

# Polar metabolomics 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: Metabolomics

## DESCRIPTION

### Method keywords

metabolomics

mass spectrometry

Liquid chromatography

metabolic profiling

Metabolism

metabolic fingerprinting  
biofluids  
urine  
feces  
saliva  
blood  
cell culture  
colon tissue

### **Scientific area keywords**

analytical chemistry  
metabolic disorders  
inflammation  
biofluids  
cancer research  
food allergy

### **Method description**

Our polar metabolomics profiling and fingerprinting methodology 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, urine, feces, plasma and saliva have been extensively validated in both a targeted as well as an untargeted fashion. The metabolomics 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**

HPLC ;  
HR-Orbitrap-MS.

### **Method status**

Internally validated

Published in peer reviewed journal

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

### **Advantages**

The metabolome is considered as the endpoint of metabolism and is therefore influenced by amongst others the genes, the diet, the environment and the residing microbiome. As such, the measurement of the metabolome provides 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**

Vanden Bussche et al (2015)  
Analytical Chemistry, 87, 10927-10934  
De Paepe et al (2018)  
Analytica Chimica Acta, 1033, 108-118  
Rombouts et al (2019)  
Analytica Chimica Acta, 1066, 79-92  
Wijnant et al (2019) submitted  
De Spiegeleer et al (2019) submitted

### **Associated documents**

[De Paepe et al, 2018.pdf](#)  
[Rombouts et al, 2019.pdf](#)  
[Vandenbussche et al, 2015.pdf](#)

### **Links**

[Rombouts et al, 2019](#)  
[De Paepe et al, 2018](#)

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