

## Technical Bulletin

## Non-Polar Metabolites QC Mix

Catalogue number SBR00073

## Product Description

Metabolomics is the profiling study of metabolites that are usually small molecules from biochemical processes and pathways<sup>1,2</sup>. Metabolites are mostly characterized from samples of stool<sup>3</sup>, serum/plasma<sup>4</sup>, urine<sup>5</sup>, cerebrospinal fluid<sup>6</sup>, and saliva<sup>7</sup>. Metabolomics deals with diverse areas like microbiome<sup>8</sup>, nutrition<sup>9</sup>, diseases<sup>10</sup> and agriculture<sup>11</sup>. Generally, metabolites are analyzed by two main approaches: Targeted<sup>12,13</sup> and untargeted<sup>14,15</sup> metabolomics. Targeted metabolomics<sup>12,13</sup> is the analysis of known specific chemical group metabolites like short chain fatty acids<sup>16</sup>, bile acids, lipids<sup>17</sup> and amino acids<sup>18</sup>. Whereas untargeted metabolomics<sup>14,15</sup> is analysis of all unknown chemical compounds in one sample.

Liquid chromatography-mass spectrometry (LC-MS) is the main method for metabolite profiling in metabolomics analysis<sup>19,20</sup>. In order to assess any variations in the LC-MS-based metabolomics analysis data, it is recommended to add an additional QC (quality control) sample at the beginning of every analytical experiment batch and should be injected every 4-10 injections in to the workflow steps<sup>19,21,22</sup>. The QC sample evaluates any drifting phenomenon like intensity values, ion suppression or any changes in the retention time of the peaks in the LC-MS data.

Here we offer a ready to use Non Polar Metabolites QC Mix in a solution of ~2:1:1 IPA:ACN:H<sub>2</sub>O for mass spectroscopy workflows. By utilizing the QC mix, the user will be able to assess drifting and ion suppression phenomena. The Non-Polar Metabolites QC Mix is comprised of 9 components (see Table 1). The Non-Polar metabolites mix contains hydrophobic type of metabolites such as, cholesterol derivatives, unsaturated fatty acids, phospholipids and ceramides.

## Components

Table 1.

Components in the Non-Polar Metabolites QC Mix

No.	Metabolite name	Empirical Formula	Exact mass	Concentration (µg/mL)	Concentration (µM)
1	Progesterone	C <sub>21</sub> H <sub>30</sub> O <sub>2</sub>	314.2246	2	6.4
2	D-Sphingosine	C <sub>18</sub> H <sub>37</sub> NO <sub>2</sub>	299.2824	10	33.4
3	1-Oleoyl-sn-glycero-3-phosphocholine (LysoPC(18:1(9Z)/0:0))	C <sub>26</sub> H <sub>52</sub> NO <sub>7</sub> P	521.3481	2.5	4.8
4	Linolenic acid	C <sub>18</sub> H <sub>30</sub> O <sub>2</sub>	278.2245	20	71.8
5	cis-4,7,10,13,16,19-Docosahexaenoic acid (DHA)	C <sub>22</sub> H <sub>32</sub> O <sub>2</sub>	328.2402	5	15.2
6	Arachidonic acid sodium salt	C <sub>20</sub> H <sub>32</sub> O <sub>2</sub>	304.2402	10	30.6
7	Sodium cholesteryl sulfate	C <sub>27</sub> H <sub>46</sub> O <sub>4</sub> S	466.3116	10	20.5
8	N-palmitoyl-D-sphingosine (C16 ceramide (D18:1/16:0))	C <sub>34</sub> H <sub>67</sub> NO <sub>3</sub>	537.5121	2	3.7
9	1,2-dioleoyl-sn-glycero-3-phosphocholine (18:1 (Δ9-Cis) PC (DOPC))	C <sub>44</sub> H <sub>84</sub> NO <sub>8</sub> P	785.5934	1	1.3

## Reagents and Equipment Required but Not Provided

- Column: Agilent® Eclipse plus-C8, 95 Å, RRHD 1.8µm 2.1x150mm
- Ammonium formate Cat# 70221
- Acetonitrile Cat# 1.00029
- Isopropanol Cat# 1.02781

## Precautions and Disclaimer

For R&D use only. Not for drug, household, or other uses. Please consult the safety data Sheet for information regarding hazards and safe handling practices.

The product is obtained in format of crimp top (Silicone/PTFE liner) amber vial which suitable for use with most of the LC-MS autosamplers.

## Storage/Stability

The product is shipped at ambient temperature. Store at -20°C upon receipt.

## Preparation Instructions

The Non-Polar Metabolites QC Mix is a ready to inject solution supplied in a crimp top (Silicone/PTFE liner) amber vial 220µL.

## Procedure

Mass Spectrometry Conditions: Instrument: Bruker™ Q-ToF Impact II

Source Type: ESI

Method A:

Ion Polarity: Positive

Capillary: 4500 V

Nebulizer: 2.2 Ba0072

Dry gas temperature: 200 °C

Dry gas: 8L/min

Method B: Ion Polarity: Negative

Capillary: 5500 V

Nebulizer: 2.2 Bar

Dry gas temperature: 220 °C

Dry gas: 8L/min

LC Conditions:

Column: Column oven temperature: 55 °C

Flow rate: 0.5 mL/min

Eluent A: 10mM Ammonium formate in water + 0.1% formic acid

Eluent B: 85% ACN, 10% IPA, 5% water + 10mM ammonium formate + 0.1% formic acid.

Injection volume: Method A (ESI+) - 1 µL

Method B (ESI-) - 2 °L

Gradient: See Table 2

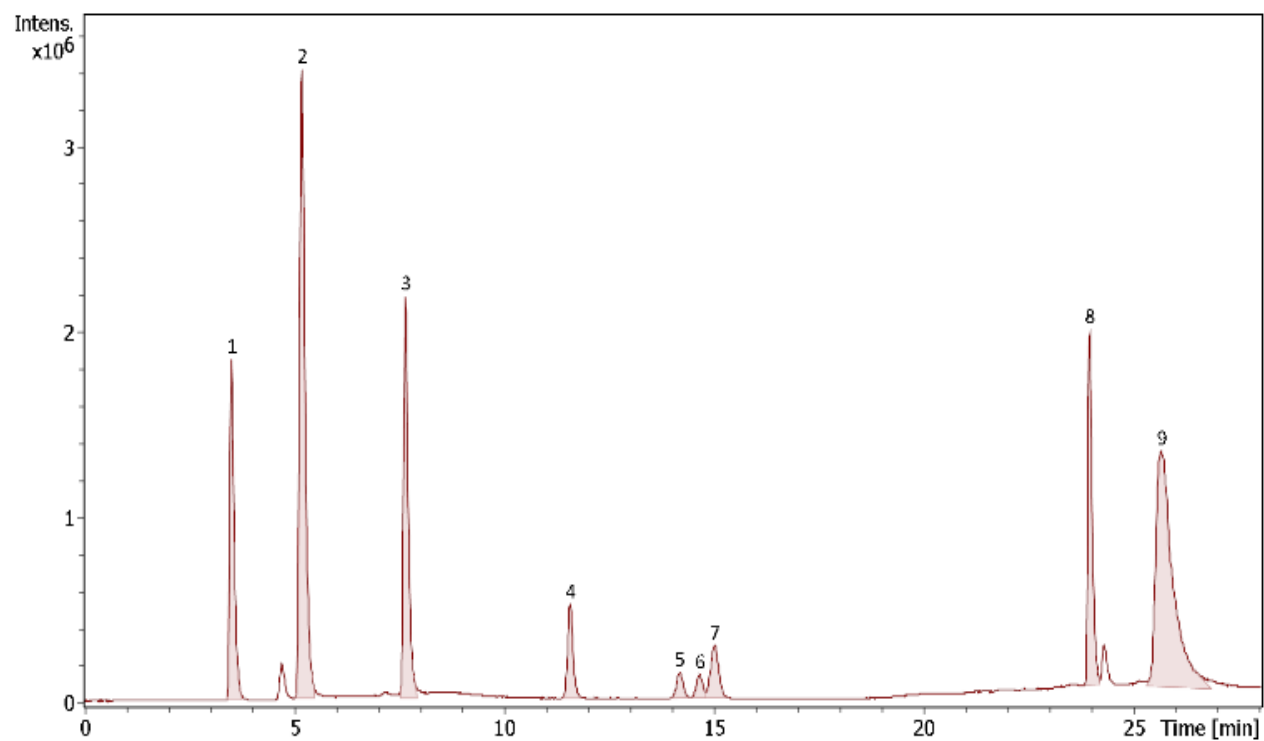
**Table 2:**

Gradient elution time is shown below for Eluent A & B.

Time (min)	A [%]	B [%]
0	47	53
2	47	53
6	35	65
16	35	65
20	0	100
27	0	100
30	47	53
35	47	53

**Figure 1:**

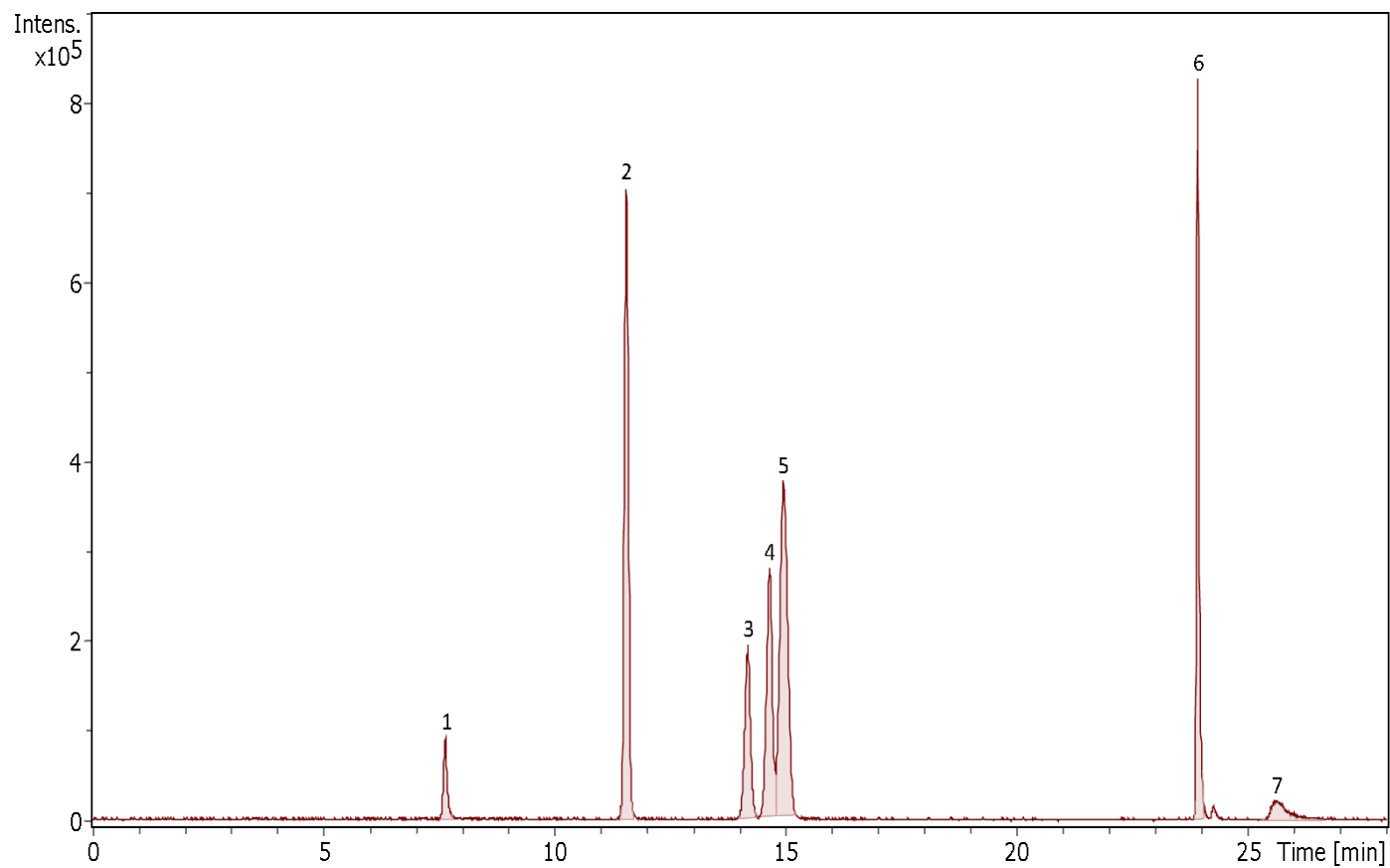
Method A: Extracted ion chromatogram (EIC) of MS ESI+ of SBR00073.



**Table 3:**

List of metabolites corresponding to the retention times in figure 1 are shown.

Peak no.	Metabolite name	Rt (min)
1	Progesterone	3.5
2	D-Sphingosine	5.2
3	LysoPC(18:1(9Z)/0:0)	7.7
4	Linolenic acid	11.6
5	DHA	14.2
6	Arachidonic acid	14.7
7	Cholesterol sulfate	15.0
8	C16 ceramide (D18:1/16:0)	23.9
9	18:1 ( $\Delta$ 9-Cis) PC (DOPC)	25.7

**Figure 2: Method B:** Extracted ion chromatogram (EIC) of MS ESI- of SBR00073

## References

1. S. G Oliver., *et al.*, Systematic functional analysis of the yeast genome. *Trends in biotechnology.*, **16(9)**, 373-378 (1998).
2. Kevin Cho., *et al.*, After the feature presentation: technologies bridging untargeted metabolomics and biology. *Current opinion in biotechnology*, 28, 143-148. (2014).
3. Karu, N., *et al.*, A review on human fecal metabolomics: Methods, applications and the human fecal metabolome database. *Analytica chimica acta*, 1030, 1-24. (2018).
4. Psychogios, N., *et al.*, The human serum metabolome. *PLoS one*, **6(2)**, e16957. (2011).
5. Bouatra, S., *et al.*, The human urine metabolome. *PLoS one*, **8(9)**, e73076. (2013).
6. Wishart, D. S., *et al.*, The human cerebrospinal fluid metabolome. *Journal of Chromatography B*, **871(2)**, 164-173. (2008).
7. Dame, Z. T., *et al.*, The human saliva metabolome. *Metabolomics*, **11(6)**, 1864-1883. (2015).
8. Bauermeister, A., *et al.*, Mass spectrometry-based metabolomics in microbiome investigations. *Nature Reviews Microbiology*, 1-18. (2021).
9. Tebani, A., & Bekri, S., Paving the way to precision nutrition through metabolomics. *Frontiers in nutrition*, 6, 41. (2019).
10. Tounta, V., *et al.*, Metabolomics in infectious diseases and drug discovery. *Molecular Omics*, **17(3)**, 376-393. (2021).
11. Hong, J., *et al.*, Plant metabolomics: an indispensable system biology tool for plant science. *International journal of molecular sciences*, **17(6)**, 767. (2016).
12. Nikolskiy, I., *et al.*, Discriminating precursors of common fragments for large-scale metabolite profiling by triple quadrupole mass spectrometry. *Bioinformatics*, **31(12)**, 2017-2023. (2015).
13. Patti, G. J., *et al.*, Metabolomics: the apogee of the omics trilogy. *Nature reviews Molecular cell biology*, **13(4)**, 263-269. (2012).
14. Roberts, L. D., *et al.*, Targeted metabolomics. *Current protocols in molecular biology*, **98(1)**, 30-2. (2012).
15. Zheng, X., *et al.*, A targeted metabolomic protocol for short-chain fatty acids and branched-chain amino acids. *Metabolomics*, **9(4)**, 818-827. (2013).
16. Schrimpe-Rutledge., *et al.*, Untargeted metabolomics strategies—challenges and emerging directions. *Journal of the American Society for Mass Spectrometry*, **27(12)**, 1897-1905. (2016).
17. Griffiths, W. J., *et al.*, Targeted metabolomics for biomarker discovery. *Angewandte Chemie International Edition*, **49(32)**, 5426-5445. (2010).
18. Klepacki, J., *et al.*, Amino acids in a targeted versus a non-targeted metabolomics LC-MS/MS assay. Are the results consistent? *Clinical biochemistry*, **49(13-14)**, 955-961. (2016).
19. Zhou, B., *et al.*, LC-MS-based metabolomics. *Molecular BioSystems*, **8(2)**, 470-481. (2012).
20. Theodoridis., *et al.* LC-MS-based methodology for global metabolite profiling in metabonomics/metabolomics. *TrAC Trends in Analytical Chemistry*, **27(3)**, 251-260. (2008).
21. Ivanisevic, J., & Want, E. J., From samples to insights into metabolism: Uncovering biologically relevant information in LC-HRMS metabolomics data. *Metabolites*, **9(12)**, 308. (2019).
22. Sarvin, B., *et al.*, Fast and sensitive flow-injection mass spectrometry metabolomics by analyzing sample-specific ion distributions. *Nature communications*, **11(1)**, 1-11. (2020).

---

## Notice

We provide information and advice to our customers on application technologies and regulatory matters to the best of our knowledge and ability, but without obligation or liability. Existing laws and regulations are to be observed in all cases by our customers. This also applies in respect to any rights of third parties. Our information and advice do not relieve our customers of their own responsibility for checking the suitability of our products for the envisaged purpose.

The information in this document is subject to change without notice and should not be construed as a commitment by the manufacturing or selling entity, or an affiliate. We assume no responsibility for any errors that may appear in this document.

### Technical Assistance

Visit the tech service page at [SigmaAldrich.com/techservice](https://SigmaAldrich.com/techservice).

### Terms and Conditions of Sale

Warranty, use restrictions, and other conditions of sale may be found at [SigmaAldrich.com/terms](https://SigmaAldrich.com/terms).

### Contact Information

For the location of the office nearest you, go to [SigmaAldrich.com/offices](https://SigmaAldrich.com/offices).

The life science business of Merck operates  
as MilliporeSigma in the U.S. and Canada.

Merck and Sigma-Aldrich are trademarks of Merck KGaA, Darmstadt, Germany or its affiliates.  
All other trademarks are the property of their respective owners. Detailed information on  
trademarks is available via publicly accessible resources.

© 2022 Merck KGaA, Darmstadt, Germany and/or its affiliates. All Rights Reserved.

sbr00073pis Rev 2/24

