



LIPIDOMICS THE COMPLEX LIPID PANEL

Unlocking Lipid Biology with a Complete Lipidomic Solution

Complex lipids are a diverse class of metabolites that serve many functions in biology and play an important role in the development of metabolic diseases, cancer, inflammation and central nervous system disorders.

Accurate measures of lipids are essential for biomarker discovery and for clarifying biological questions. But, because they have a diverse array of chemical structures and a high degree of isomeric overlap, lipids are exceptionally challenging to accurately identify and quantify. The obstacles inherent in lipid profiling make high-quality lipidomic platforms extremely rare.

The Complex Lipid Panel: Complete, Quantitative Lipidomic Analysis

Metabolon has overcome the challenges of lipid profiling to create the only lipidomic platform able to provide both quantitative compositional analysis **and** complete speciation data: the Complex Lipid Panel.



The Complex Lipid Panel is the only lipidomics solution able to provide both quantitative compositional analysis and complete speciation data. By combining SelexIon differential mobility spectroscopy (DMS) with an extensive library of lipid masses and more than 50 custom-synthesized internal standards, the Complex Lipid Panel identifies up to 1,100 individual lipid species.

This unique platform provides single point quantitation of 14 lipid classes, including principal phospholipid, sphingolipid and neutral lipid classes. It also provides molecular species concentrations and complete fatty acid composition of each lipid class, thereby offering unparalleled insight into the lipidome.

This exceptional data is then imported into our Surveyor Web Tools for intuitive data visualization and easier interpretation. The combination of data and tools represents a unique environment for understanding complex lipid metabolism—a true "next generation" lipidomic solution.

A NEW KIND OF LIPIDOMICS

- Identify up to 1,100 molecular species of lipids
- Accurate quantitation of lipid class & molecular species concentrations
- Complete fatty acid composition of each lipid class
- Pathway mapping and discovery tools for easy interpretation

COMPLEX LIPID PANEL ANALYTE COVERAGE AND METHODS

Analyte Coverage

The Complex Lipid Panel provides the lipid concentration (e.g. TAG), fatty acid composition, and molecular species (e.g. PC(16:0/22:6)) of each of the 14 covered lipid classes.

The panel uses 50 μL of plasma/serum or 10 to 50 mg of tissue depending on the matrix.

In studies using 50 μ L of serum or plasma, the %CVs of lipid class concentrations are all below 10%. The median %CV of species at a 1uM concentration in serum or plasma is approximately 5%.

Ceramide (CER)	12 species
Cholesteryl Esters (CE)	26 species
Diacylglycerols (DAG)	58 species
Dihydroceramide (DCER)	12 species
Hexosylceramide (HCER)	12 species
Lactosylceramide (LCER)	12 species
Lysophosphatidylcholine (LPC)	26 species
Lysophosphatidylethanolamine (LPE)	26 species
Monoacylglycerol (MAG)	26 species
Phosphatidylcholine (PC)	140 species
Phosphatidylethanolamine (PE)	216 species
Phosphatidylinositol (PI)	28 species
Sphingomyelin (SM)	12 species
Triacylglycerols (TAG)	519 species

Methods



Lipids are extracted from samples in the presence of internal standards. The extracts are concentrated under nitrogen and reconstituted in 0.25mL of 10mM ammonium acetate dichloromethane:methanol (50:50).

The extracts are transferred to inserts and placed in vials for infusion-MS analysis, performed on a Shimadzu LC with nano PEEk tubing and the Sciex SelexIon-5500 QTRAP. The samples are analyzed via both positive and negative mode electrospray. The 5500 QTRAP scan is performed in MRM mode with a total of more than 1,100 MRMs.

Individual lipid species are quantified by taking the intensity ratios of target compounds and their assigned internal standards, then multiplying by the concentration of internal standard added to the sample. Lipid class concentrations are calculated from the sum of all molecular species within a class, and fatty acid compositions are determined by calculating the proportion of each class comprised by individual fatty acids.



In addition to a quantitative results table, the Complex Lipid Panel also comes with access to Surveyor, a suite of custom-designed data visualization and analysis software tools. Two primary tools exist within Surveyor for interpreting the data—Pathway Mapping Tools and Discovery Tools.

Pathway Mapping Tools

The Surveyor pathway maps allow clients to understand their lipidomic data in the context of lipid metabolic pathways.

Each pathway has been curated and annotated by Metabolon experts, and each element of the map is interactive, providing both data analysis (boxplots and difference testing) and additional information on each metabolite or activity.

Using Pathway Mapping tools, researchers can investigate the effect of their comparisons on the concentration and fatty acid composition of different pathways, including:

- Complex Lipid Metabolism (phospholipids and neutral lipids)
- **Sphingolipid Metabolism** (ceramides and sphingomyelin)
- Fatty Acid Metabolism

Discovery Tools

Discovery tools allow clients to perform an unbiased evaluation of the performance of each lipid, and layer in biological information and structure when desired. The tools plot all of the measured lipids and allow clients to filter and sort results to aid in the identification of biomarkers.

The **Biomarker Performance page** provides a comprehensive view of the performance of each lipid marker in separating the treatment groups.

The **Time Course/Multiple Comparisons page** improves the analysis of time-course and multiple-treatment comparisons studies by allowing clients to simultaneously plot multiple comparisons between groups.

In both tools, each plot point is interactive, linking a selected lipid marker to additional information about their structure and biology, including related box plots.





OUR SURVEYOR TOOLS PROVIDE A RICH COLLECTION OF ADDITIONAL CAPABILITIES, INCLUDING THE ABILITY TO CREATE YOUR OWN ALGORITHMS AND FILTERS, SHARE ACCESS AND NOTES ON THE STUDY WITH COLLEAGUES, AND DOWNLOAD PUBLICATION-QUALITY GRAPHICS.





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