

# Lipidomics profiling and fingerprinting methodology

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## Contact person

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## Organisation

**Name of the organisation** Ghent University (UGent)

**Department** Faculty of Veterinary Medicine, Department of Veterinary Public Health and Food Safety

**Country** Belgium

**Geographical Area** Flemish Region

## SCOPE OF THE METHOD

<b>The Method relates to</b>	Animal health, Environment, Human health
<b>The Method is situated in</b>	Basic Research, Translational - Applied Research
<b>Type of method</b>	In chemico: Lipidomics

## DESCRIPTION

### Method keywords

metabolomics

lipidomics

Lipids

profiling

fingerprinting

feces

urine

mass spectrometry

Liquid chromatography

cell culture

colon tissue

### **Scientific area keywords**

analytical chemistry

metabolic disorders

inflammation

biofluids

food allergy

cancer research

### **Method description**

Our lipidomics profiling and fingerprinting methodology enables the analysis of all lipids within a biological matrix. These lipids can then be compared between an individual or condition with a specific metabolic state and healthy controls to find biomarkers or pathways that can be related to diseases. It applies ultra-high performance liquid chromatography coupled to hybrid quadrupole-Orbitrap high-resolution mass spectrometry. Both the instrumental method, as well as generic extraction protocols for colon tissue, cell cultures, blood, urine and feces have been extensively validated in both a targeted as well as an untargeted fashion. The lipidomics workflow consists of a sample preparation, followed by the UPHLC-HRMS analysis, after which multivariate statistical analysis will be performed to identify potential biomarker candidates or altered pathways, associated with a specific metabolic state.

### **Lab equipment**

UHPLC ;

HR-Orbitrap-MS.

### **Method status**

History of use

Internally validated

Published in peer reviewed journal

## **PROS, CONS & FUTURE POTENTIAL**

### **Advantages**

Lipids are involved in a plethora of biological processes, including energy homeostasis, immune response, membrane architecture, enzyme activity, inflammation, cellular signaling and transduction of cellular events. Evidently, a dysregulated lipid metabolism has been implicated in a variety of pathological conditions. Therefore, the measurement of this lipidome, which is at the end of the genome-transcriptome-proteome cascade, will provide the most holistic image of the phenotype of a patient. Additionally, it provides both a qualitative as well as a quantitative functional read-out. Therefore, it can be considered the method of choice for hypothesis testing and hypothesis generation.

### **Challenges**

Multi-step procedure => Long analysis time, extensive sample preparation.

Big data handling.

### **Modifications**

The method can be adapted to other matrices or other animal species when necessary.

## **REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION**

### **References**

Van Meulebroek et al (2017)

Analytical Chemistry Rombouts et al (2019)

Analytica Chimica Acta De Spiegeleer et al (2019) submitted

### **Associated documents**

[Van Meulebroek et al. 2017.pdf](#)

[Rombouts et al, 2019.pdf](#)

## Links

[Van Meulebroek et al, 2017](#)

[Rombouts et al, 2019](#)

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