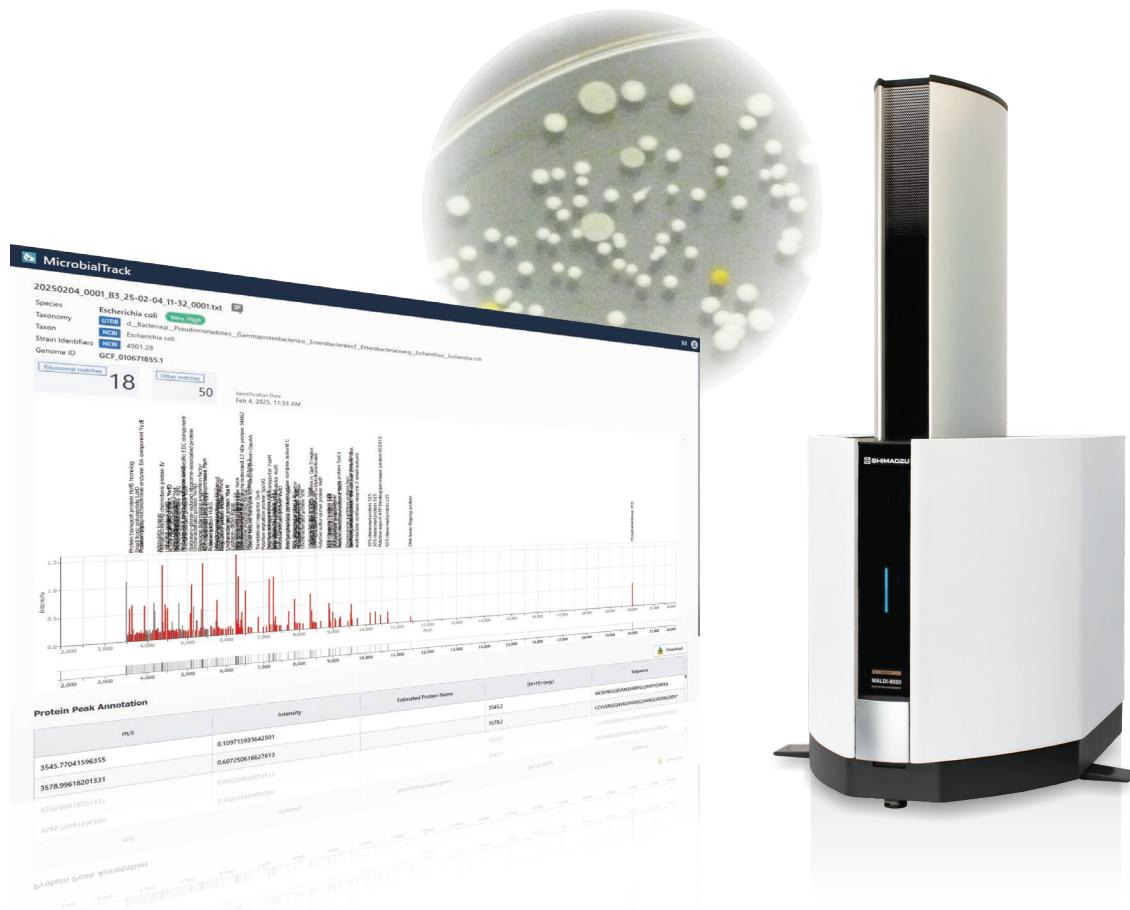


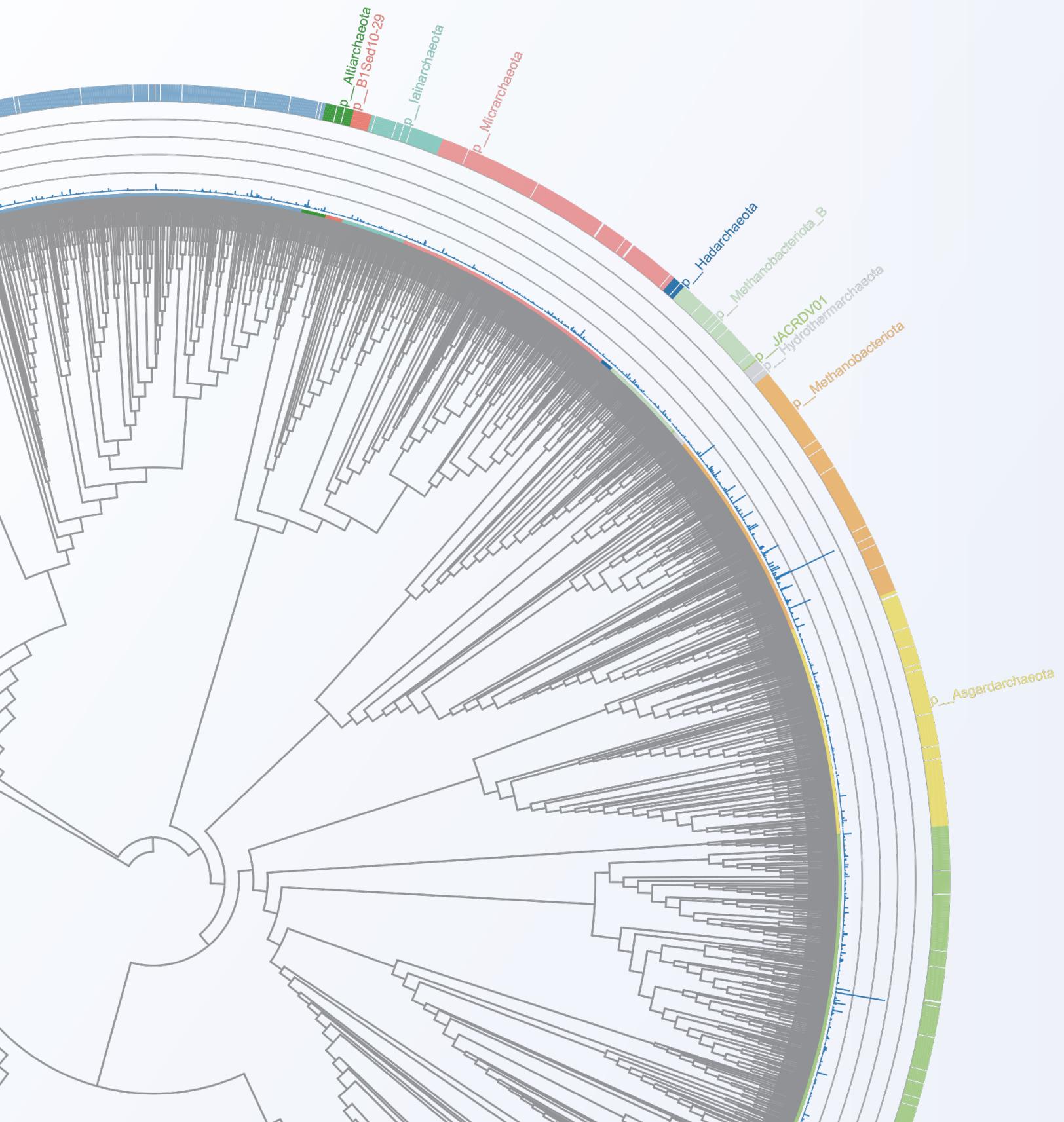
MALDI-TOF MS Microbial Identification Software

# MicrobialTrack



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## MALDI-TOF MS Microbial Identification Platform

MicrobialTrack is a new analytical platform that utilizes a vast database of theoretical prokaryotic protein masses predicted from genome sequences for MALDI-TOF MS-based identification of prokaryotic microorganisms. The database encompasses a wide array of previously unidentifiable bacterial and archaeal phylogenetic taxa, enabling the identification of uncultured and hard-to-culture microorganisms. Since the identification algorithm employed by MicrobialTrack depends on the masses of genetically predicted proteins, the identification performance is not primarily affected by culture conditions and MALDI-TOF MS models. In addition to identification results, MicrobialTrack can conduct a detailed mass spectral analysis using theoretical protein masses to assign proteomic information.

## Database Built from Genomic Data

Genomic data from approximately 400,000 *Bacteria* and *Archaea* were used to build a database of theoretical protein masses. The database encompasses approximately 85,000 species of prokaryotes (*Bacteria* and *Archaea*), including taxa with valid published taxonomic names according to the International Code of Nomenclature of Prokaryotes, as well as uncultured and difficult-to-culture taxa inferred from genomic information.

## Accessible Everywhere Via a Cloud Service

MicrobialTrack is a cloud-based service that enables the identification of microorganisms in a web browser. The service does not require a dedicated PC or software installation. Users simply register and then access the designated URL to proceed with the analysis. Several hundred thousand new prokaryotic genome sequences are published yearly and added to public databases. The MicrobialTrack database is updated regularly to include newly added taxa as genome sequences and to reflect the most recent taxonomic system, which is continually evolving. Users will have access to the latest MicrobialTrack database during the license period.

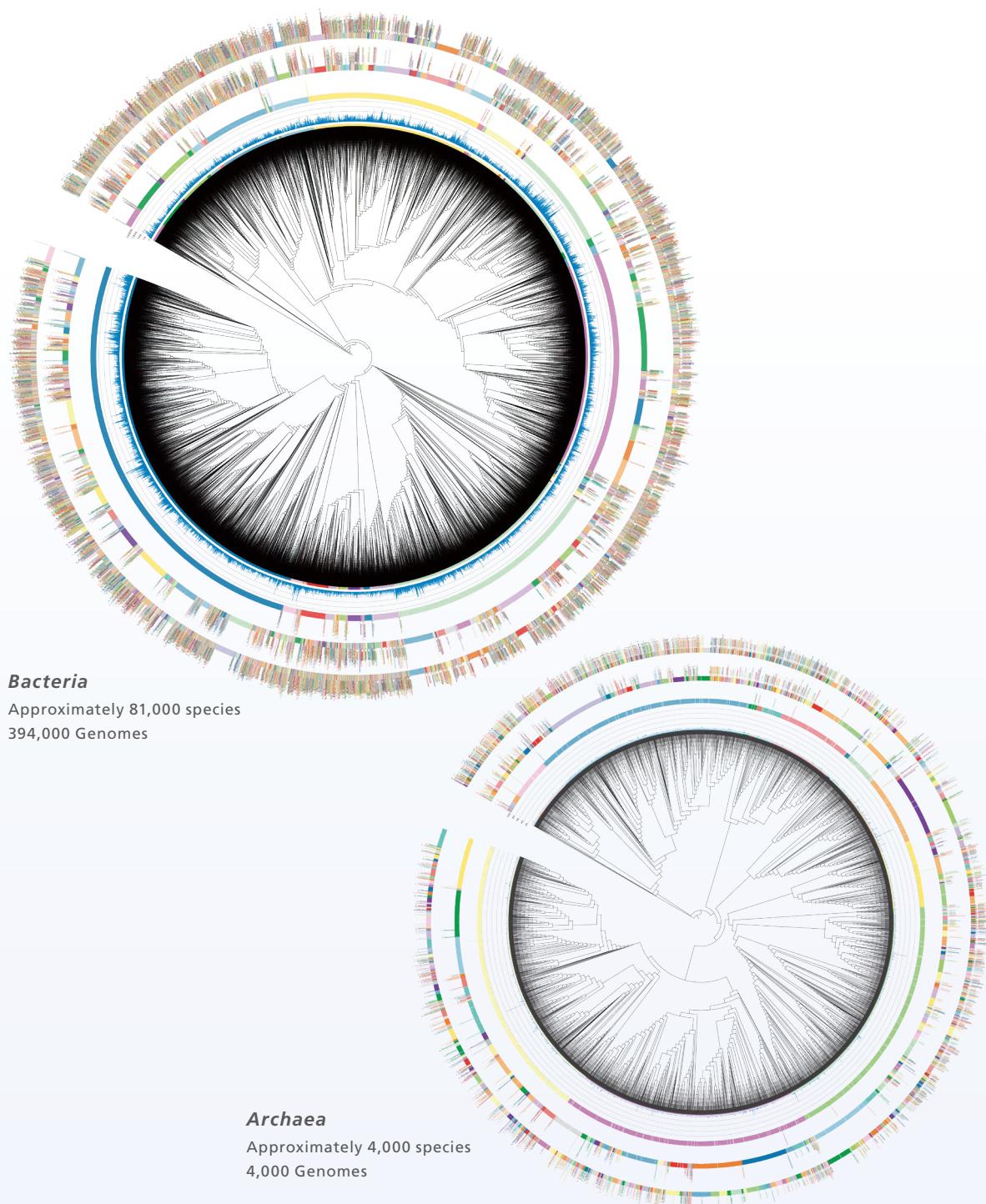
## Simple Operation

MicrobialTrack identifies microorganisms from MALDI mass spectra in three data analysis steps. The identification results display a ranked list of the most likely microbial species and their species-level taxa, along with icons color-coded based on the degree of confidence in the results.

# Database Built from Genomic Data

The MicrobialTrack database includes approximately 18,000 prokaryotic species (*Bacteria* and *Archaea*) with valid published taxonomic names, as well as about 85,000 prokaryotic species predicted based on genomic information, including difficult-to-culture and uncultured microorganisms. This database facilitates the identification of a wide variety of phylogenetic taxa beyond the capabilities of previous MALDI-TOF MS microorganism identification systems. Conventionally, identifying 96 cultures of isolates using nucleic acid-based techniques takes around 2 days, but MALDI-TOF MS with MicrobialTrack mass spectral analysis software can identify those 96 isolates within 3 hours<sup>Note</sup>.

Note: Throughput time for processing bacterial liquid culture using formic acid and acetonitrile.



## Taxonomy Framework Based on Genomics

Identification results are displayed with taxonomic names according to the Genome Taxonomy Database (GTDB, <https://gtdb.ecogenomic.org>). The GTDB defines species-level taxa based on the closeness of genomic sequences using average nucleotide identity (ANI: percentage identity of homologous regions between two genome sequences) and alignment factor (AF: percentage of homologous regions shared by two genome sequences). In the GTDB, the criteria for the species level are defined as having an ANI of 95% or higher and an AF of 65% or higher. MicrobialTrack uses the same criteria for defining species-level taxa and employs the same taxonomy string as the GTDB for other taxonomic ranks.

The MicrobialTrack database contains predicted theoretical protein masses derived from genomic data of uncultured and difficult-to-culture microorganisms, such as metagenome-assembled genomes (MAGs) and single-cell assembled genomes (SAGs). Many of these uncultured microorganisms lack valid taxonomic names and are instead assigned placeholder genus or species names in the GTDB (e.g., MGIIa-L1 and sp002965065). It is important to note that these placeholder names do not qualify as valid taxonomic names. Additional information regarding taxa with placeholder names is available on the GTDB website (<https://gtdb.ecogenomic.org>). The designations of these taxa may change as new research uncovers further information and valid published taxonomic names are assigned.

## Optimized for Different Purposes

- Users can select either of the two databases, "All" and "Reps", for microbial identification. The "All" database contains theoretical masses predicted from all genome sequences. In contrast, the "Reps" database includes those derived only from a single genome sequence representing a species-level taxon.
- For most species-level taxa, "All" contains protein information from multiple strains (genomes). For example, the taxon *Escherichia coli* contains protein information from over 30,000 genome sequences in the "All" database. "All" searches for the most closely matched strains in the database.
- In contrast, the "Reps" database contains only protein information from a single strain (genomic information) for one species. The "Reps" database is utilized to quickly estimate taxonomic identification at the genus and species levels. Searching within the "Reps" database allows evaluating which species closely match the measured spectrum against a list of potential candidates.



Note: The number of data points in the figure is based on information as of March 2025.

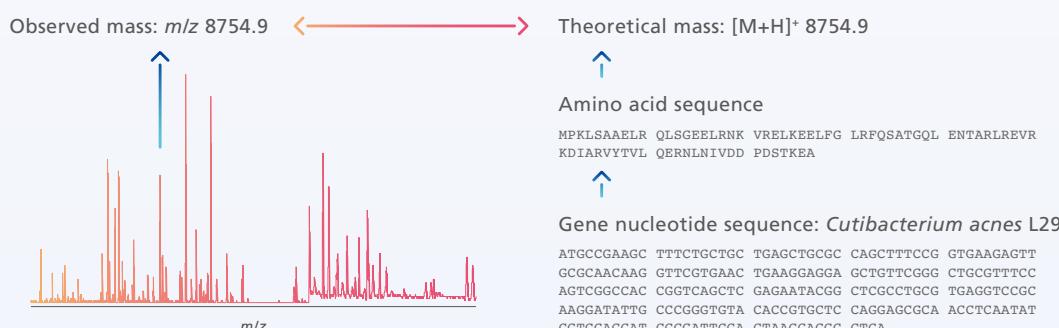
## Regular Updates, Aligned with the Latest Taxonomic Framework

The MicrobialTrack database is regularly updated to introduce newly identified bacterial and archaeal taxa and to reflect the latest GTDB taxonomy framework. The database is managed on a server, ensuring users have seamless access to the latest version during the license period.



## Proteomics-Based Identification

MicrobialTrack utilizes a database of theoretical masses predicted from genomic information to identify unknown microorganisms. Identification is achieved by comparing the observed masses from microbial cell MALDI-TOF MS analysis with theoretical masses. Advancements in genome sequencing technologies have greatly expanded prokaryotic genome sequence entries in public nucleotide sequence databases<sup>1)</sup>. A large-scale database of theoretical masses developed for MicrobialTrack and an original identification algorithm enable the rapid identification of a wide range of microbial species, independent of culture conditions or MALDI-TOF MS models<sup>2)</sup>.



1) PA. Demirev *et al.*, *Anal. Chem.* 71, 2732 (1999).

2) Y. Sekiguchi *et al.*, *Genome Biolog.* 24, 257 (2023).

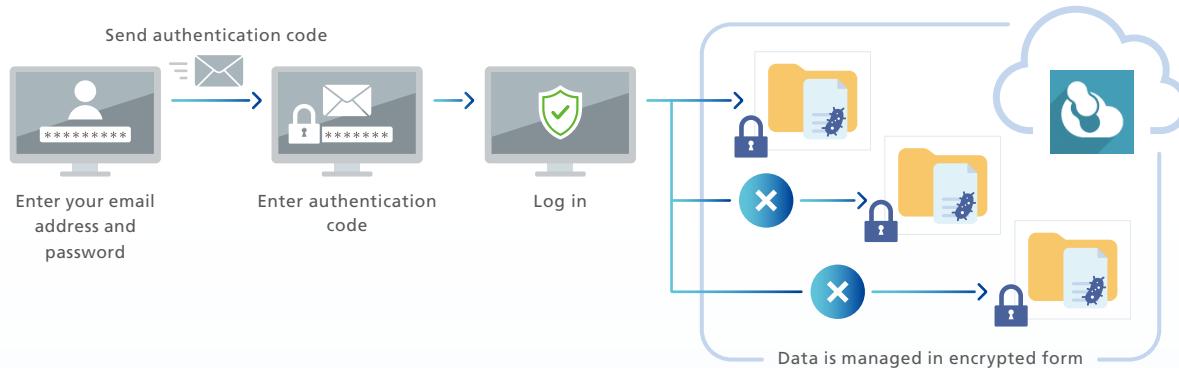
# Accessible Everywhere as a Cloud Service

## No Matter the Location, Easy to Implement

As a cloud-based service, there is no need to purchase a dedicated PC or install software. Users can access the dedicated URL from their own PC in any location as long as they have an internet-connected environment.

## Robust Security

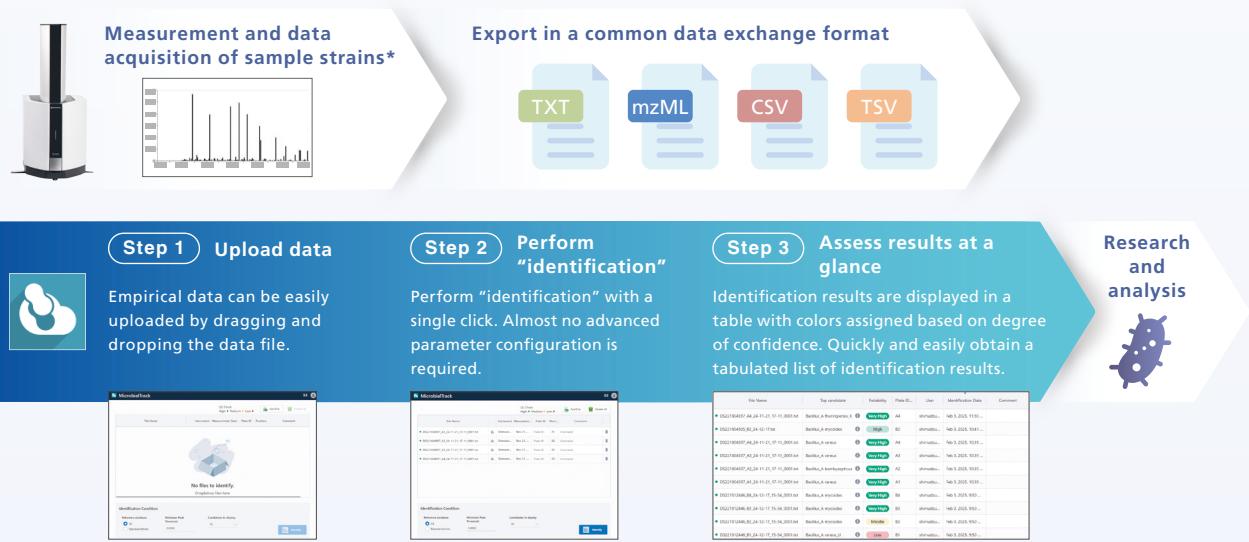
MicrobialTrack operates on a reliable cloud infrastructure with strict security features, including access controls. It maintains safety through regular monitoring of access logs, vulnerability assessments, and software updates, ensuring that the data of other users is not referenced, allowing you to use it with confidence. Furthermore, by utilizing multi-factor authentication (MFA), you can obtain an even higher level of security.



## Simple Operation

### Identification Completed in Just Three Steps

Microbial cells are analyzed using MALDI-TOF MS. Since it supports a universal format, the platform is vendor neutral. The resulting peak lists are compared to a theoretical mass database to identify the microorganisms. The identification process can be completed in just three steps. The identification results present a ranked list of candidate species, along with icons that are color-coded based on the degree of confidence. The results also allow users to verify which proteins from the microbial species were detected as the peaks.



Note: MicrobialTrack is not guaranteed to read data from all third-party equipment. Please refer to the product information website for a track record of previously read data.

## Advanced Identification of "Species Complexes"

MicrobialTrack redefines the "species complex" as taxa that comprise multiple species-level taxa, which are genetically distinct but often difficult to distinguish based solely on theoretical protein masses. MicrobialTrack identifies such species complexes based on theoretical protein masses and notifies users of this information.

Candidates Resampling General Info					
Rank	Species	NCBI Strain Identifiers	Reliability	Reliability Value	Details
1	Bacillus_A cereus	Staal7-6	Very High	15>	<a href="#">View</a>
2	Bacillus_A bombbysepticus	4XXS	Very High	15>	<a href="#">View</a>
3	Bacillus_A cereus	AFS099306	Very High	15>	<a href="#">View</a>

**Complex**

1 Bacillus\_A Bacillus\_A sp006494425, Bacillus\_A bombbysepticus, Bacillus\_A proteolyticus, Bacillus\_A albus, Bacillus\_A sp02584985, Bacillus\_A sp002571225, Bacillus\_A thuringiensis, Bacillus\_A cereus, Bacillus\_A cereus\_AZ, Bacillus\_A cereus\_K, Bacillus\_A cereus\_AT, Bacillus\_A thuringiensis\_K, Bacillus\_A cereus\_AG.

## Multifaceted Evaluation of Identification Results

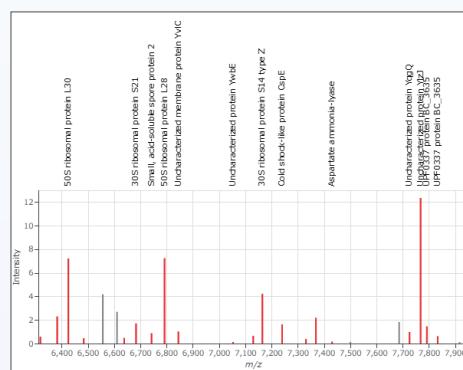
Identification results vary based on several factors, including the condition of the sample microorganisms, the preparation of the samples, and the quality of the MALDI mass spectra. Therefore, MicrobialTrack employs multiple performance metrics to evaluate each identification result from various perspectives. One of these methods involves using a portion of randomly selected observed peaks to repeat the identification process, and then displays which genus and species are identified as top-hit organisms during resampling, along with their frequency of occurrence. Based on this random resampling, the software provides an estimate of the identification certainty level at both the genus and species levels.

Candidates	Resampling	General Info
Genus	Bacillus_A	100%
Species	Bacillus_A cereus	60%
	Bacillus_A bombbysepticus	40%

## Advanced Proteomics Platform

MicrobialTrack uses the theoretical masses in the database to estimate which peak corresponds to which protein. Such a list of inferred protein names is displayed on the mass spectrum and in a tabular list. Mass peaks that match theoretical protein masses are also displayed in red for easy recognition in a mass peak graph in the software. As an optional feature, MicrobialTrack also allows users to view protein names, theoretical masses, and amino acid sequences for mass peaks.

Protein Peak Annotation				
m/z	Intensity	Estimated Protein Name	[M+H]+(avg.)	Sequence
8215.39939038538	0.377086745116754	UPF0410 protein YwzA	8218.1	MIWSLIVGGILGWLASL...
8644.49166379267	0.468668492767455	Dihydroorotate dehyd...	8646.9	DKVMNSDLPVVEQFD...
8644.49166379267	0.468668492767455	Uncharacterized mem...	8646.4	MAQLLGQQALIAVSH...
8644.49166379267	0.468668492767455	RNA-binding protein ...	8647	MKQSINIQDQFLNQLR...
8682.32021554924	2.41841376492772	Uncharacterized prote...	8684.4	MKELKKGKIEDYTRFGQI...
8682.32021554924	2.41841376492772	30S ribosomal protein...	8683.3	MAGRKGGRAKRRKVC...



## License Types and Periods of Validity

License	Duration	No. of Identifications	Display Estimated Protein Information
DEMO	30 days	100	No
BASIC 1 year	1 year	10,000	No (Yes*)
BASIC 3 years	3 years	35,000	No (Yes*)
BASIC 5 years	5 years	60,000	No (Yes*)
PRO 1 year	1 year	30,000	Yes
PRO 3 years	3 years	120,000	Yes
PRO 5 years	5 years	200,000	Yes

Note: Please contact your sales representative for a demo license.

\* This campaign is valid until March 31, 2027. Please note that the campaign may change without advance notice.

## Recommended System Requirements

Operating System	Windows 11, 64-bit
Browser	Microsoft Edge
Resolution	1920×1080 pixels

## Supported Microorganisms

Prokaryotes (*Bacteria* and *Archaea*)

\*Fungi (mold and yeast) are not supported

## Related Products

### MALDI-TOF MS



- MALDI-8020
- MALDI-8030
- MALDI-8020 EasyCare
- MALDI-8030 EasyCare

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- SampleStation™
- AuraSolution™

[Product >](#)

### Statistical Analysis Software for Direct Ionization Mass Spectrometry

- eMSTAT Solution™

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### Highly Accurate Bacterial Characterization Software

- Strain Solution Ver. 2

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