BRUKER

# Clinical Microbiology

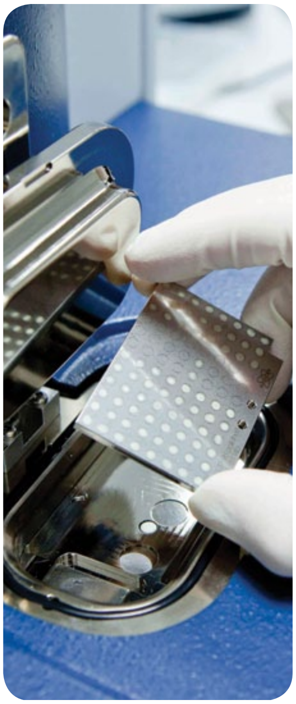
## MALDI Biotyper

- Fast & Accurate Identification of Microorganisms

MALDI-TOF

Innovation with Integrity

# In Microbiology, Every Minute Counts



### A Powerful Technology for Better Results

To help answer key challenges in Clinical Microbiology, Bruker has utilized its many years of experience to create the truly ground breaking **MALDI Biotyper** system. With its combination of performance and utility, the **MALDI Biotyper** has changed the way microbial identification is done in laboratories around the world.

### Identifying Microorganisms by Their Molecular Fingerprint

The **MALDI Biotyper** identifies microorganisms using MALDI-TOF (Matrix Assisted Laser Desorption Ionization-Time of Flight) Mass Spectrometry to measure a unique molecular fingerprint of an organism. Specifically, the **MALDI Biotyper** measures highly abundant proteins that are found in all microorganisms.

The characteristic patterns of these highly abundant proteins are used to reliably and accurately identify a particular microorganism by matching the respective pattern with an extensive open database to determine the identity of the microorganism down to the species level.

## The MALDI Biotyper System:

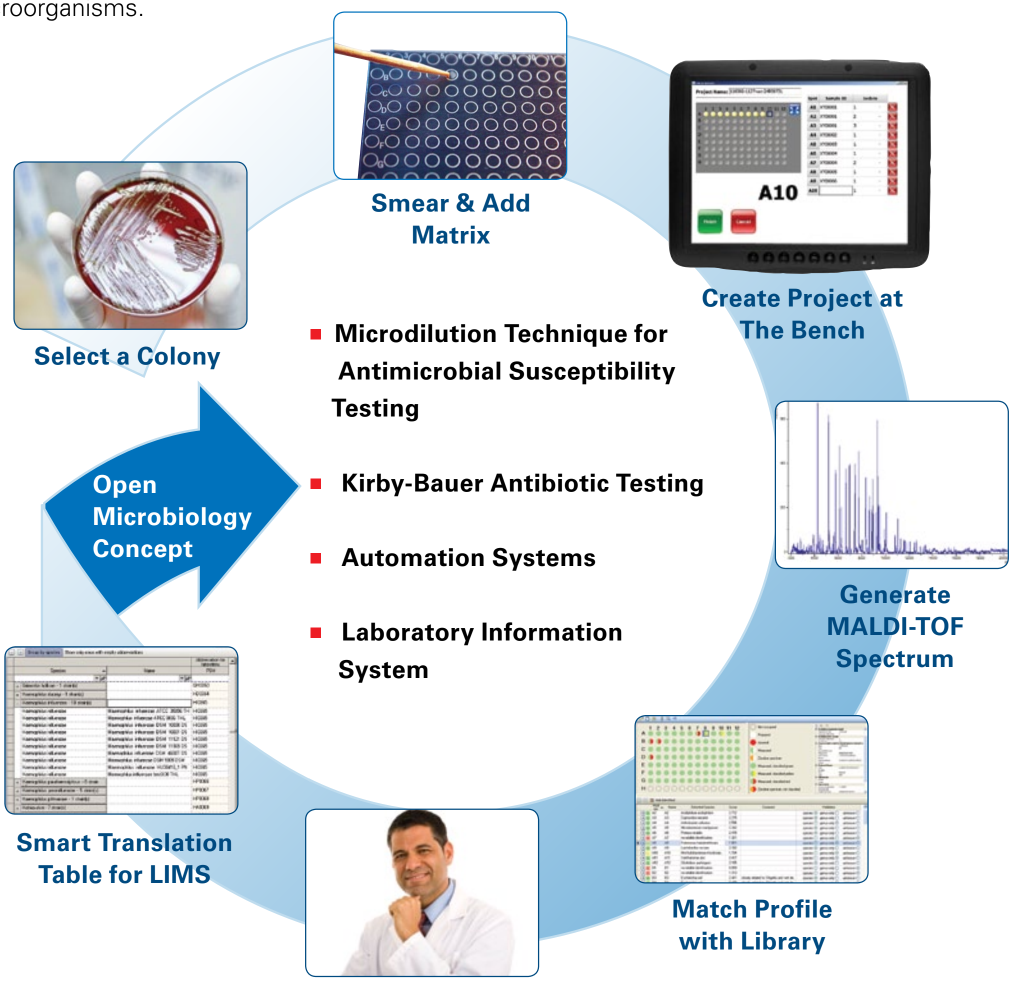
- **Highly Accurate**
- **Applicable to a Wide Range of Microorganisms**
- **Much Faster than Traditional Methods**
- **Cost Effective**
- **Robust and Easy to Use**

# A Simple Procedure for A Sophisticated Platform

## Innovative Design Leads to Enhanced Performance and Productivity

The **MALDI Biotyper** workflow has been designed to be as robust and easy to perform as possible. No previous experience with Mass Spectrometry is required. The workflow has been streamlined and requires only a few simple steps to generate high quality species identifications, our dedicated microbiology software automates the process of acquiring the mass spectrum and performing the library matching providing a report showing the closest matches to the extensive library of microorganisms.

Typically no more than a single colony from a plate or a small aliquot from a broth is required, the entire procedure requires only a few minutes to complete. Additional workflows are also available for the processing of positive blood cultures as well as other traditionally difficult to analyze groups of organisms including fungi and mycobacterium.



**Select a Colony**

**Smear & Add Matrix**

**Create Project at The Bench**

**Generate MALDI-TOF Spectrum**

**Match Profile with Library**

**Final Review by Microbiologist**

**Smart Translation Table for LIMS**

**Open Microbiology Concept**

- **Microdilution Technique for Antimicrobial Susceptibility Testing**
- **Kirby-Bauer Antibiotic Testing**
- **Automation Systems**
- **Laboratory Information System**

### CE-IVD Workflow

A fully validated workflow according to the European Union IVD Directive 98/79/EC is also available and utilizes most of the same strains contained within the combined database.

## Easy System Setup

# A Workflow that Empowers Microbiology Laboratories

### Choosing the Right Sample Platform

Bruker offers a selection of bar-coded, disposable, or reusable 24, 48, or 96 position Sample Targets to best suit your individual requirements. All sample positions can be randomly accessed by the system, in any combination, for maximum assay flexibility.

### Have an Urgent Sample?

No problem. Just pause the running project, exchange the sample target, and get results in a few minutes. The unique system design facilitates on-the-fly changes to handle urgent samples.

### Matches Your Sample Project

With on board barcode reading, the **MALDI Biotyper** matches your sample with its corresponding target, ensuring you never analyse the wrong samples.

# Make A Difference in Analyzing Positive Blood Cultures

**The efficient pathway for fast, reliable, unambiguous species identification from positive blood culture bottles**

## MALDI Sepsityper™ Kit

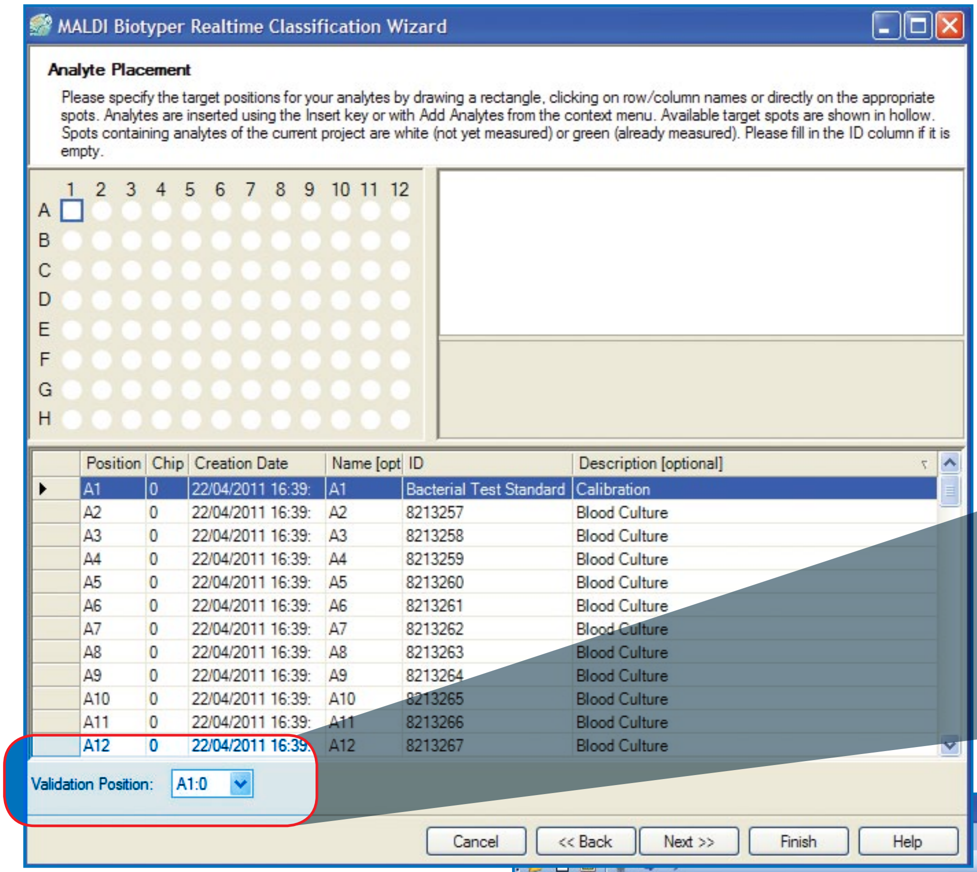
Using the MALDI Sepsityper Kit in combination with the **MALDI Biotyper**, can result in a 70-90% identification rate in positive blood culture samples,

This high confidence result is available much earlier than with conventional technology. Use of the Sepsityper Kit can typically save at least one day in the time-to-result for the crucial identification step in analyzing blood borne infections.

**Result Overview**

1 Harvest 1 ml blood culture liquid in a test tube
2 Add Lysis Buffer and centrifuge
3 Add Washing Buffer and centrifuge
4 Suspend pellet in water
5 Standard Bruker extraction protocol for MALDI bacterial profiling
6 Spotting of 1µl extract onto MALDI target, overlay with HCCA matrix
7 MALDI-TOF measurement
8 Receive Result, ID

# Easy to Use Software That's Dedicated to Microbiology…



**Analyte Placement**

Please specify the target positions for your analytes by drawing a rectangle, clicking on row/column names or directly on the appropriate spots. Analytes are inserted using the Insert key or with Add Analytes from the context menu. Available target spots are shown in hollow. Spots containing analytes of the current project are white (not yet measured) or green (already measured). Please fill in the ID column if it is empty.

| Position | Chip | Creation Date | Name [opt | ID | Description [optional] |
|---|---|---|---|---|---|
| A1 | 0 | 22/04/2011 16:39: | A1 | Bacterial Test Standard | Calibration |
| A2 | 0 | 22/04/2011 16:39: | A2 | 8213257 | Blood Culture |
| A3 | 0 | 22/04/2011 16:39: | A3 | 8213258 | Blood Culture |
| A4 | 0 | 22/04/2011 16:39: | A4 | 8213259 | Blood Culture |
| A5 | 0 | 22/04/2011 16:39: | A5 | 8213260 | Blood Culture |
| A6 | 0 | 22/04/2011 16:39: | A6 | 8213261 | Blood Culture |
| A7 | 0 | 22/04/2011 16:39: | A7 | 8213262 | Blood Culture |
| A8 | 0 | 22/04/2011 16:39: | A8 | 8213263 | Blood Culture |
| A9 | 0 | 22/04/2011 16:39: | A9 | 8213264 | Blood Culture |
| A10 | 0 | 22/04/2011 16:39: | A10 | 8213265 | Blood Culture |
| A11 | 0 | 22/04/2011 16:39: | A11 | 8213266 | Blood Culture |
| A12 | 0 | 22/04/2011 16:39 | A12 | 8213267 | Blood Culture |

Validation Position: A1:0

## The Wizard

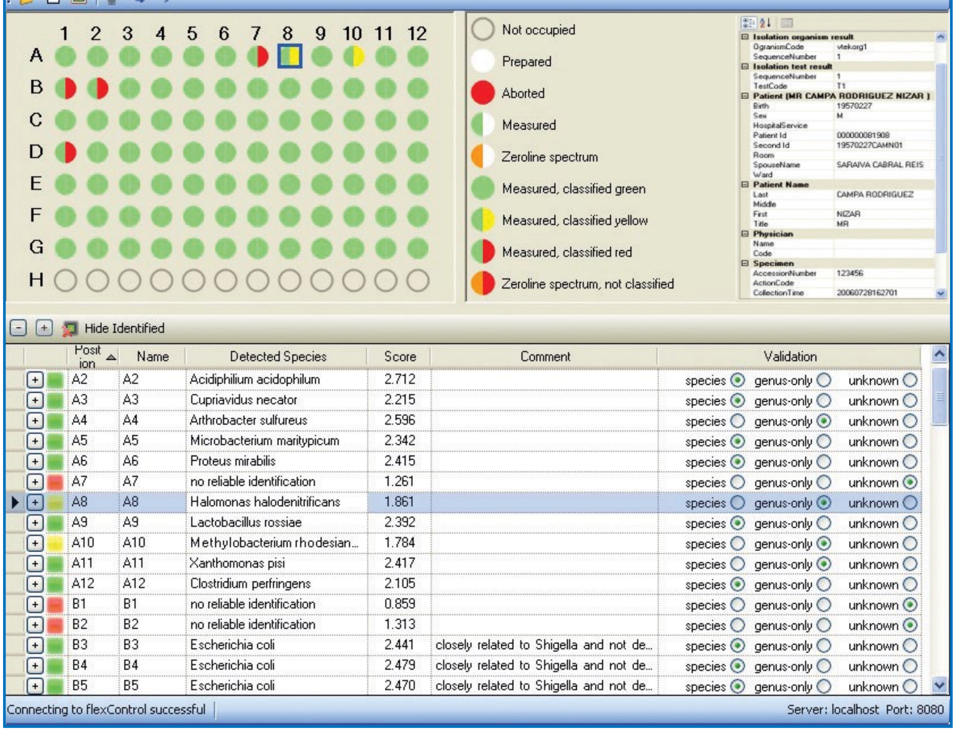
A simple to use Real Time Classification wizard guides you through setting up a sample for analysis in just a few easy steps. Import sample information from LIMS or Excel or even enter it manually using a barcode reader.

## Automatic Calibration

Using the Bruker Bacterial Test Standard, you can select any position on your target, and the **MALDI Biotyper** will automatically calibrate the system.

## Validate Your Results

The **MALDI Biotyper** expert system supports both the identification and validation of results. Make better, more informed decisions with the help of "matching hints" and view relevant sample data or information from your LIMS.



- ○ Not occupied
- ○ Prepared
- ● Aborted
- ◐ Measured
- ◐ Zeroline spectrum
- ● Measured, classified green
- ◐ Measured, classified yellow
- ◐ Measured, classified red
- ◐ Zeroline spectrum, not classified

| | |
|---|---|
| **⊟ Isolation organism result** | |
| OgranismCode | vitekorg1 |
| SequenceNumber | 1 |
| **⊟ Isolation test result** | |
| SequenceNumber | 1 |
| TestCode | T1 |
| **⊟ Patient (MR CAMPA RODRIGUEZ NIZAR )** | |
| Birth | 19570227 |
| Sex | M |
| HospitalService | |
| Patient Id | 000000081908 |
| Second Id | 19570227CAMN01 |
| Room | |
| SpouseName | SARAIVA CABRAL REIS |
| Ward | |
| **⊟ Patient Name** | |
| Last | CAMPA RODRIGUEZ |
| Middle | |
| First | NIZAR |
| Title | MR |
| **⊟ Physician** | |
| Name | |
| Code | |
| **⊟ Specimen** | |
| AccessionNumber | 123456 |
| ActionCode | |
| CollectionTime | 20060728162701 |

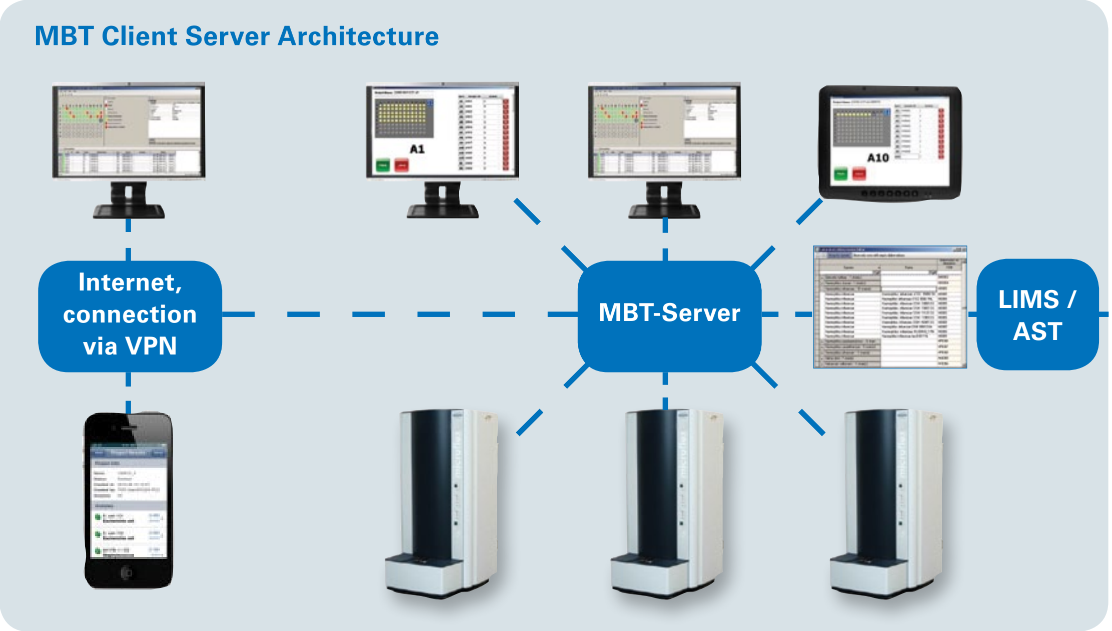
| | Position | Name | Detected Species | Score | Comment | Validation |
|---|---|---|---|---|---|---|
| 🟩 | A2 | A2 | Acidiphilium acidophilum | 2.712 | | species ● genus-only ○ unknown ○ |
| 🟩 | A3 | A3 | Cupriavidus necator | 2.215 | | species ● genus-only ○ unknown ○ |
| 🟩 | A4 | A4 | Arthrobacter sulfureus | 2.596 | | species ○ genus-only ● unknown ○ |
| 🟩 | A5 | A5 | Microbacterium maritypicum | 2.342 | | species ● genus-only ○ unknown ○ |
| 🟩 | A6 | A6 | Proteus mirabilis | 2.415 | | species ● genus-only ○ unknown ○ |
| 🟥 | A7 | A7 | no reliable identification | 1.261 | | species ○ genus-only ○ unknown ● |
| 🟨 | A8 | A8 | Halomonas halodenitrificans | 1.861 | | species ○ genus-only ● unknown ○ |
| 🟩 | A9 | A9 | Lactobacillus rossiae | 2.392 | | species ● genus-only ○ unknown ○ |
| 🟨 | A10 | A10 | Methylobacterium rhodesian… | 1.784 | | species ○ genus-only ● unknown ○ |
| 🟩 | A11 | A11 | Xanthomonas pisi | 2.417 | | species ○ genus-only ● unknown ○ |
| 🟩 | A12 | A12 | Clostridium perfringens | 2.105 | | species ● genus-only ○ unknown ○ |
| 🟥 | B1 | B1 | no reliable identification | 0.859 | | species ○ genus-only ○ unknown ● |
| 🟥 | B2 | B2 | no reliable identification | 1.313 | | species ○ genus-only ○ unknown ● |
| 🟩 | B3 | B3 | Escherichia coli | 2.441 | closely related to Shigella and not de… | species ● genus-only ○ unknown ○ |
| 🟩 | B4 | B4 | Escherichia coli | 2.479 | closely related to Shigella and not de… | species ● genus-only ○ unknown ○ |
| 🟩 | B5 | B5 | Escherichia coli | 2.470 | closely related to Shigella and not de… | species ● genus-only ○ unknown ○ |

Connecting to flexControl successful

Server: localhost Port: 8080

# …With A Powerful & Flexible Data System Architecture

### MBT Client Server Architecture



### Direct Connection to LIMS

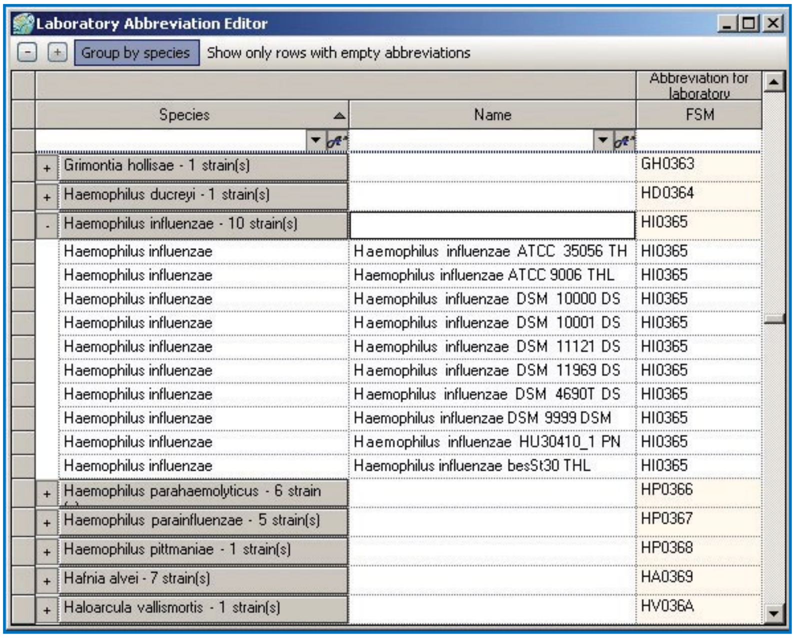
All LIMS integration is handled by the MBT Server.  CSV and ASTM are supported as exchange formats and have established connections to many LIMS providers.

## Easy Integration with Laboratory Informatics

The central **MALDI Biotyper** Server manages all requests for information and stores all data. The Server also manage requests and processes data from several instruments or remote clients. Installation of  remote clients on existing computers in the laboratory is supported. This enables system set up and operation directly from the lab bench, or allows for the validation of an already completed run.

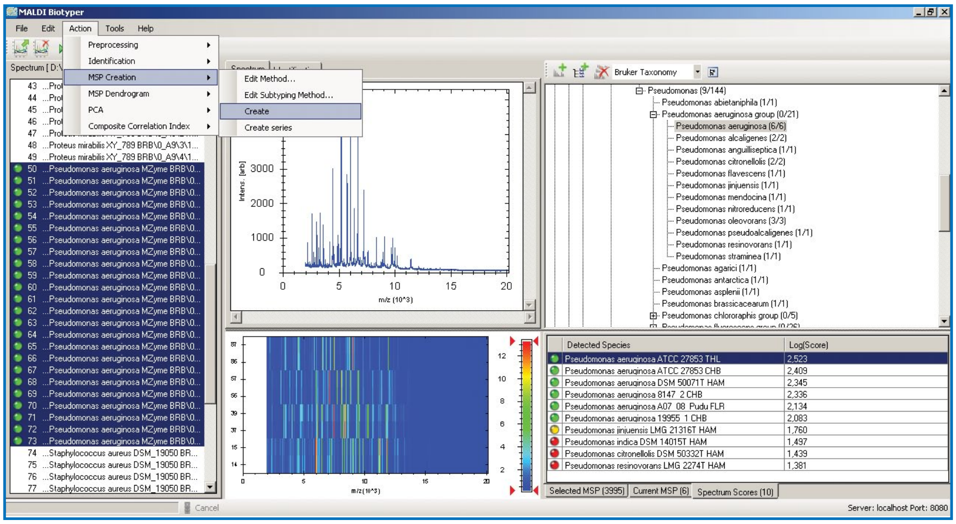
## Translate Your Results

Using the customizable smart translation tool, the thousands of species covered by the **MALDI Biotyper** are automatically converted into a format that a LIS, an expert system, or an AST System can understand.



| | | | Abbreviation for laboratory |
|---|---|---|---|
| | Species | Name | FSM |
| + | Grimontia hollisae - 1 strain(s) | | GH0363 |
| + | Haemophilus ducreyi - 1 strain(s) | | HD0364 |
| - | Haemophilus influenzae - 10 strain(s) | | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae ATCC 35056 TH | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae ATCC 9006 THL | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 10000 DS | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 10001 DS | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 11121 DS | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 11969 DS | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 4690T DS | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae DSM 9999 DSM | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae HU30410_1 PN | HI0365 |
| | Haemophilus influenzae | Haemophilus influenzae besSt30 THL | HI0365 |
| + | Haemophilus parahaemolyticus - 6 strain | | HP0366 |
| + | Haemophilus parainfluenzae - 5 strain(s) | | HP0367 |
| + | Haemophilus pittmaniae - 1 strain(s) | | HP0368 |
| + | Hafnia alvei - 7 strain(s) | | HA0369 |
| + | Haloarcula vallismortis - 1 strain(s) | | HV036A |

# An Open Microbiology Platform and Database



43 ...Pro
44 ...Pro
45 ...Pro
46 ...Pro
47 ...Pro
48 ...Proteus mirabilis XY_789 BRB\0_A9\3\1...
49 ...Proteus mirabilis XY_789 BRB\0_A9\4\1...
50 ...Pseudomonas aeruginosa MZyme BRB\0...
51 ...Pseudomonas aeruginosa MZyme BRB\0...
52 ...Pseudomonas aeruginosa MZyme BRB\0...
53 ...Pseudomonas aeruginosa MZyme BRB\0...
54 ...Pseudomonas aeruginosa MZyme BRB\0...
55 ...Pseudomonas aeruginosa MZyme BRB\0...
56 ...Pseudomonas aeruginosa MZyme BRB\0...
57 ...Pseudomonas aeruginosa MZyme BRB\0...
58 ...Pseudomonas aeruginosa MZyme BRB\0...
59 ...Pseudomonas aeruginosa MZyme BRB\0...
60 ...Pseudomonas aeruginosa MZyme BRB\0...
61 ...Pseudomonas aeruginosa MZyme BRB\0...
62 ...Pseudomonas aeruginosa MZyme BRB\0...
63 ...Pseudomonas aeruginosa MZyme BRB\0...
64 ...Pseudomonas aeruginosa MZyme BRB\0...
65 ...Pseudomonas aeruginosa MZyme BRB\0...
66 ...Pseudomonas aeruginosa MZyme BRB\0...
67 ...Pseudomonas aeruginosa MZyme BRB\0...
68 ...Pseudomonas aeruginosa MZyme BRB\0...
69 ...Pseudomonas aeruginosa MZyme BRB\0...
70 ...Pseudomonas aeruginosa MZyme BRB\0...
71 ...Pseudomonas aeruginosa MZyme BRB\0...
72 ...Pseudomonas aeruginosa MZyme BRB\0...
73 ...Pseudomonas aeruginosa MZyme BRB\0...
74 ...Staphylococcus aureus DSM_19050 BR...
75 ...Staphylococcus aureus DSM_19050 BR...
76 ...Staphylococcus aureus DSM_19050 BR...
77 ...Staphylococcus aureus DSM_19050 BR...

- Pseudomonas (9/144)
  - Pseudomonas abietaniphila (1/1)
  - Pseudomonas aeruginosa group (0/21)
    - Pseudomonas aeruginosa (6/6)
    - Pseudomonas alcaligenes (2/2)
    - Pseudomonas anguilliseptica (1/1)
    - Pseudomonas citronellolis (2/2)
    - Pseudomonas flavescens (1/1)
    - Pseudomonas jinjuensis (1/1)
    - Pseudomonas mendocina (1/1)
    - Pseudomonas nitroreducens (1/1)
    - Pseudomonas oleovorans (3/3)
    - Pseudomonas pseudoalcaligenes (1/1)
    - Pseudomonas resinovorans (1/1)
    - Pseudomonas straminea (1/1)
  - Pseudomonas agarici (1/1)
  - Pseudomonas antarctica (1/1)
  - Pseudomonas asplenii (1/1)
  - Pseudomonas brassicacearum (1/1)
  - Pseudomonas chlororaphis group (0/5)

| | Detected Species | Log(Score) |
|---|---|---|
| ● | Pseudomonas aeruginosa ATCC 27853 THL | 2,523 |
| ● | Pseudomonas aeruginosa ATCC 27853 CHB | 2,409 |
| ● | Pseudomonas aeruginosa DSM 50071T HAM | 2,345 |
| ● | Pseudomonas aeruginosa 8147 2 CHB | 2,336 |
| ● | Pseudomonas aeruginosa A07 08 Pudu FLR | 2,134 |
| ● | Pseudomonas aeruginosa 19955 1 CHB | 2,083 |
| ● | Pseudomonas jinjuensis LMG 21316T HAM | 1,760 |
| ● | Pseudomonas indica DSM 14015T HAM | 1,497 |
| ● | Pseudomonas citronellolis DSM 50332T HAM | 1,439 |
| ● | Pseudomonas resinovorans LMG 2274T HAM | 1,381 |

Selected MSP (3995) | Current MSP (6) | Spectrum Scores (10)

Server: localhost Port: 8080

## The Main Spectra Concept

Database entries in the MALDI Biotyper are stored as Main Spectra (MSP). These MSPs are based on multiple measurements of a single defined strain to ensure that the true biological variability of an organism has been captured.

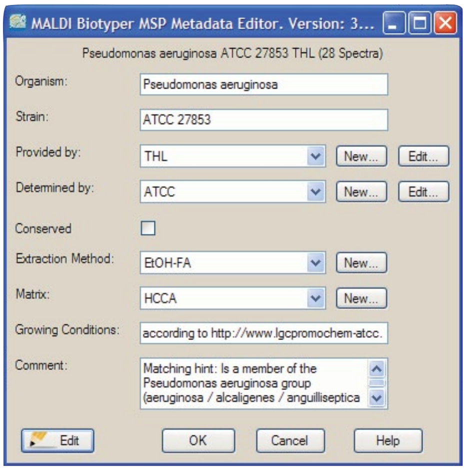
An unbiased sophisticated algorithm creates the MSP completely unsupervised by extracting information about peak position, intensity and frequency, while employing very effective de-noising and patented mass corrections to the peak data.

Unknowns are then compared to the MSP library using a superior pattern matching approach which is based on true statistical multi-variant analysis; and includes peak positions, intensities and frequencies ensuring the highest possible levels of accuracy and reproducibility across the complete range of microbes.

## An Open and Comprehensive Database

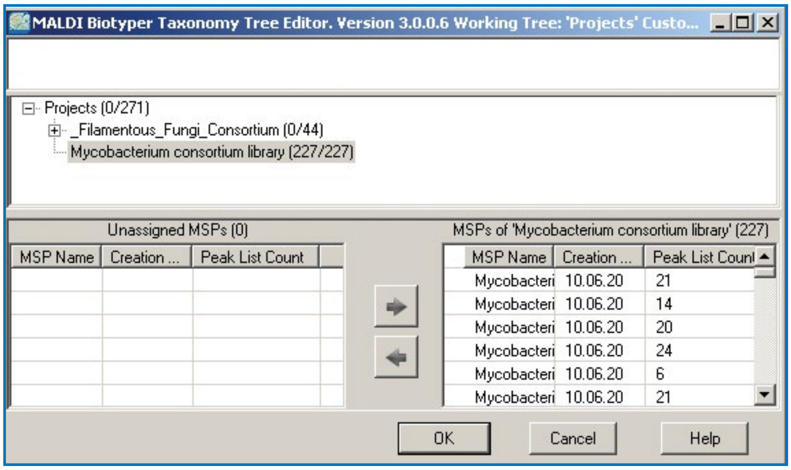
**MALDI Biotyper** integrates a ready to use reference library of microorganisms comprising thousands of individual strains of microorganisms. The library is constantly maintained and updated with contributions from many collaborating partners from countries around the world.

MSPs can be created and added to the database by users. This process is simple and highly automated within the software. MSP's can then be associated into their unique libraries with just a few additional mouse clicks.



Pseudomonas aeruginosa ATCC 27853 THL (28 Spectra)

Organism: Pseudomonas aeruginosa
Strain: ATCC 27853
Provided by: THL
Determined by: ATCC
Conserved ☐
Extraction Method: EtOH-FA
Matrix: HCCA
Growing Conditions: according to http://www.lgcpromochem-atcc.
Comment: Matching hint: Is a member of the Pseudomonas aeruginosa group (aeruginosa / alcaligenes / anguilliseptica



- Projects (0/271)
  - _Filamentous_Fungi_Consortium (0/44)
  - Mycobacterium consortium library (227/227)

Unassigned MSPs (0)

| MSP Name | Creation ... | Peak List Count |
|---|---|---|

MSPs of 'Mycobacterium consortium library' (227)

| MSP Name | Creation ... | Peak List Count |
|---|---|---|
| Mycobacteri | 10.06.20 | 21 |
| Mycobacteri | 10.06.20 | 14 |
| Mycobacteri | 10.06.20 | 20 |
| Mycobacteri | 10.06.20 | 24 |
| Mycobacteri | 10.06.20 | 6 |
| Mycobacteri | 10.06.20 | 21 |

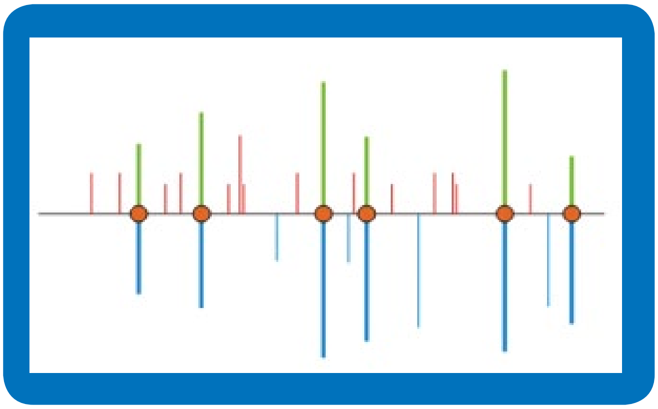
## Continuous Database Expansion and Expert Support

Bruker is fully committed to the future development of the database. An active program of library generation culminates in regular database updates for **MALDI Biotyper** users. These updates are especially focused in areas of major clinical importance.

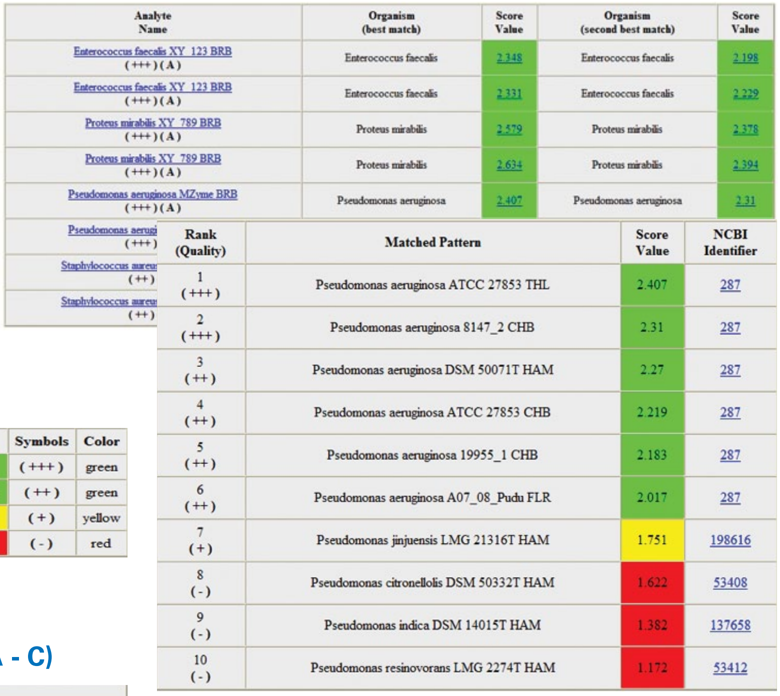
# Rigorous and Sophisticated Data Analysis Assures Accuracy

## Analyzing and Displaying Results

Sample data can be displayed against different reference strains. Sample data is displayed above the axis, while Reference data is displayed below in blue. Perfect matches between the sample data and the reference standard are indicated in green. Differences between the sample and reference are highlighted in red. Light blue indicates peaks found in the reference, but not the sample.



## Result Overview



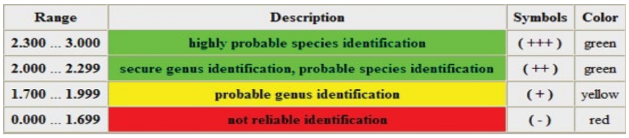
| Analyte Name | Organism (best match) | Score Value | Organism (second best match) | Score Value |
|---|---|---|---|---|
| Enterococcus faecalis XY_123 BRB<br>( +++ ) ( A ) | Enterococcus faecalis | 2.348 | Enterococcus faecalis | 2.198 |
| Enterococcus faecalis XY_123 BRB<br>( +++ ) ( A ) | Enterococcus faecalis | 2.331 | Enterococcus faecalis | 2.229 |
| Proteus mirabilis XY_789 BRB<br>( +++ ) ( A ) | Proteus mirabilis | 2.579 | Proteus mirabilis | 2.378 |
| Proteus mirabilis XY_789 BRB<br>( +++ ) ( A ) | Proteus mirabilis | 2.634 | Proteus mirabilis | 2.394 |
| Pseudomonas aeruginosa MZyme BRB<br>( +++ ) ( A ) | Pseudomonas aeruginosa | 2.407 | Pseudomonas aeruginosa | 2.31 |
| Pseudomonas aerugi<br>( +++ ) | | | | |
| Staphylococcus aureu<br>( ++ ) | | | | |
| Staphylococcus aureu<br>( ++ ) | | | | |

| Rank (Quality) | Matched Pattern | Score Value | NCBI Identifier |
|---|---|---|---|
| 1<br>( +++ ) | Pseudomonas aeruginosa ATCC 27853 THL | 2.407 | 287 |
| 2<br>( +++ ) | Pseudomonas aeruginosa 8147_2 CHB | 2.31 | 287 |
| 3<br>( ++ ) | Pseudomonas aeruginosa DSM 50071T HAM | 2.27 | 287 |
| 4<br>( ++ ) | Pseudomonas aeruginosa ATCC 27853 CHB | 2.219 | 287 |
| 5<br>( ++ ) | Pseudomonas aeruginosa 19955_1 CHB | 2.183 | 287 |
| 6<br>( ++ ) | Pseudomonas aeruginosa A07_08_Pudu FLR | 2.017 | 287 |
| 7<br>( + ) | Pseudomonas jinjuensis LMG 21316T HAM | 1.751 | 198616 |
| 8<br>( - ) | Pseudomonas citronellolis DSM 50332T HAM | 1.622 | 53408 |
| 9<br>( - ) | Pseudomonas indica DSM 14015T HAM | 1.382 | 137658 |
| 10<br>( - ) | Pseudomonas resinovorans LMG 2274T HAM | 1.172 | 53412 |

## Scoring the Results

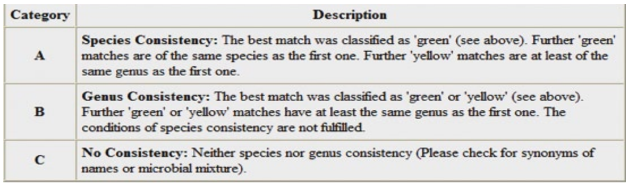
The resultant report for each sample shows the top two matches along with their respective matching score. The top ten matches, along with precise information about the closest matching strain, can also be displayed.

## Meaning of Score Values



| Range | Description | Symbols | Color |
|---|---|---|---|
| 2.300 ... 3.000 | highly probable species identification | ( +++ ) | green |
| 2.000 ... 2.299 | secure genus identification, probable species identification | ( ++ ) | green |
| 1.700 ... 1.999 | probable genus identification | ( + ) | yellow |
| 0.000 ... 1.699 | not reliable identification | ( - ) | red |

## Meaning of Consistency Categories (A - C)



| Category | Description |
|---|---|
| A | **Species Consistency:** The best match was classified as 'green' (see above). Further 'green' matches are of the same species as the first one. Further 'yellow' matches are at least of the same genus as the first one. |
| B | **Genus Consistency:** The best match was classified as 'green' or 'yellow' (see above). Further 'green' or 'yellow' matches have at least the same genus as the first one. The conditions of species consistency are not fulfilled. |
| C | **No Consistency:** Neither species nor genus consistency (Please check for synonyms of names or microbial mixture). |

## Grading the Results

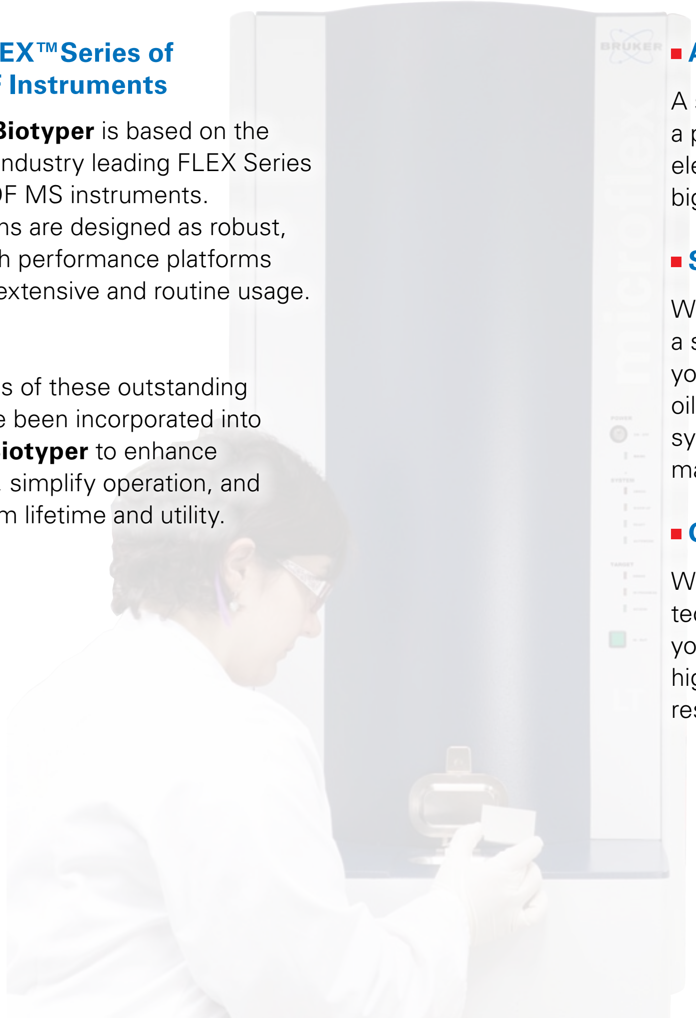
In addition to the score, the sample match result is also given a Consistency Category. This data parameter gives a indication of the degree of consistency. The categories are rated as Species Consistent, Genus Consistent, or No Consistency.

# The Best Technology from The Market Leader in MALDI-TOF

## Bruker's FLEX™ Series of MALDI-TOF Instruments

The **MALDI Biotyper** is based on the well proven, industry leading FLEX Series of MALDI-TOF MS instruments. These systems are designed as robust, compact, high performance platforms intended for extensive and routine usage.

Many features of these outstanding systems have been incorporated into the **MALDI Biotyper** to enhance performance, simplify operation, and extend system lifetime and utility.



## A True Bench Top System

A smart compact design that packs a punch. Employs the same high end electronics and developments from its big brothers.

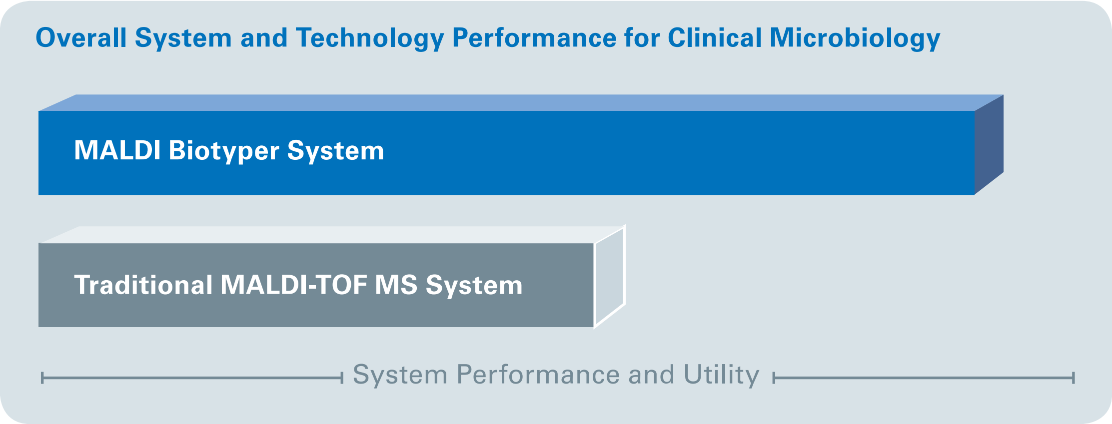
## Silent and Pleasant Operation

With WhisperMode™ you really have a system that can sit on bench next to you almost silently. By eliminating noisy oil based vacuum pumps, the vacuum system is not only quiet, but virtually maintenance free.

## Greatly Enhanced Sensitivity

With the most sensitive detector technology available (FlashDetector™) you can benefit from having the same high performance technology as large research grade instruments.

# Size Doesn't Equal Performance



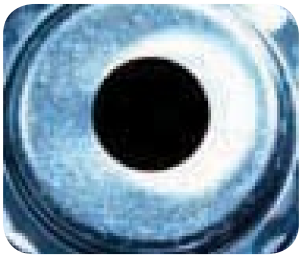
### Full Spectrum Resolution

Patented, intelligent pulsed Ion Extraction across a wide protein mass range. This unique technology enhances peak resolution and separation, and mitigates the need for unnecessarily long and bulky instrument flight tubes.

# Maximize Laboratory Productivity and Return on Investment

### Self Cleaning Source

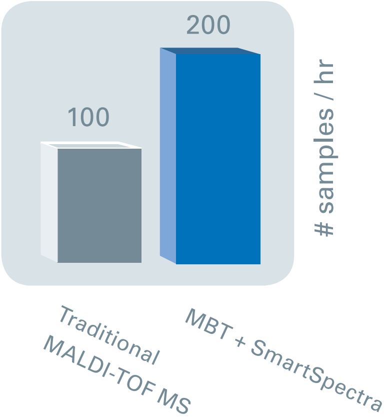
The Perpetual™ Ion Source* is a unique, automated self cleaning instrument source. This technology enables routine maintenance of the system to insure peak performance in less than 15 minutes without the costly and time consuming need to break system vacuum. *Patent pending

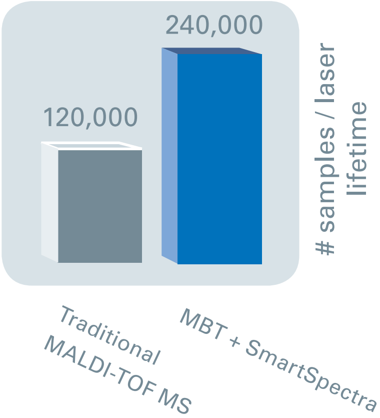

Before Cleaning

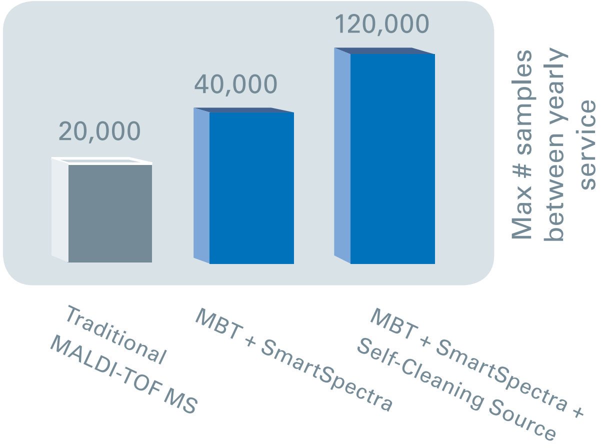

After Cleaning

### SmartSpectra™ Acquisition

This capability accelerates data acquisition speed by minimizing the time and amount of sample needed to generate a signal. Typically, 96 samples can be fully analyzed in well under 30 minutes.







# Technical Specifications

## Dimensions & Operating Parameters

| | |
|---|---|
| LxWxH: | 510 x 680 x 1093mm [20.1" x 26.8" x 43"] |
| Weight: | 84kg (185 lb) net weight |
| Noise: | <30 dB under normal operating conditions |
| Temp Range: | 10-30°C (50-86°F) |
| Operating Humidity: | 15-85% non-condensing @ 30°C |

### Instrument: Microflex LT

- Nitrogen Laser with 60Hz repetition rate
- Full Spectrum Resolution (FSR) with broadband focusing mode (PAN™)
- Smart Spectra Acquisition™
- Perpetual Ion Source™ with IR-laser self-cleaning functionality
- FlashDetector™
- Whispermode™
- Oil-free membrane pre-vacuum pump and turbo pump
- Manufactured under all cGMP and QSR regulations

### Microbial Identification Applications:

- Gram +/- Bacteria, Yeast, Fungi, Filamentous Fungi, Mycobacteria, Direct from Blood Culture

### Computer, Software & Database:

- Windows XP operating system with Quad-Core CPU 2.66 GHz, Laser printer and Remote Service Capability via 128-bit SSL
- **MALDI Biotyper** Database
- **MALDI Biotyper** Client Server

### Optional System Upgrades and Accessories:

- IVD **MALDI Biotyper** Software according to the European Union IVD Directive 98/79/EC
- Sepsityper Kit for processing samples directly from Blood Cultures

### Sample Targets:

- Reusable Polished Stainless Steel Targets: 48 & 96 position with and without barcode
- Disposable 48 position Biotargets with individual barcode
- 24 and 96 position BigAnchorChip™ Targets

**Frank Laukien, President & CEO**
**Bruker Corporation**

> "Bruker is a pioneer and leader in providing mass spectrometry systems for the clinical laboratory. Bruker optimizes and enhances its systems to bring the analytical power and utility of sophisticated, high performance instruments to bear on improving the capabilities, time to result, and data quality in clinical laboratories.
>
> Bruker systems are not just leading technology, they can be the pathway to delivering the answers needed to manage and treat serious health issues around the world."

For research use only. Not for use in diagnostic procedures.

**Bruker Daltonik GmbH**

Bremen · Germany
Phone +49 (0)421-2205-0
Fax +49 (0)421-2205-103
sales@bdal.de

**Bruker Daltonics Inc.**

Billerica, MA · USA
Phone +1 (978) 663-3660
Fax +1 (978) 667-5993
ms-sales@bdal.com

Fremont, CA · USA
Phone +1 (510) 683-4300
Fax +1 (510) 687-1217
cam-sales@bruker.com

**www.bruker.com**