

Jun 12, 2025

Lipidomic analysis in WM115 cells

 Forked from [Lipidomic analysis in HeLa cells](#)

DOI

<https://dx.doi.org/10.17504/protocols.io.bp2l6dmn5vqe/v1>

Rosanne Wouters^{1,2}, Igor Beletchi¹, Chris Van den Haute^{3,4,2}, Veerle Baekelandt^{3,4,2}, Shaun Martin¹,
Jan Eggermont¹, Peter Vangheluwe^{1,2}

¹Laboratory of Cellular Transport Systems, Department of Cellular and Molecular Medicine, KU Leuven;

²Aligning Science Across Parkinson's (ASAP) Collaborative Research Network;

³Research Group for Neurobiology and Gene Therapy, Department of Neurosciences, KU Leuven;

⁴Leuven Viral Vector Core, KU Leuven



Rania Abou El Asrar

KU Leuven

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

[Create free account](#)

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.bp2l6dmn5vqe/v1>

Protocol Citation: Rosanne Wouters, Igor Beletchi, Chris Van den Haute, Veerle Baekelandt, Shaun Martin, Jan Eggermont, Peter Vangheluwe 2025. Lipidomic analysis in WM115 cells . **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.bp2l6dmn5vqe/v1>

License: This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

We use this protocol and it's working

Created: January 12, 2025

Last Modified: June 12, 2025

Protocol Integer ID: 118148

Keywords: lipidomic analysis in wm115 cell, lipidomic analysis, protocol for the lipidomic analysis, wm115 cell

Funders Acknowledgements:

Aligning Science Across Parkinson's

Grant ID: ASAP-000458

C1 KU Leuven grant

Grant ID: C15/15/073

Fonds voor Wetenschappelijk Onderzoek (FWO) Flanders

Grant ID: S006617N

Michael J. Fox Foundation

Grant ID: MJFF-008610

Abstract

A protocol for the lipidomic analysis in WM115 cells

Troubleshooting

Lipidomic analysis in WM115 cells

- 1 Collect cells and homogenize cell pellets in 0.7 ml water with a handheld sonicator.
- 2 To the homogenate, add 0.8 ml HCl(1 M):CH₃OH 1:8 (v/v), 0.9 ml CHCl₃, 0.2 mg/ml of the antioxidant 2,6-di-tert-butyl-4-methylphenol (BHT; Sigma Aldrich), 3 µl of SPLASH[®] LIPIDOMIX[®] Mass Spec Standard (Cat No: 330707, Avanti Polar Lipids), 3 µl of Ceramides and 3 µl of Hexosylceramides internal Standards (#5040167 and #5040398, AB SCIEX).
- 3 After vortexing and centrifugation, collect the lower organic fraction.
- 4 Evaporate the lower fraction using a Savant Speedvac spd111v (Thermo Fisher Scientific) at room temperature.
- 5 Store the remaining lipid pellet at -20 °C under argon.
- 6 Just before mass spectrometry, reconstitute the lipid pellets in 100% ethanol.
- 7 Analyze lipid species by liquid chromatography electrospray ionization tandem mass spectrometry (LC-ESI/MS/MS) on a Nexera X2 UHPLC system (Shimadzu) coupled with hybrid triple quadrupole/linear ion trap mass spectrometer (6500+ QTRAP system; AB SCIEX).
- 8 Perform chromatographic separation on a XBridge amide column (150 mm × 4.6 mm, 3.5 µm; Waters) maintained at 35 °C using mobile phase A [1 mM ammonium acetate in water-acetonitrile 5:95 (v/v)] and mobile phase B [1 mM ammonium acetate in water-acetonitrile 50:50 (v/v)] in the following gradient: (0–6 min: 0 % B → 6 % B; 6–10 min: 6 % B → 25 % B; 10–11 min: 25 % B → 98 % B; 11–13 min: 98 % B → 100 % B; 13–19 min: 100 % B; 19–24 min: 0 % B) at a flow rate of 0.7 ml/min which was increased to 1.5 ml/min from 13 min onwards.
- 9 Measure phosphatidylserine, phosphatidylcholine and phosphatidylinositol in negative ion mode by fatty acyl fragment ions.
- 10 Perform phospholipid quantification by **multiple reactions monitoring** (MRM), the transitions being based on the neutral losses or the typical product ions.



- 11 The following instrument parameters are used: Curtain Gas = 35 psi; Collision Gas = 8 a.u. (medium); IonSpray Voltage = 5500 V and -4500 V; Temperature = 550 °C; Ion Source Gas 1 = 50 psi; Ion Source Gas 2 = 60 psi; Declustering Potential = 60 V and -80 V; Entrance Potential = 10 V and -10 V; Collision Cell Exit Potential = 15 V and -15 V.
- 12 The following fatty acyl moieties were taken into account for the lipidomic analysis: 14:0, 14:1, 16:0, 16:1, 16:2, 18:0, 18:1, 18:2, 18:3, 20:0, 20:1, 20:2, 20:3, 20:4, 20:5, 22:0, 22:1, 22:2, 22:4, 22:5 and 22:6. Data Analysis:
- 13 Perform peak integration with the MultiQuantTM software version 3.0.3. Lipid species signals were corrected for isotopic contributions (calculated with Python Molmass 2023.8.30;DOI|:<https://doi.org/10.5281/zenodo.7135495>) and were quantified based on internal standard signals and adheres to the guidelines of the Lipidomics Standards Initiative (LSI) (level 2 type quantification as defined by the LSI).