



MetaboScape® Bibliography

• 2019 - 2020

MetaboScape Bibliography

The peer-reviewed and in-peer-reviewing communications listed below is a non-exhaustive list from the work empowered by MetaboScape® in the years 2019-2020 and many more are to come.

MetaboScape is a fully integrated SW solution which can be used across application areas, including discovery metabolomics, lipidomics, phenomics, foodomics, environmental and imaging.

The MetaboScape all-in-one software provides users with the flexibility to support semi-targeted discovery and non-targeted screening workflows ranging from processing, compound identification, statistics to pathway mapping. MetaboScape supports data acquired from both LC and high-throughput flow injection (FIA) MRMS aXelerate workflows, MS/MS data acquired on Bruker's QTOF and timsTOF systems and using high-speed PASEF on the timsTOF Pro and timsTOF fleX. In addition, SpatialOMx MALDI imaging workflows from Bruker's MRMS & timsTOF fleX are supported.

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The aim of non-targeted profiling is to identify features that are characteristic of a particular physiological state or sample. As there is no single workflow to enable access to the dynamic temporal and spatial fingerprints for all compounds, there is a need to evaluate data from complementary platforms. MetaboScape® addresses these needs by allowing for the evaluation of complementary data from both ESI and MALDI Imaging, as well as confidently assigning relevant markers in their biological context.



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