Lipid Analysis

Glycerophospholipids

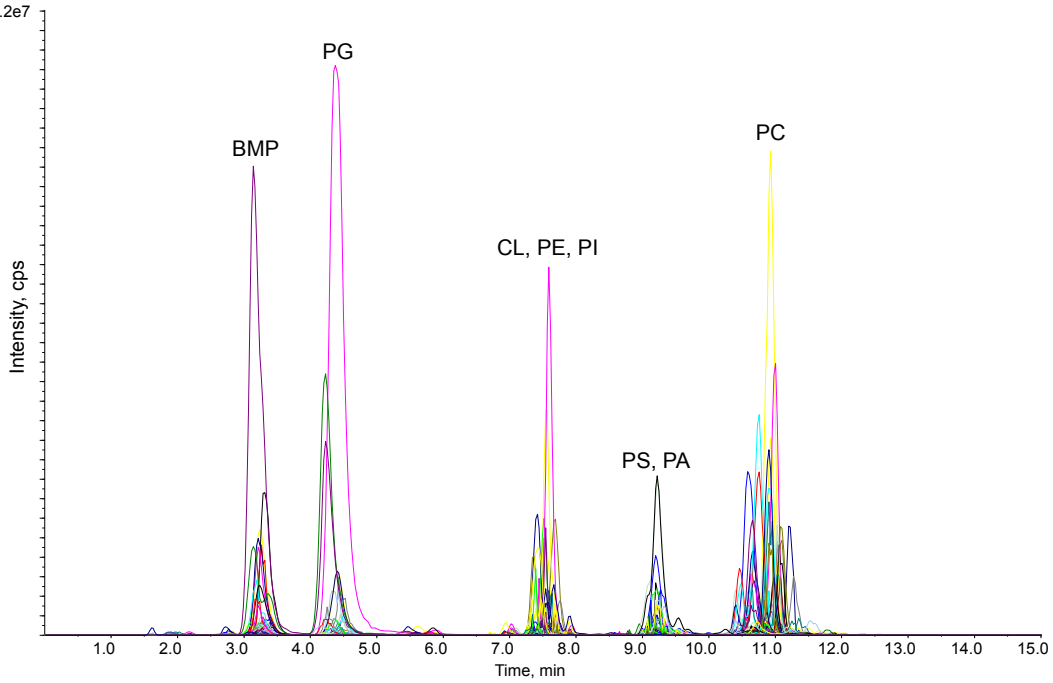
Glycerophospholipids (GP), often simply referred to as phospholipids, are the major structural building blocks of most cellular membranes in both eukaryotes and prokaryotes, and they are therefore essential for all life. Many phospholipids are also mediators involved in inflammation and disease, or precursors of other lipid mediators such as oxylipins. The GP category of lipids includes a great variety of molecular species, which is determined both by the polar heads and by the content of glycerol-linked acyl or alkyl chains. Because of this complexity, only an analytical approach targeting several hundred analytes can provide an adequate profile of the relative contents of these lipids, as well as their possible changes in different physiological or pathological situations.

This service can be of interest to a wide variety of scientists, including researchers exploring the fundamental mechanisms of biology, clinicians looking for biomarkers or following up on a treatment, or companies testing potential therapeutic tools.

Analyte Coverage

This service uses LC-MS/MS to analyze a customizable list of molecular species of glycerophospholipids, including lysoglycerophospholipids, across all major classes in this category: phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylserine (PS), phosphatidylglycerol (PG), including *bis*(monoacylglycerophosphate) (BMP), phosphatidylinositol (PI), phosphatidic acid (PA), and cardiolipin (CL). The method can be easily customized, for instance to focus on specific classes or to include additional radyl chains.

Class	Common *sn*-1 Radyl Chains	Common *sn*-2 Radyl Chains
PC	16:0, 16:1, O-16:0, P-16:0 (or O-16:1), 18:0, 18:1, O-18:0, P-18:0 (or O-18:1), 18:2	OH, 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:4, 20:5, 22:6
PE		
PS	16:0, 16:1, 18:0, 18:1, 18:2	
PG		
PI		
PA		
CL		OH, 16:0, 16:1, 18:0, 18:1, 18:2



LC-MS/MS chromatogram of phospholipids extracted from mammalian cells, showing the approximate retention times of the different classes.

Our Approach

Samples are extracted using a well-established liquid-liquid method. The method has been validated from a variety of matrices including plasma, cells, bronchoalveolar lavage fluid, and a variety of mammalian tissues.

Normal-phase HPLC and tandem mass spectrometry resolve most analytes and enable independent integration.

The use of isotopically labeled internal standards helps achieve precise relative quantitation of the endogenous analytes present in biological samples.

Our Advantages

- Our scientists are expertly trained and have decades of collective experience in the analysis, synthesis, and evaluation of biological roles of lipids.
- State-of-the-art instrumentation, reagents, and methods for all aspects of sample preparation, lipid extraction, LC-MS analysis, and data review ensure consistent, high-quality data.
- Method is scalable, from pilot studies with a few samples to high-throughput studies with hundreds of samples.
- High-quality standards produced in-house enable accurate calibration curve preparation and reliable quantitation.
- Collaborative, flexible approach. The method can be customized to include, remove or substitute analytes, or to be used with samples other than plasma. Please inquire for specific details.

Contact us for more information at **www.caymanchem.com/lipidomics**

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