+1,050
molecules
included

MetaSci

Providing high quality metabolite library

Plant Metabolite Library

standards for mass spectrometry

Exploring the presence and the quantity of primary and secondary metabolites in plants can enable accurate genomic and metabolic engineering, resulting in higher productivity of crops. We provide more than 1,050 plant metabolite standards for various metabolomics methods such as metabolic pathway analysis and high-throughput analysis. Our standards are compatible with many analysis platforms using a LC or GC coupled to any type of mass spetrometer including single quadropole, triple quadropole (QQQ), QTOF and Orbitraps. The standards can be used for various applications such as method development, instrument specific in-house spectral collection and generating calibration curves.

5-10 mg of compound in autosampler vials

CONTACT US
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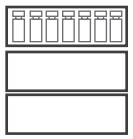
110 West Beaver Creek Rd, Unit 7
Richmond Hill, ON
L4B 1J9, CANADA

Providing high quality metabolite library

INCLUDES:
Flavonoids
Terpenoids
Polyphenols
Amino acids
Sugars
Dipeptides
Glycosides
Lipids

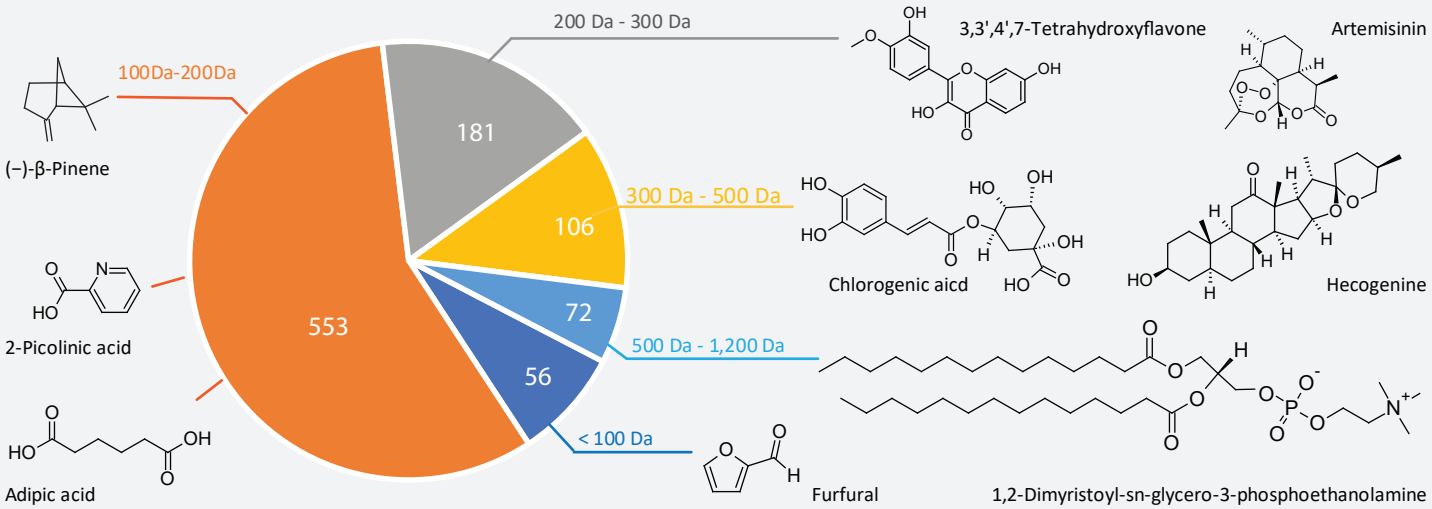
SUITABLE FOR:
Metabolomics Analysis
Method Development
NMR, GC-MS, LC-MS, CE-MS
Biomarker Discovery
Targeted & Un-targeted Studies
In-House Spectra Library
High-Throughput Screening
Drug Discovery

WHAT'S IN THE BOX?

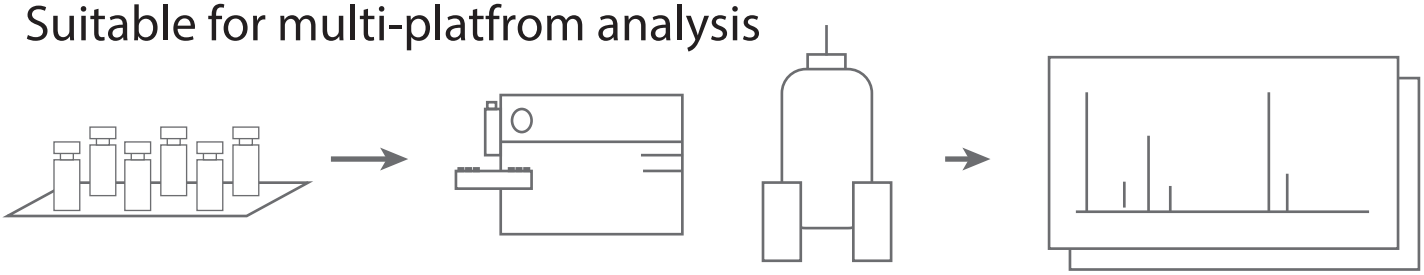

+1,050 samples
in 11 boxes


User's manual

Laboratory Information
Management System



Suitable for multi-platfrom analysis



+950 SAMPLES, ACQUIRE ALL OR SOME JUST IN 3 DAYS

We provide the standards in autosampler vials in 5-10 mg. The quantity of each vial is enough for preparation of multiple solutions in desired concentration, for method development and for other applications such as derivatization. The user can make high concentration solution to offset dilution effect upon pooling solutions. MetaSci Library is one of the few collections in the world that provides enough material for NMR studies. Unlike 96-well plate format (i.e., all-or-non packaging!) the customer can refill single compounds easily and can customize the library to acquire only the compounds in need.

HMDB AND MSI+ SUPPORT

We provide all bioinformatics data through major partner databases such as HMDB, YMDB, ECMDB,, FoodDb T3Db. This includes annotation, taxonomy, CAS number, other identifiers used by PubChem and METLIN ID, corresponding biofluid and structure. Accessing our proprietary Library Information Management System will help the research team to identify each compound, prepare solution, calculate concentration and view all spectral data for each compound.

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