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Product Information

LSMLS™ Plate 7 (Lipophilic)
Supplied by IROA Technologies, LLC.

Catalog Number **LSMLS07**
Storage Temperature –20 °C

Product Description

LSMLS07 (Large Scale Metabolite Library Plate 7) is a collection of high quality, small biochemical molecules that span a broad range of primary metabolism. These are high purity (>95%) compounds supplied in an economical, ready-to-use format.

The library is most commonly used to provide retention times and spectra for key metabolic compounds, help optimize analytical mass spectrometry protocols, and qualify and quantify mass spectrometry sensitivity and limit of detection.

LSMLS™ Plate 7 comes with MLSDiscovery™, a software tool to support the extraction, manipulation, and storage of the data generated when using the LSMLS07. For further information on the software, to download, and for manual and video links please visit: www.sigmaaldrich.com/catalog/product/sigma/lsmls07

Components

LSMLS Plate 7 compounds are conveniently provided at 1 mg per well, enough for multiple injections, suitable for manual and automated workflow.

The library is intended to be used for mass spectrometry metabolomics applications and provides a broad representation of primary metabolism.

Occasionally the plate map will change due to the availability of compounds. The compounds of each row have distinct molecular masses and can be multiplexed, but users should refer to the plate map for their specific lot before proceeding.

The plate map contains descriptors and represents information gathered from multiple databases. Please note this data may contain some errors. It is recommended for users to carefully review plate composition and description information prior to use. To help build a better database, please report any observed discrepancies.

LSMLS07 includes:

- 1 polypropylene plate in 96 well format
  Polypropylene deepwell (1.2 mL, total volume per well) plate (MasterBlock®, Greiner Number 780215) in combination with seals (VIEWseal™, Greiner Number 676070)
- 1 mg (dried weight) of each metabolite

MLSDiscovery software includes:

- Plate map
- Alpha-numeric assigned position
- Descriptors:
  Name
  Parent CID
  KEGG ID where available or ChemSpider ID
  Molecular formula
  Molecular mass
  CAS Registry number
  ChEBI
  HMDB ID/YMDB ID
  PubChem Compound and Substance ID
  Metlin ID

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.

Preparation Instructions

The following are suggestions and dependent on user chromatography and instrumentation.

These plates contain primarily lipid-like compounds. It is recommended to solubilize these compounds using a chloroform:methanol (1:1) mixture.

Pool compounds for multiplexing. Be sure to check the plate map to ensure one can adequately separate the compounds using the chromatographic system prior to pooling.

Storage/Stability
Store the plate at –20 °C.

Once the metabolites are dissolved, the plate should be resealed and kept at –20 °C or –80 °C for long-term storage and protected from light. Avoid repeated freeze/thaw cycles.

Procedure
The compounds of LSMLS Plate 7 can either be used as standards and injected individually or mixed in such a way that the entire library may be examined with reasonable efficiency. Mixing compounds by row mixtures allows multiple compounds to be analyzed per injection. Again, be sure to check the plate map to ensure one can adequately separate the compounds using the chromatographic system prior to pooling.

The following are only suggestions and depend on user chromatography and instrumentation.

1. Individual Injections
   As standards, each well represents a single compound. The entire library may be examined in great detail with several injections, one for each of the unique metabolites (Total volumes for each well of 250 µL–1 mL may be considered).

2. Simple multiplex injections
   If the rows of the plate are pooled, then the entire collection may be analyzed with 5 injections of simple mixtures. Keep the total volume for each well to 150 µL or less to prevent loss due to dilution and use 5-10 µL of each well for the pooled sample. Then, inject 2, 4, or 6 µL of the pooled material as needed.

References

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6. Tautenhahn, R. et al., An accelerated workflow for untargeted metabolomics using the METLIN database. Nature Biotechnology, 2012, 30: 826–828. doi:10.1038/nbt.2348.
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