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Draft a mini review about the relevance of lipidomics analysis in dermatologic



### The Relevance of Lipidomics Ana **Dermatological Research**

### Introduction

Lipidomics, the comprehensive study of lipid profiles, has emerged as a pivotal to including ceramides, cholesterol, and fatty acids, play essential roles in maintainir Dysregulation of these lipids is linked to various skin disorders, such as atopic de advanced analytical techniques like mass spectrometry, lipidomics enables precis anatomical sites, depths, and individuals. This mini review explores the methodological applications of lipidomics, highlighting its transformative potential in understand

### Analytical Methods and Technologies in Skin Lipide

Shotgun mass spectrometry is a cornerstone of high-throughput skin lipidomic sebaceous and stratum corneum lipids. This technique involves direct infusion o without prior chromatographic separation, allowing rapid acquisition of complex as the QExactive mass spectrometer, are essential for resolving overlapping signa lipid species, including ceramides, cholesterol, and triacylglycerols In Sadowski, 2017

The advantages of shotgun lipidomics include broad lipid coverage, absolute qua unprecedented throughput, which is critical for large-scale studies and clinical ap been used to analyze over 268 skin samples, revealing depth-dependent lipid gra

M Sadowski, 2017 p2; M Sadowski, 2017 p8. Additionally, tape-stripping combined v



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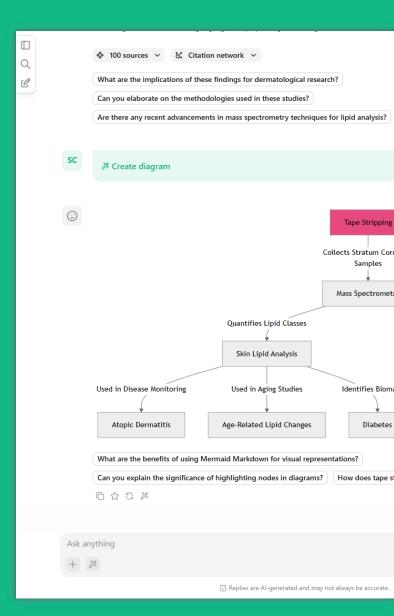
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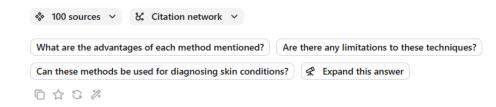


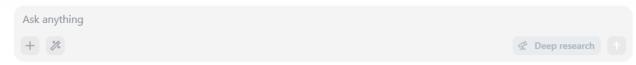
Several non-invasive methods are available for quantifying different lipid classes in the skin:

- Tape Stripping Combined with Mass Spectrometry: Tape stripping collects stratum corneum samples, which can be
  analyzed using high-throughput shotgun mass spectrometry to quantify up to 16 lipid classes, including sebaceous
  and stratum corneum lipids Sadowski, 2017.
- Cyanoacrylate Stripping and Thin-Layer Chromatography: Cyanoacrylate stripping collects skin surface lipids, which
  are then separated and quantified using high-performance thin-layer chromatography and densitometric methods
  Röpke, 1996.
- 3. Raman Microspectroscopy: This technique provides in vivo analysis of lipid content, conformation, and organization in the stratum corneum, offering insights into lipid-protein ratios and skin barrier function Verzeaux, 2018.
- Short-Wave Infrared (SWIR) Spectroscopy: SWIR spectroscopy, combined with tape stripping, enables depth profiling
  of lipids and water in the stratum corneum, with high sensitivity and specificity compared to other methods

   Ezerskaia, 2018
- Skin Surface Lipid RNA Analysis: Lipids collected from skin surface can also be analyzed for RNA content, providing
  molecular insights into lipid synthesis and skin conditions Shima, 2022.

These methods vary in their focus, from lipid quantification to molecular profiling, and are suitable for different research and clinical applications.



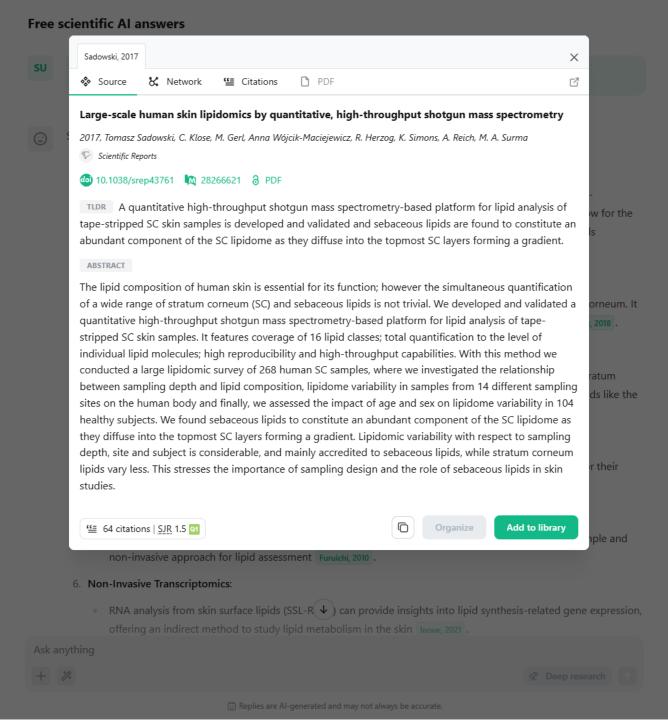




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Create a table with further papers that made use of mass spectrometry-based quantification of skin lipids.



Here is a table summarizing studies that utilized mass spectrometry for quantification of skin lipids:

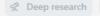
Study	Methodology	Key Findings	Link
Sadowski, 2017	High-throughput shotgun mass spectrometry	Quantified 16 lipid classes in stratum corneum samples; analyzed lipid variability by sampling depth, site, age, and sex	M\ Sadowski, 2017
Kendall, 2018	Various mass spectrometry approaches	Explored targeted and untargeted lipidomics, including imaging techniques for anatomical lipid distribution	Kendall, 2018
Li, 2016	Lipidomics profiling	Investigated lipid alterations in inflammatory skin diseases like atopic dermatitis and psoriasis	Li, 2016
Sjövall, 2018	Time-of-flight secondary ion mass spectrometry (ToF-SIMS)	Imaged spatial distribution of lipids and topically applied compounds in skin layers	Sjövall, 2018
Michael- Jubeli, 2011	High-temperature gas chromatography-mass spectrometry	Profiled skin surface lipids, identifying over 200 compounds in a single run	Michael-Jubeli, 2011
Li, 2022	UPLC-QTOF-MS	Identified sphingolipids as potential biomarkers for type 2 diabetes through skin lipid analysis	Li, 2022
Chen, 2023	UPLC-QTOF-MS	Explored lipid differences in hand skin surface among females of different ages	Chen, 2023
Yang, 2021	UPLC-QTOF-MS	Analyzed lipid alterations in pregnant women, revealing weakened skin barrier function	Yang, 2021
Mitchell, 2015	MALDI-MS imaging	Studied lipid distribution in living skin equivalents during development and maturation	Mitchell, 2015

These studies highlight the versatility of mass spectrometry techniques in analyzing skin lipids for various applications, including disease monitoring, aging, and physiological changes.

Ask anything









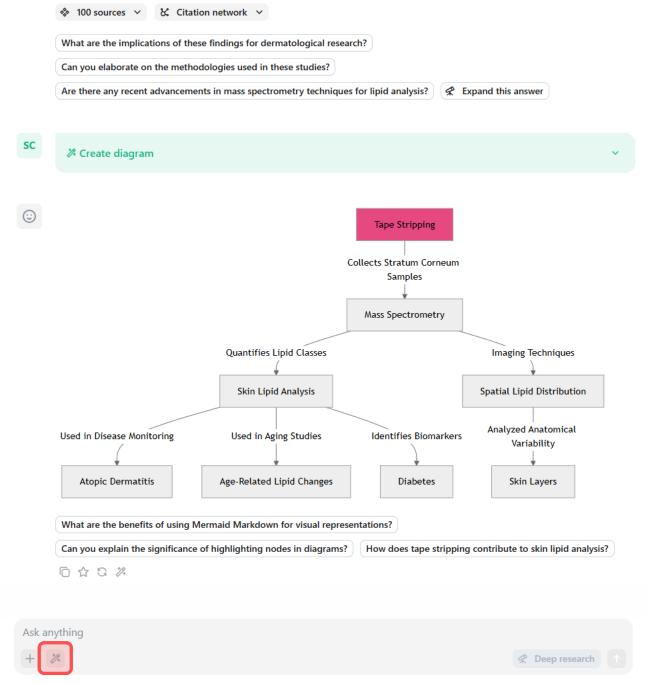


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Provide a comprehensive overview about mass spectrometry-based lipid analysis in dermatology research.

### Mass Spectrometry-Based Lipid Analysis in Dermatology Research

### Introduction

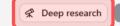
Mass spectrometry-based lipid analysis has become a cornerstone in dermatology research, offering unparalleled insights into the complex lipid compositions of skin. Lipids play critical roles in maintaining the epidermal barrier, regulating hydration, and modulating inflammation, making their study essential for understanding skin health and disease. Advances in lipidomics, driven by techniques like electrospray ionization (ESI) and matrix-assisted laser desorption ionization (MALDI), have enabled precise quantification and spatial mapping of lipids. This report explores the transformative impact of these methodologies on dermatological research, highlighting their potential to uncover biomarkers, elucidate disease mechanisms, and inform therapeutic strategies.

### **Mass Spectrometry Techniques for Lipid Analysis**

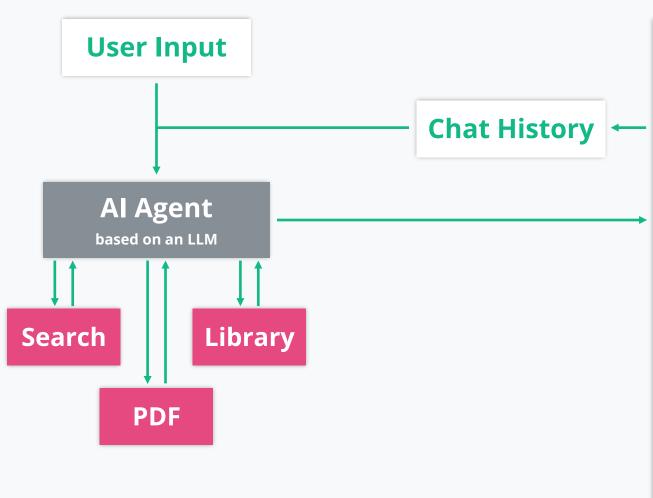
Electrospray ionization (ESI) has revolutionized lipidomics by enabling highly sensitive and precise quantification of lipid species. ESI operates by ionizing lipids directly from biological extracts, allowing for the analysis of complex lipid mixtures without extensive sample preparation. Advances in ESI have improved ionization efficiency and reduced matrix effects, particularly through the use of internal standards and chemical modifiers, which enhance the accuracy of lipid quantification ( Yang, 2011 ; Wang, 2017 ). Direct infusion methods, combined with tandem mass spectrometry, further streamline lipid profiling, enabling rapid and comprehensive analysis of lipid compositions ( Brügger, 2014 ).

Matrix-assisted laser desorption ionization (MALDI) complements ESI by providing spatial resolution of lipid distributions in tissues. MALDI imaging mass spectrometry (IMS) has been instrumental in dermatology research, revealing lipid

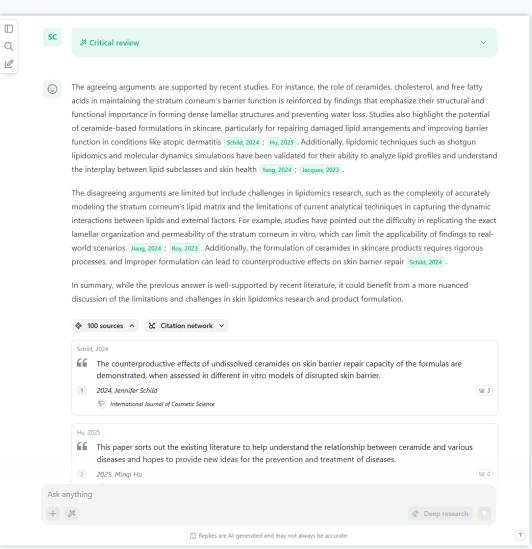




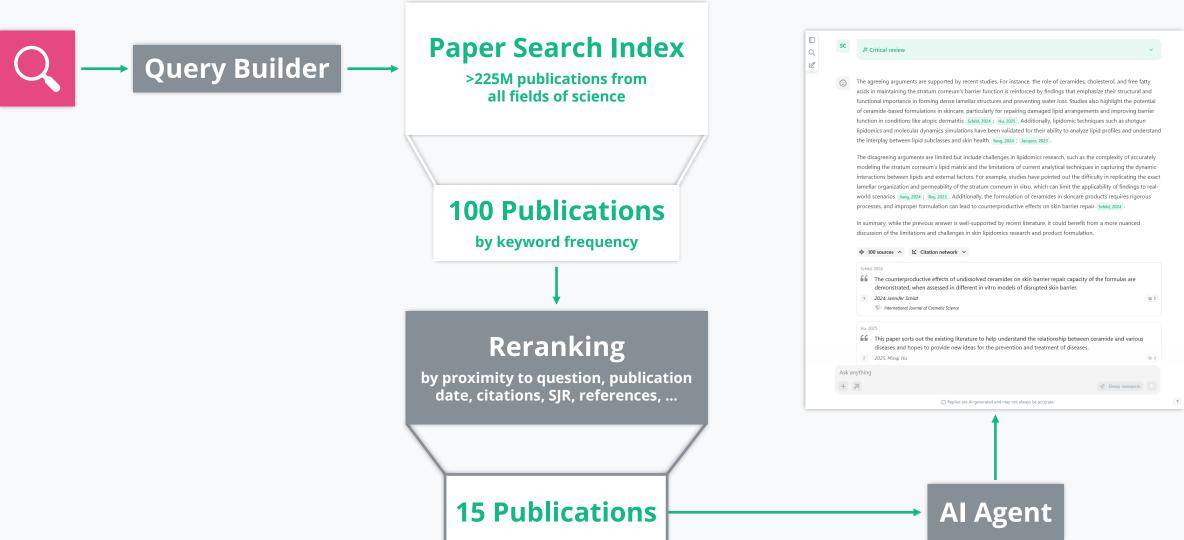
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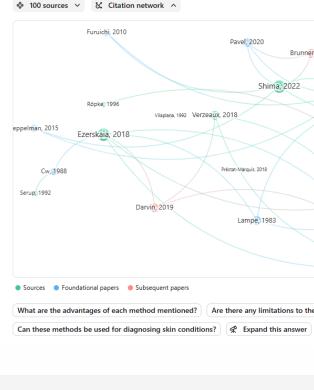
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- Skin Surface Lipid RNA Analysis: Lipids collected from skin surface can also molecular insights into lipid synthesis and skin conditions Shima, 2022.

These methods vary in their focus, from lipid quantification to molecular profiling and clinical applications.



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Which non-invasive methods allow for quantification of different lipid classes in the skin?

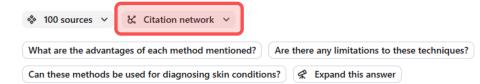


Several non-invasive methods are available for quantifying different lipid classes in the skin:

- Cyanoacrylate Stripping and Thin-Layer Chromatography: Cyanoacrylate stripping collects skin surface lipids, which
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These methods vary in their focus, from lipid quantification to molecular profiling, and are suitable for different research and clinical applications.









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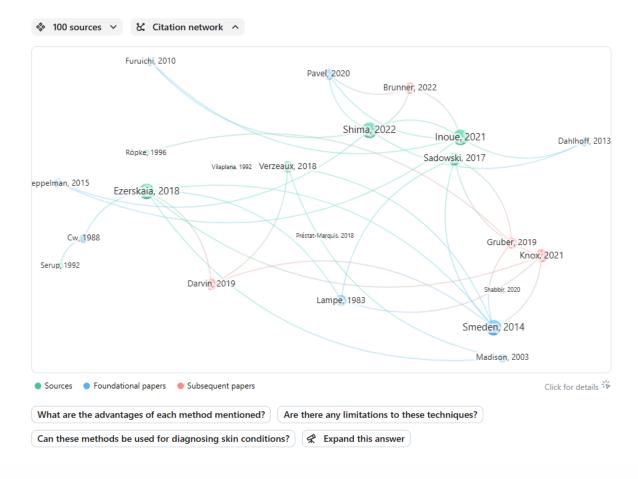
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- of lipids and water in the stratum corneum, with high sensitivity and specificity compared to other methods

  Ezerskaia, 2018.
- 5. **Skin Surface Lipid RNA Analysis**: Lipids collected from skin surface can also be analyzed for RNA content, providing molecular insights into lipid synthesis and skin conditions Shima, 2022.

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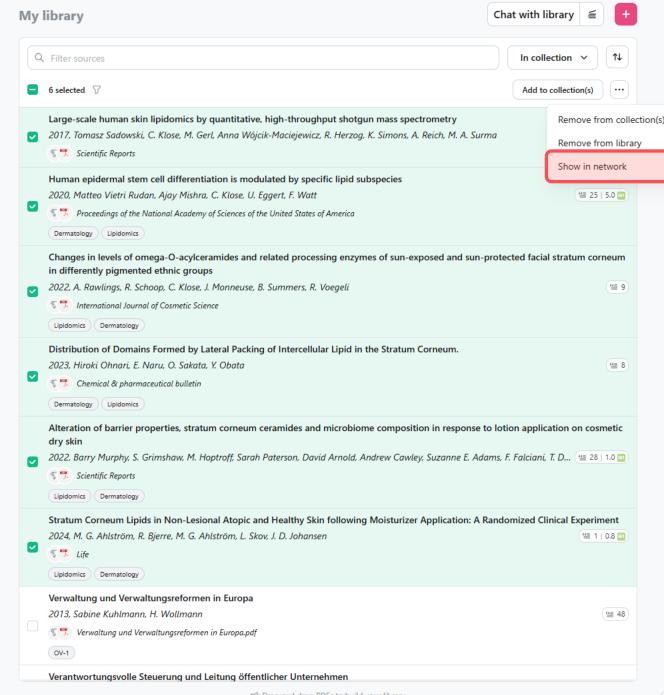


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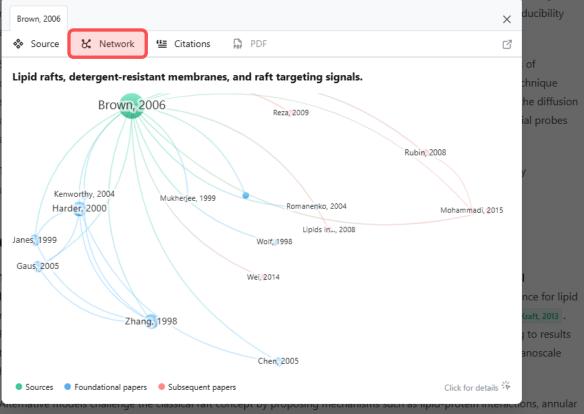


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rafts in nonionic detergents like Triton X-100, followed by density gradient centrifugation. While this method identifies cholesterol- and sphingolipid-rich domains, it often disrupts native membrane structures, leading to artifacts that may not



lipid shells, and mesoscale domains. These models emphasize the role of active cellular processes and cytoskeletal interactions in membrane organization, rather than passive lipid-driven segregation Mayor, 2004. For instance, studies show that sphingolipid domains depend on cytoskeletal support rather than cholesterol interactions, contradicting key aspects of the raft hypothesis Kraft, 2017. Additionally, dynamic nanoclusters regulated by actin cytoskeleton have been proposed as a more accurate representation of membrane compartmentalization Plowman, 2005.

These findings suggest that plasma membrane organization is more complex and dynamic than the lipid raft hypothesis alone can explain, necessitating a broader framework to integrate emerging evidence.





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5

rafts in nonionic detergents like Triton X-100, followed by density gradient centrifugation. While this method identifies

Brown, 2006 

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### Lipid rafts, detergent-resistant membranes, and raft targeting signals.

### Supporting

Several citations support the findings of Brown (2006), emphasizing the importance of lipid rafts in cellular signaling, protein localization, and membrane dynamics. These studies validate the role of palmitoylation and other post-translational modifications in targeting proteins to lipid rafts <a href="Bhattacharyya">Bhattacharyya</a>, 2013 , Hornemann, 2015 , Sanders, 2014 , Young, 2012 . Additionally, they confirm the utility of DRMs as a tool for studying lipid raft-associated proteins, despite their limitations <a href="Domingues">Domingues</a>, 2010 , Nikolaev, 2017 , Rieke, 2011 , Xu, 2012 , Zadravec, 2010 . These citations highlight the paper's contribution to understanding the biochemical and functional properties of lipid rafts.

### Mentioning

The cited paper by Deborah A. Brown (2006) is frequently mentioned in discussions about lipid rafts and detergent-resistant membranes (DRMs). It is referenced as a foundational work in understanding the biochemical properties and functional roles of lipid rafts, particularly their resistance to detergents and their association with cholesterol and sphingolipids Agarwal, 2018, Bhaskar, 2009, Botto, 2010, Chan, 2010, Cresawn, 2007, Delint-Ramírez, 2015, Rajamanickam, 2016, Sanders, 2014, Storch, 2007, Yu, 2007. The paper is often cited in research contexts involving signal transduction, protein trafficking, and membrane organization, highlighting its relevance across various biological processes.

### ? Contrasting

Several citations contrast with Brown (2006), questioning the equivalence of DRMs to native lipid rafts and highlighting methodological artifacts associated with detergent-based isolation techniques. These studies argue that DRMs may not accurately represent the in vivo organization of lipid rafts and caution against overinterpreting results derived from DRM analysis Asano, 2009, Bauwens, 2013, Lingwood, 2010, Scholz, 2021, Sprenger, 2010, Tanner, 2011, Urbanus, 2012, Rozentsvet, 2023, Langowski, 2012, Heberle, 2017. These critiques highlight ongoing debates about the validity of DRM-based approaches and the dynamic nature of lipid rafts in

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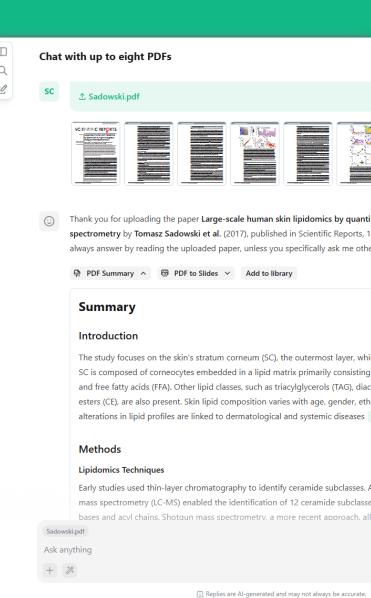
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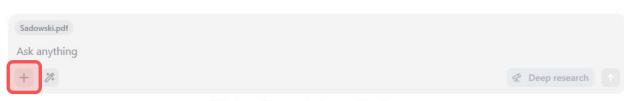




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### **Summary**

### Introduction

The study focuses on the skin's stratum corneum (SC), the outermost layer, which is critical for its barrier function. The SC is composed of corneocytes embedded in a lipid matrix primarily consisting of ceramides (Cer), cholesterol (Chol), and free fatty acids (FFA). Other lipid classes, such as triacylglycerols (TAG), diacylglycerols (DAG), and cholesterol esters (CE), are also present. Skin lipid composition varies with age, gender, ethnicity, and environmental factors, and alterations in lipid profiles are linked to dermatological and systemic diseases Sadowski, 2017 p1.

### Methods

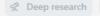
### Lipidomics Techniques

Early studies used thin-layer chromatography to identify ceramide subclasses. Advances in liquid chromatographymass spectrometry (LC-MS) enabled the identification of 12 ceramide subclasses based on combinations of sphingoid bases and acvl chains. Shotaun mass spectrometry, a more recent approach, allows high-throughput analysis but lacks

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<table-of-contents> PDF Summary 🗸 🖾 PDF to Slides 🗸

Write a brief description of the study design.

- The study by Sadowski et al. utilized a quantitative, high-throughput shotgun mass spectrometry-based platform to analyze human skin lipidomics. The design involved:
  - Sampling Method: Skin samples were collected using tape-stripping, a non-invasive method allowing control over sampling depth and reproducibility. Samples were taken from 104 subjects, including 65 females and 39 males, across 14 body sites and different depths of the stratum corneum (SC) Sadowski, 2017 p2.
  - Lipid Analysis: Lipids were extracted using methanol and analyzed via shotgun mass spectrometry, enabling absolute
    quantification of 16 lipid classes, including ceramides, cholesterol, and sebaceous lipids. Internal standards ensured
    accuracy in Sadowski, 2017 p3
  - 3. **Study Objectives**: The research investigated lipidome variability with respect to sampling depth, body site, and interindividual differences based on age and sex. Statistical analyses, including principal component analysis, were used to assess lipid profiles M Sadowski, 2017 p5.

This design enabled the largest SC lipidomic study to date, providing insights into lipid composition variability and its physiological implications.

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Lipid extraction. Lipid extraction of tape-stripping samples containing one stripping disc each and scraps biopsy samples alike was carried out in 2 mL polypropylene tubes where 900 µL of methanol including internal standards was added to each sample. The samples were shaken at 1400 rpm at 4°C for one hour. Thereafter, extracts were transferred to a multi-well plate and dried in a speed vacuum concentrator. Dried extracts were re-suspended in an acquisition mixture of 7.5 mM ammonium acetate in chloroform-methanol-propan-2-od (1:24, V-V-V). For cholesterol, the dried extract was acetylated to the dried extract was acetylated again and re-suspended in the above acquisition mixture. All liquid handling steps were performed using Hamilton Robotics STARlet robotic platform with Anti Droplet Control for pipetting of organic solvents.

MS data acquisition. Samples were analyzed by direct infusion with a QExactive mass spectrometer (Thermo Scientific) equipped with a TriVersa NanoMate ion source (Advion Biosciences) in a single acquisition for both positive and negative ion modes with a resolving power of  $R_{th^{-}}$  and  $R_{th}$  and  $R_{th}$  and  $R_{th}$  are already for MSMS. MSMS fragmentation was performed at normalized collision energy of 35% and was triggered by an inclusion list encompassing corresponding MS mass ranges' Both MS and MSMS data were combined to monitor CE, DAG and TAG ions as ammonium adducts and all ceramide sub-classes as acetate adducts. Precursor ions and confirmatory MSMS fragments as reported previously  $^{\rm MSM}$  are summarized in Supplementary Table 1. Cholesterol was identified in a separate acquisition as cholesterol-acetate after a derivatization procedure.

Lipid identification and quantification. The resolving power used allows for identification of lipids based on precursor masses<sup>21</sup>. Combining MSMS fragmentation data with the high resolution MS precursor data followed by isotopic correction (type I and II according to the strategy described previously<sup>he,22</sup>), permitted structural elucidation of lipid molecular species. It increased the identification specificity, but also made it possible to unambiguously distinguish all 12 ceramide sub-classes; including NP/AGS and NH/AGS pairs.

Internal standards used in this study were chosen not to be natively present in skin samples. Per sample 42 pmol of EOS D9 68-3;2 (18:1;2, 18:20), 18:20), 14 pmol NS D3 36:1;2 (18:1;2, 18:0;0), 50 pmol DAG D5 34:0;0 (17:0,0, 17:0,0), 100 pmol CE 20:09, 1000 pmol cholesterol D6 and 100 pmol TAG D5 51:00,0 (17:0,0, 17:1,0), 17:0,0) were delivered as internal standards. Quantification was conducted via normalization of the isotopically corrected intensity of the monoisopic peak of each native species to the isotopically corrected intensity of the monoisopic peak of the internal standard. The quantities of lipid molecular species were calculated from ratios between their respective characteristic MSMS fragments, as described previously<sup>10</sup>. Non-hydroxy and alpha-hydroxy ceramide sub-classes were normalized to deuterated NS, whereas omega-hydroxy ceramides were normalized to deuterated EOS. Quantitative lipidomic data of the study can be found in Supplementary Table 2.

Data analysis and post-processing. Data were analyzed with in-house developed lipid identification software based on LipidXplorer<sup>23,24</sup>. Only lipid identifications with measured mass deviations below 3 ppm from the theoretical mass for MS and 8 ppm for MSMS peaks in scans where lock mass was available, and 5 and 12, respectively, where it was not; signal-to-noise ratio greater than 5; and an amount at least 5-fold higher than in corresponding blank samples were considered as positive hits, yielding 862 unique lipids across all samples from all experiments. Further, unless stated otherwise, only lipids present in at least two replicates and above 2 pmo all experiments. Further, unless stated otherwise, only lipids present in at least two replicates and above 2 pmo per sample were included in subsequent data analysis, resulting in 509 unique lipids. Data visualization, linear regression (linear least squares method), and correlation (two-tailed Pearson and Spearman correlation) calculations were performed on Prism6.0h software (GraphPad Software, Inc.). Where it does not lower figure clarity, individual data points are shown<sup>25</sup>.

Statistical models were trained with the R Environment for Statistical Computing (R version 3.3.2 (2016-10-31)), by the caret package (version  $6.0-72)^{2n}$ , which in turn uses the randomForest package (version  $4.6-12)^{2r}$ . For statistical modeling only lipids present in at least 50% of samples per cohort were used. If a lipid was present in one cohort, it was also included for other cohorts, even if its occurrence rate was lower. During model training with 5 times repeated 10 times cross validation, the resampled data were preprocessed by centering and scaling, missing values were imputed with the median, and near zero variance predictors were removed.

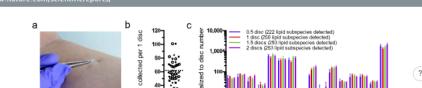
### Result

High throughput-compatible skin sampling and sample processing. In order to take advantage of the quick spectra acquisition capabilities of shotgun mass spectrometry, the sampling procedure and all other sample-handling steps were optimized for speed, throughput and convenience utilizing automation whenever possible. Automation of procedures also benefits in higher reproducibility<sup>28</sup>.

Tape-stripping was used as it was simultaneously the most convenient and non-invasive sampling method (Fig. 1a). It also had the additional advantage of allowing for control over the sampling depth (by collecting the appropriate stratum corneum layer by sequential stripping) and collecting comparable sample amounts. As surface furrows might affect the amount of material collected<sup>29</sup>, we gravimetrically determined the reproducibility of sample amount collected via tape-stripping of the second layer with one stripping disc to be 62 ± 14 µg (mean ± s.d.) (Fig. 1b). Extraction of lipids with commonly used organic solvents from a polymeric tape with adhesive (i.e. stripping disc) was complicated because established methods utilizing chloroform<sup>80,11</sup> or methyl eter-butyl ether<sup>21</sup> interfered with tape constituents, physically dissolving them. We found, however, that methanol extraction successfully used for skin lipidomics in previous studies<sup>11</sup> allowed for efficient extraction of skin lipido

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### Comparing the results of papers

Create a table to compare the results for all twelve ceramide subclasses. Sort the subclasses by alphabet.

The results for the twelve ceramide subclasses from both studies are summarized below. The table is sorted alphabetically by subclass name.

Ceramide Subclass	Observations from Ahlström et al. (2024)	Observations from Sadowski et al. (2017)
AdS	No significant difference observed between AD and controls  M Ahlström, 2024  p4 .	Included in analysis; no specific results highlighted  N Sadowski, 2017 p5 .
АН	No significant difference observed between AD and controls  M Ahlström, 2024  p4 .	Included in analysis; no specific results highlighted  Intluded in analysis; no specific results highlighted  p5 .
AP	No significant difference observed between AD and controls  M Ahlström, 2024  p4	Included in analysis; no specific results highlighted  Intluded in analysis; no specific results highlighted  Intluded in analysis; no specific results highlighted
AS	Higher levels in AD compared to controls (p = 0.011)  M Ahlström, 2024 p4 .	Included in analysis; no specific results highlighted  In Sadowski, 2017 p5 .
EOdS	No significant difference observed between AD and controls  M Ahlström, 2024  p4	Low abundance in samples; detected in deeper layers  [8] Sadowski, 2017 p4 .
EOH	No significant difference observed between AD and controls  M Ahlström, 2024 p4 .	Increased with sampling depth In Sadowski, 2017 p5
EOS	Higher relative abundance in controls compared to AD (p = 0.024) Ahlström, 2024 p4	Increased with sampling depth In Sadowski, 2017 p5
EOP	No significant difference observed between AD and controls  M Ahlström, 2024 p4 .	Included in analysis; no specific results highlighted  M Sadowski, 2017 p5 .
NH	Higher levels in AD compared to controls (p = 0.01)	Included in analysis; no specific results highlighted
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### Is this in line with other papers?



I will review the findings from other studies to determine whether they align with the results of Ahlström et al. (2024) and Sadowski et al. (2017). Please hold on.

The findings from Ahlström et al. (2024) and Sadowski et al. (2017) align with broader trends observed in other studies on ceramide subclasses in atopic dermatitis (AD) and healthy skin. Key points include:

### 1. Altered Ceramide Profiles in AD:

- Ahlström et al. reported higher levels of ceramide subclasses such as NS and NH in AD, consistent with studies showing altered ceramide profiles in AD due to immune-driven effects and skin barrier dysfunction Toncic, 2020.
   Imokawa, 2021.
- Decreased levels of ceramide EOS in AD, as noted by Ahlström et al., are also supported by findings of reduced ultra-long-chain ceramides in AD, which are critical for skin barrier integrity Bakar, 2024, Kondo, 2024.

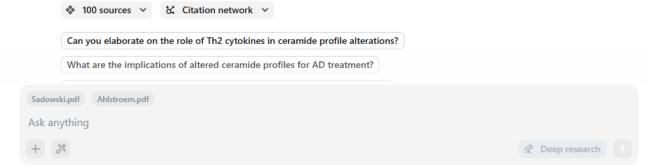
### 2. Impact of Inflammation and Cytokines:

 Studies highlight the role of Th2 cytokines in modifying ceramide profiles, particularly reducing ceramide EOS and altering ceramide NS composition, which mirrors the trends observed in Ahlström et al. Bakar, 2024, Chu, 2023.

### 3. Variability Across Studies:

 While Sadowski et al. focused on healthy skin variability, other studies emphasize the disease-specific changes in ceramide subclasses, such as increased unsaturated ceramides in AD Kondo, 2024.

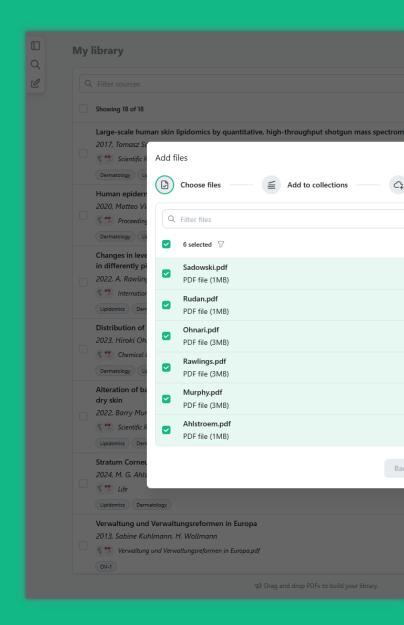
Overall, the findings from both papers are consistent with the literature, emphasizing the importance of ceramide composition in skin health and AD pathogenesis. Let me know if you'd like further details on specific studies!



HOW TO

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4 Example





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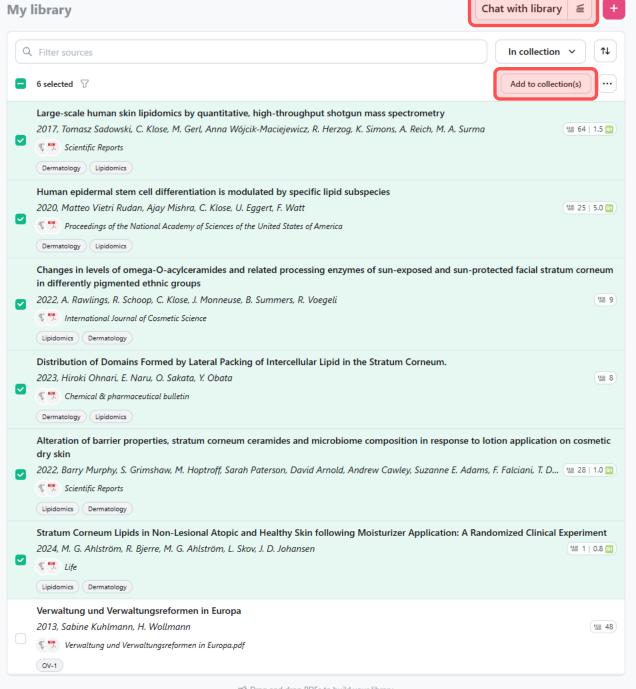


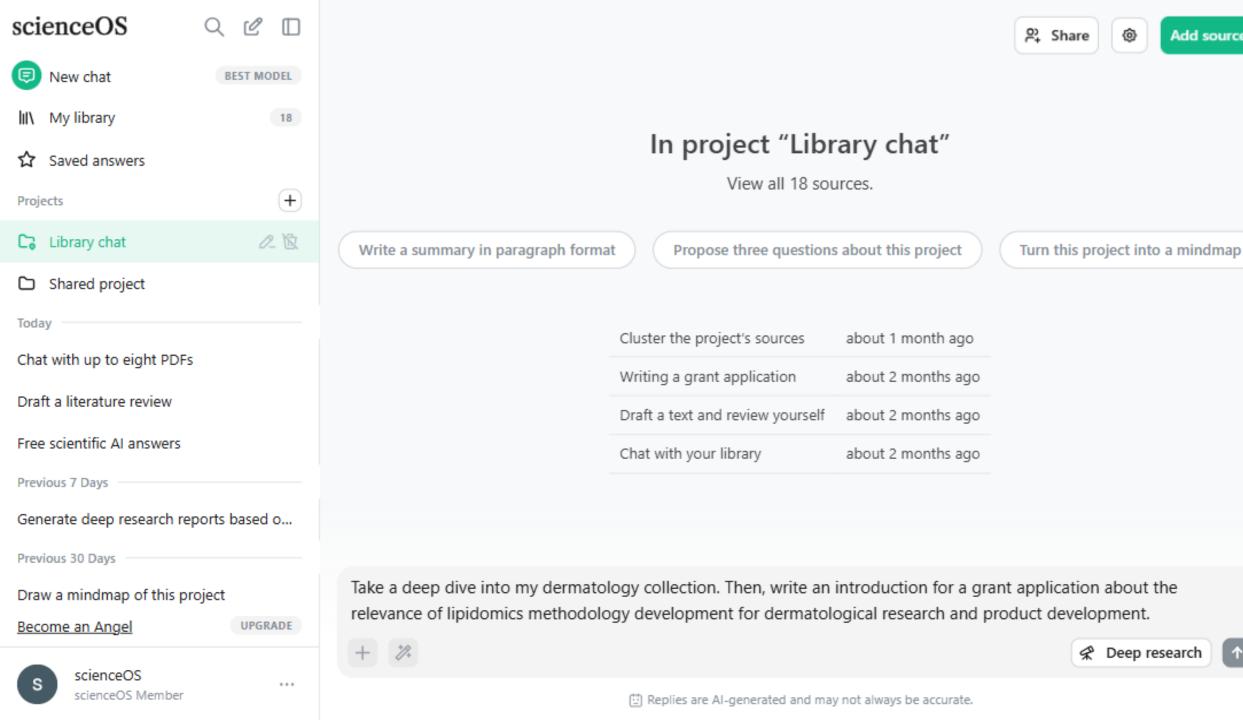
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### Writing a grant application



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Take a deep dive into my dermatology collection. Then, draft the introduction for a grant application about the relevance of lipidomics methodology development for dermatological research and product development.

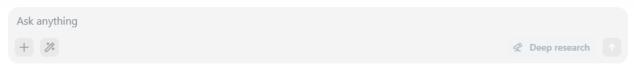
### Draft Introduction for Grant Application

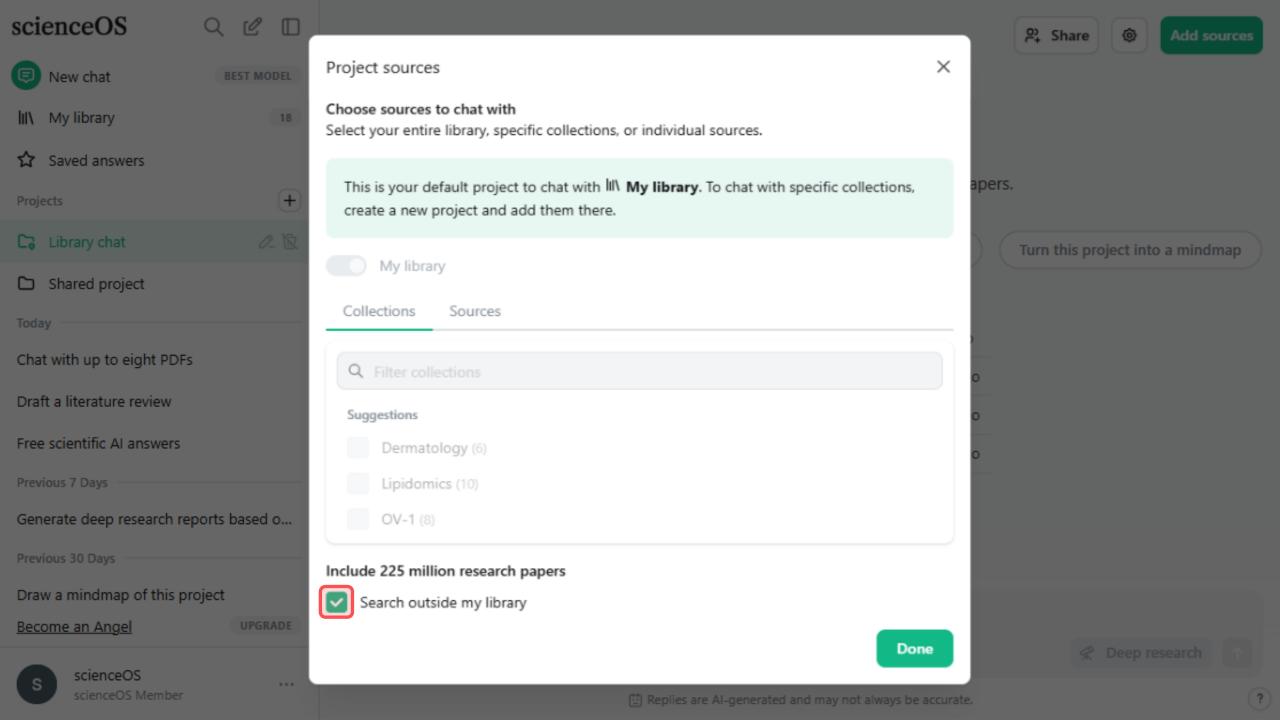
The stratum corneum (SC), the outermost layer of human skin, plays a critical role in maintaining barrier function, hydration, and protection against environmental insults. This functionality is largely governed by its lipid composition, which includes ceramides, cholesterol, and free fatty acids organized into lamellar structures. Dysregulation of these lipids is implicated in various dermatological conditions, such as atopic dermatitis, xerosis, and impaired barrier function, highlighting the need for advanced methodologies to study lipid dynamics (M) Sadowski, 2017 (p8), (M) Murphy, 2022 (p2).

Recent advances in lipidomics, particularly shotgun mass spectrometry, have enabled high-throughput, quantitative analysis of lipid species, offering unprecedented insights into their roles in skin physiology and pathology. For example, lipidomic profiling has revealed site-specific and age-related variations in lipid composition, as well as the regulatory potential of individual lipid subspecies in keratinocyte differentiation (MRudan, 2020 p3), (MSadowski, 2017 p6). Furthermore, lipidomics has demonstrated the impact of topical treatments on lipid profiles, suggesting therapeutic avenues for restoring skin barrier integrity (MAhlström, 2024 p7).

This grant proposal aims to advance lipidomics methodologies tailored for dermatological research, focusing on their application in understanding skin diseases and optimizing cosmetic and pharmaceutical product development. By integrating cutting-edge lipidomics with dermatological science, this initiative seeks to uncover novel biomarkers and therapeutic targets, ultimately enhancing skin health and treatment efficacy.









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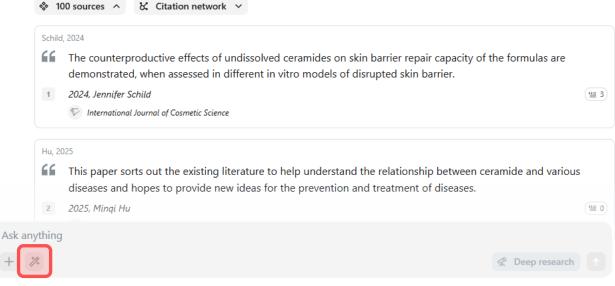
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The agreeing arguments are supported by recent studies. For instance, the role of ceramides, cholesterol, and free fatty acids in maintaining the stratum corneum's barrier function is reinforced by findings that emphasize their structural and functional importance in forming dense lamellar structures and preventing water loss. Studies also highlight the potential of ceramide-based formulations in skincare, particularly for repairing damaged lipid arrangements and improving barrier function in conditions like atopic dermatitis Schild, 2024; Hu, 2025. Additionally, lipidomic techniques such as shotgun lipidomics and molecular dynamics simulations have been validated for their ability to analyze lipid profiles and understand the interplay between lipid subclasses and skin health Yang, 2024; Jacques, 2023.

The disagreeing arguments are limited but include challenges in lipidomics research, such as the complexity of accurately modeling the stratum corneum's lipid matrix and the limitations of current analytical techniques in capturing the dynamic interactions between lipids and external factors. For example, studies have pointed out the difficulty in replicating the exact lamellar organization and permeability of the stratum corneum in vitro, which can limit the applicability of findings to real-world scenarios Jiang, 2024; Roy, 2023. Additionally, the formulation of ceramides in skincare products requires rigorous processes, and improper formulation can lead to counterproductive effects on skin barrier repair Schild, 2024.

In summary, while the previous answer is well-supported by recent literature, it could benefit from a more nuanced discussion of the limitations and challenges in skin lipidomics research and product formulation.





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5

Dermatology collection

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Draft a mini review about the relevance of lipidomics analysis in dermatological research.

### The Relevance of Lipidomics Analysis in Dermatological Research

### Introduction

Lipidomics, the comprehensive study of lipid profiles, has emerged as a pivotal tool in dermatological research. Skin lipids, including ceramides, cholesterol, and fatty acids, play essential roles in maintaining barrier function and overall skin health. Dysregulation of these lipids is linked to various skin disorders, such as atopic dermatitis and xerosis. By leveraging advanced analytical techniques like mass spectrometry, lipidomics enables precise characterization of lipid variability across anatomical sites, depths, and individuals. This mini review explores the methodologies, biological insights, and clinical applications of lipidomics, highlighting its transformative potential in understanding skin physiology and pathology.

### **Analytical Methods and Technologies in Skin Lipidomics**

Shotgun mass spectrometry is a cornerstone of high-throughput skin lipidomics, enabling comprehensive analysis of sebaceous and stratum corneum lipids. This technique involves direct infusion of lipid extracts into a mass spectrometer without prior chromatographic separation, allowing rapid acquisition of complex spectra. High-resolution instruments, such as the QExactive mass spectrometer, are essential for resolving overlapping signals and ensuring accurate identification of lipid species, including ceramides, cholesterol, and triacylglycerols [MN Sadowski, 2017] p3; [MN Ohnari, 2023] p2.

The advantages of shotgun lipidomics include broad lipid coverage, absolute quantification using internal standards, and unprecedented throughput, which is critical for large-scale studies and clinical applications. For example, this method has been used to analyze over 268 skin samples, revealing depth-dependent lipid gradients and inter-individual variability

M. Sadowski, 2017 p2; M. Sadowski, 2017 p8 . Additionally, tape-stripping combined with shotgun lipidomics provides a non-





# CONCLUSION

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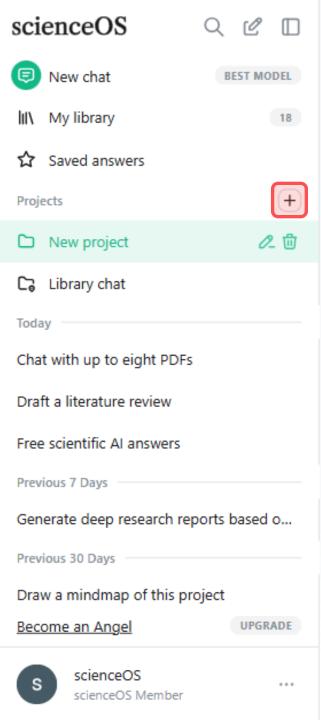
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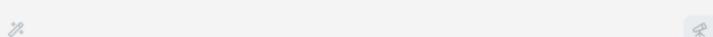


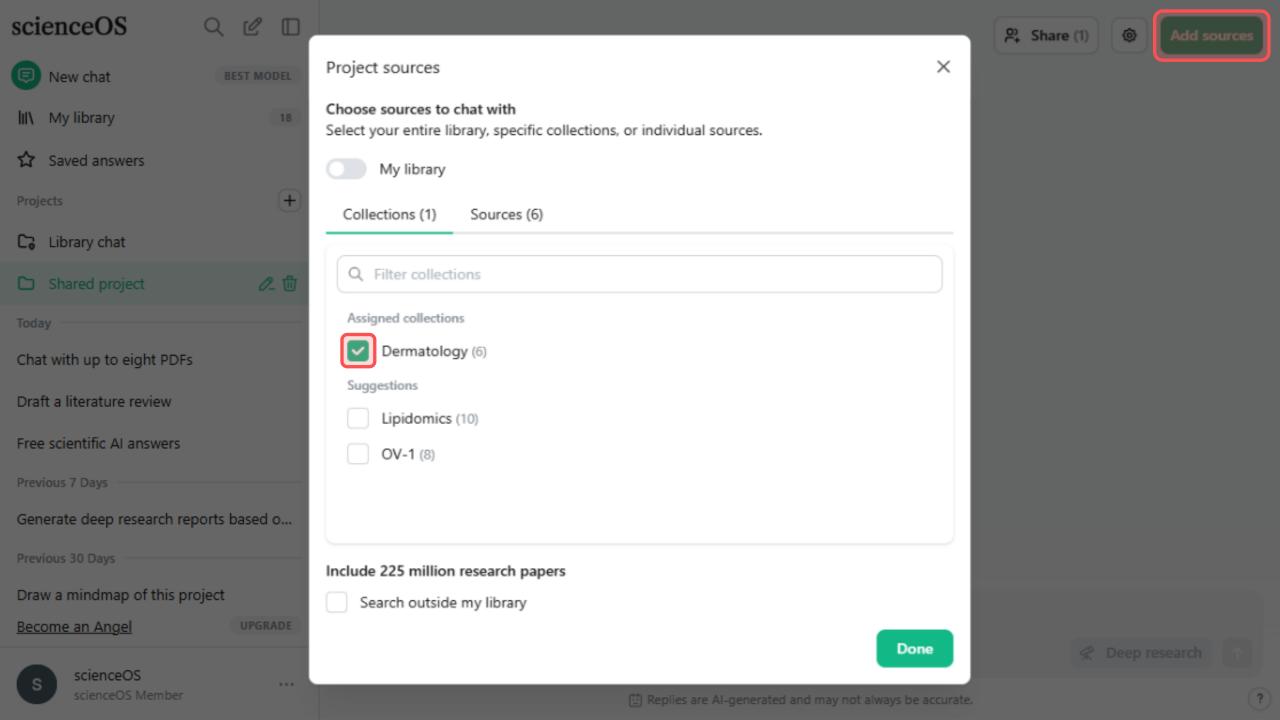


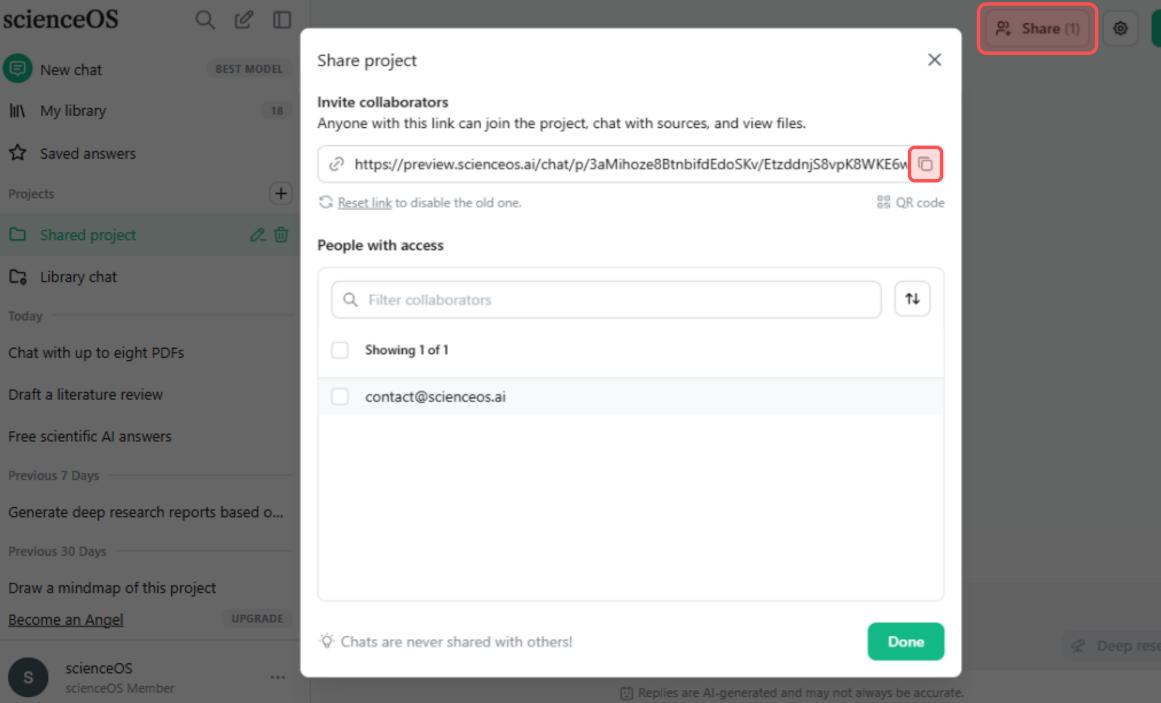


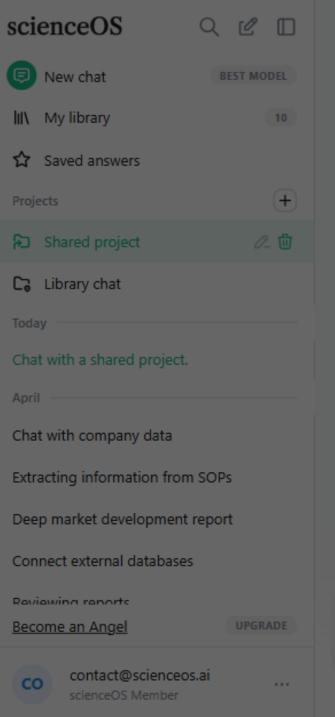
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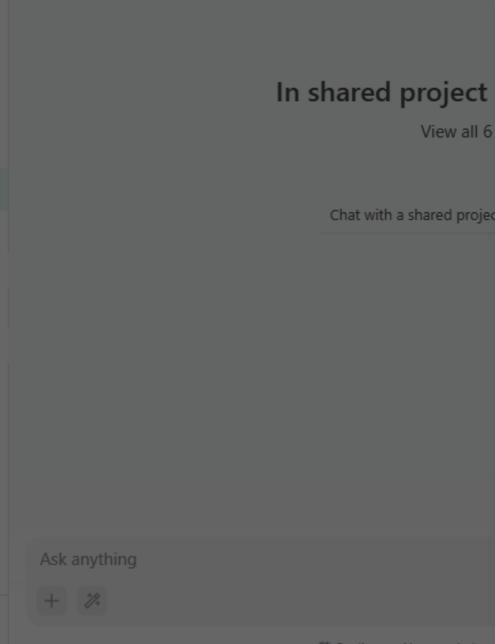
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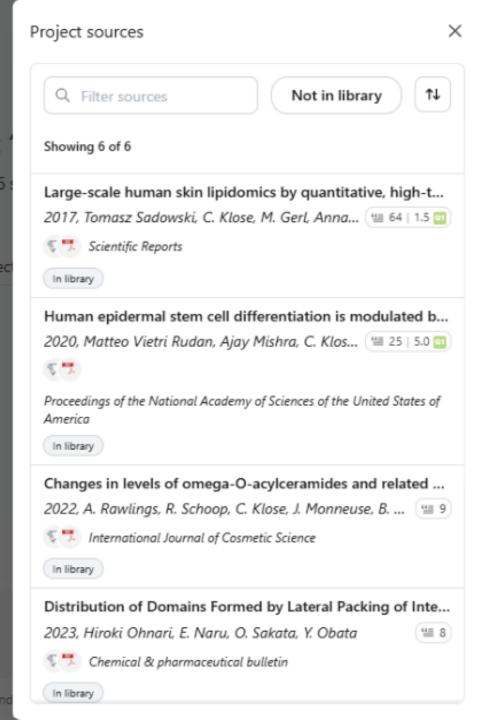










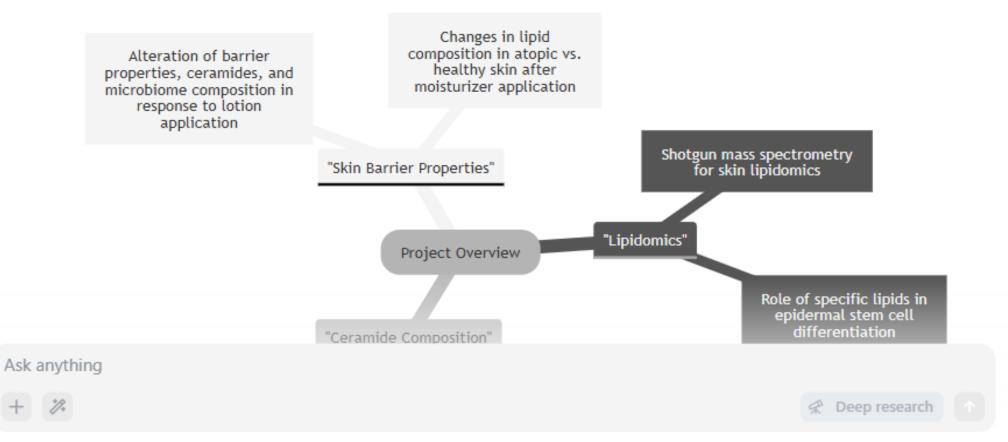




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