FACT SHEET

SAPIENT

Metabolite identification to **enhance & accelerate** small molecule biomarker discovery

Expanding identification to enhance your discovery insights.

Accurate metabolite identification is needed to **maximize the impact of discovery metabolomics and lipidomics,** to effectively map the role of key biomarkers identified in a study and support translation to clinical use.

Sapient has focused extensively on building capabilities to **enhance the speed, quality, and extent of metabolite identification** so that more statistically significant metabolites and lipids can be effectively interrogated and advanced to validation studies.

Eludicating **the most biologically important signals** in patient cohorts.

With Sapient's rapid liquid chromatography-mass spectrometry (rLC-MS) systems, we can **now measure >15,000 chromatographic features in a single sample, greatly expanding biomarker discovery potential** but also increasing the likelihood of finding important but unidentified molecules.

Our metabolite identification services are central in mapping the biological role of discovered novel biomarkers and their involvement in disease processes. We focus on accuracy to mitigate misidentifications or false hits and ensure that the marker can be **reproducibly measured in validation studies.**

How We Maximize IDs

In-house library of >13,000 chemical reference standards

- Enriched for key human metabolic pathways, biochemical processes, and disease drivers
- Strong coverage across endogenous human metabolites, lipids, and FDA approved drugs
- All standards have been extensively analyzed using Sapient's rLC-MS

Up to 1,400 metabolites identified in large studies

- Identified using retention time (RT), MS1 mass-to-charge ratio (m/z), and MS2 chemical fingerprint

Database of >6 million MS2 spectra

- Representing 850K+ compounds
- Used for putative structural identification of unidentified metabolites and lipids

Maximizing translability.

Sapient's metabolite identification capabilities have been **developed to maximize definitive identifications for a study and to elucidate more unknown molecules** to advance novel discoveries.

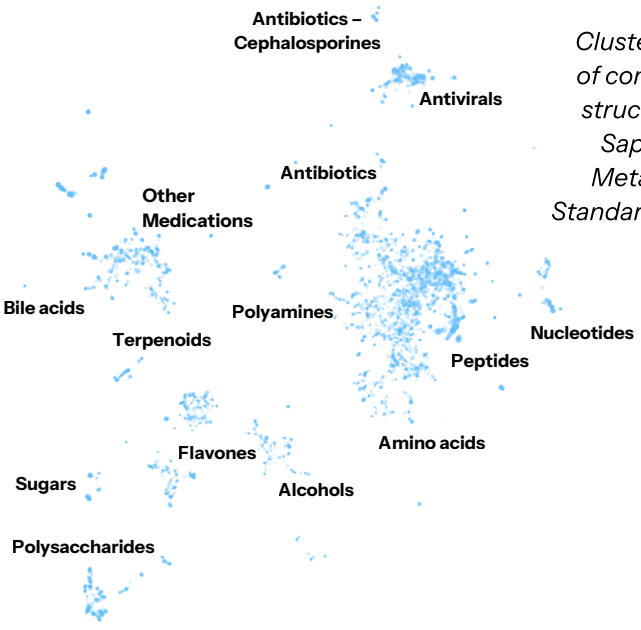
Metabolite identifications at the **highest confidence levels.**

By generating multi-parameter rLC-MS data on >13,000 chemical reference standards, we are able to assign MSI Tier 1 identification to **up to 1,400 metabolites and lipids** measured in plasma and tissue biosamples.

All identified compounds undergo **rigorous quality control** including visual inspection of peak shape and retention time consistency across all samples, as well as confirmation that no identified compound represents an isotope, adduct, or in-source fragment of another signal.

Extensive data to **elucidate unannotated molecules.**

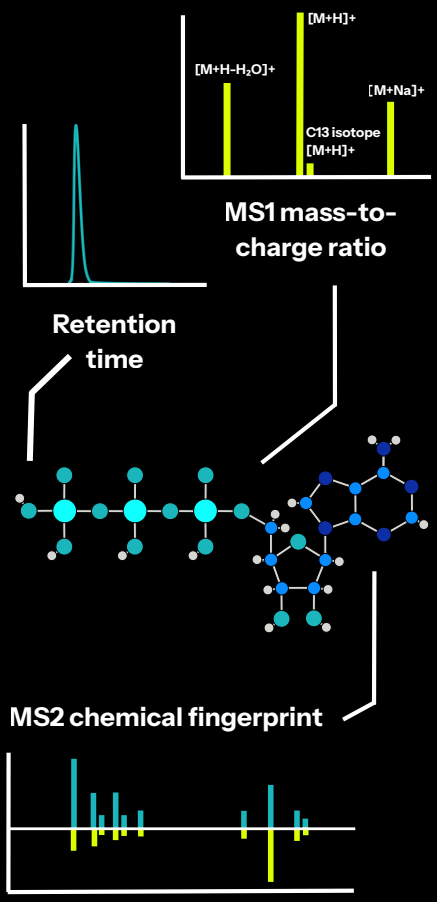
For those molecules that remain unannotated, Sapient leverages our database of over 6 million MS2 spectra across 850,000+ compounds to **provide putative structural insights for hundreds to thousands of additional metabolites.** We also offer custom studies to identify signficant unknown compounds observed in discovery studies and not yet captured in our reference databases.



Cluster graph of compound structures in Sapient's Metabolite Standards Library

What makes an identification Tier 1?

The molecule is matched to a reference standard under the same analytical conditions via multiple chemical parameters including:



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