. This portal can help researchers to construct a complete lipidomics data analysis workflow starting with lipid identification and quantification till advanced visualization and data integration using open-access software solutions with the clickable graphical user interface. The Lipidomics Tools Guide will be regularly reviewed and updated to reflect new developments in the field as well as continuous support for the listed tools. Moreover, the Guide can be updated upon request by authors of the software within the scope of this resource. The LIPID MAPS interactive Lipidomics Tools Guide ([https://www.lipidmaps.org/resources/tools?page=flow\\_chart](https://www.lipidmaps.org/resources/tools?page=flow_chart)) summarizes essential information about each tool to assist beginners in lipidomics as well as advanced data scientists in selecting the most suitable tool for each of the steps in the processing of MS-derived lipidomics data.

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## Author contributions

The manuscript was written with contributions from all authors who have given approval to the final version of the manuscript. M.F. and V.B.O. conceived the original idea and supervised the project. Z.N., M.F., and V.B.O. contributed to review of the tools and data collection. M.F., Z.N. and M.W. contributed to figures. M.W. designed and tested the workflows and tutorials. G.J., K.M.E., and R.An. developed the website with the help from Z.N. and M.F. Software developers Z.N., R.Ah., L.A., J.A.J., S.A., A.B., G.C.C., M.J.C., E.F., C.G., L.G., J.H., N.H., D.K., A.K., A.F.L., A.M., J.M.A., M.R.M., C.O., T.P., A.S., D.S., G.S., M.K., H.T., E.L.W., and J.X. contributed to sections on software tools in both the manuscript and website.

## Competing interests

A.K. is employed at Bruker Daltonics GmbH & Co. KG, Bremen, Germany. Other authors declare no competing interests.

## Additional information

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