青源峰达
Quenda

Beyond 5000

Automatic Clinical Microbial Mass Spectrometry

One hardware platform can complete the identification of viruses, bacteria and fungi

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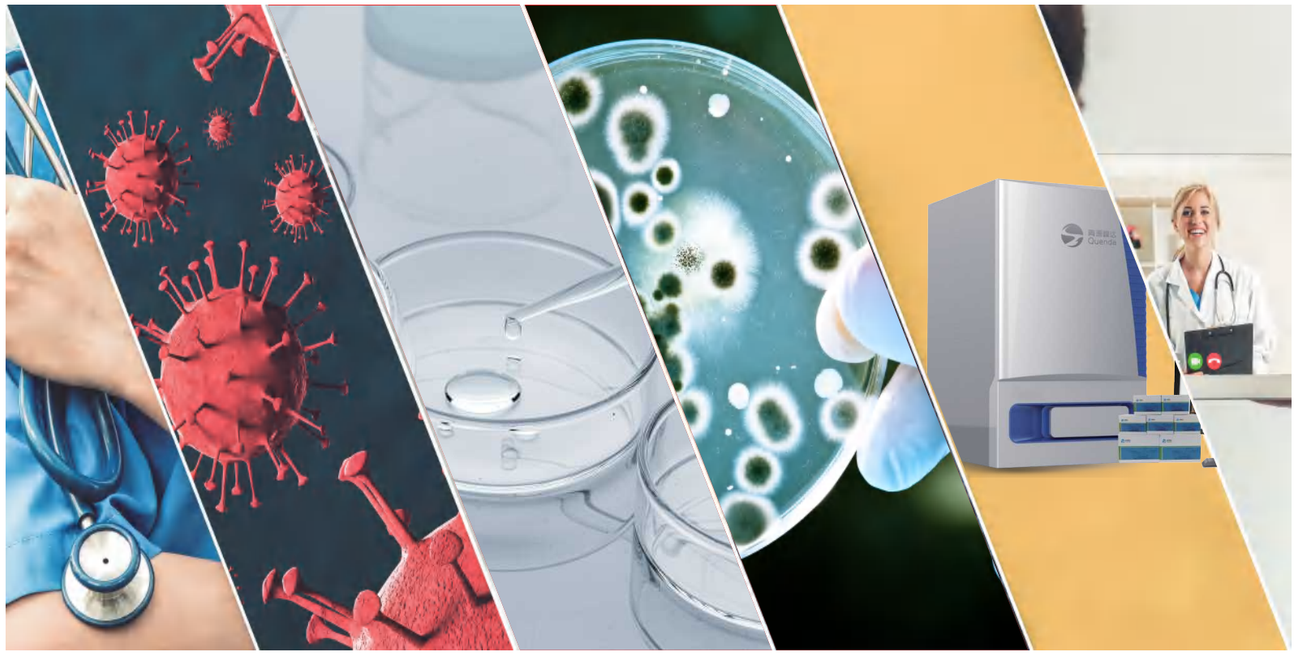
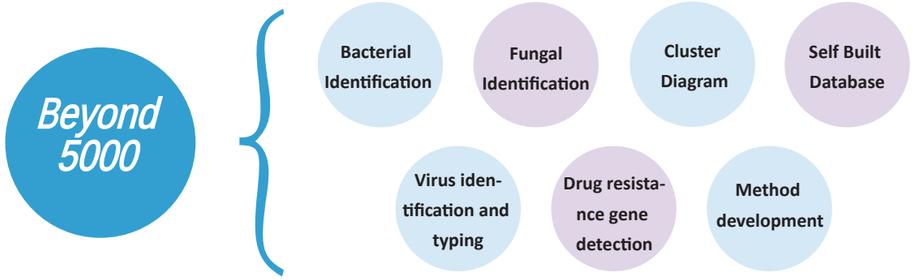


Beyond 5000

HAVE CLASS II INSTRUMENT REGISTRATION CERTIFICATE AND CLASS II KIT REGISTRATION CERTIFICATE

- One device can complete the identification of viruses, bacteria and fungi, and provide accurate diagnostic reports for clinic
- Accurately identify the bacteria to the species level within ten minutes
- Mass spectrometry virus identification system with independent intellectual property rights



Gram positive bacteria identification Kit	**CLASS II**
Gram negative bacilli identification Kit	**CLASS II**
Yeast identification Kit	**CLASS II**
Mycobacterium and nocardia sample processing kit	**CLASS I**
Filamentous fungi sample processing kit	**CLASS I**

Special stainless steel target plate for microbial identification

CORE ADVANTAGES

1. One device can identify viruses, bacteria and fungi;

2. The detection cycle is short, and 96 samples can be detected in 10 minutes. It features fast data processing without waiting;

3. High reproducibility without frequent calibration, CV < 3%;

4. The data acquisition and analysis are completed with one key, and the sample pretreatment is simple, time-saving and labor-saving;

5. 5000Hz semiconductor laser is free for replacement, reagent cost is low and with no special consumables.

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A NEW GENERATION OF AUTOMATIC MICROBIAL MASS SPECTROMETRY IDENTIFICATION SYSTEM

Wide spectrum:

The new generation MALDI-TOF MS with wide mass range (10-1000000 Da) detection ability still has high sensitivity in high mass region (especially when the molecular weight is greater than 400000 Da)

Tailored for clinical applications:

Revolutionary improvement of MALDI-TOF MS sensitivity, reproducibility, detection time and accuracy

Accurate Results

Fast Detection

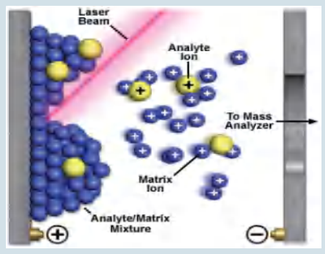
Easy to Use

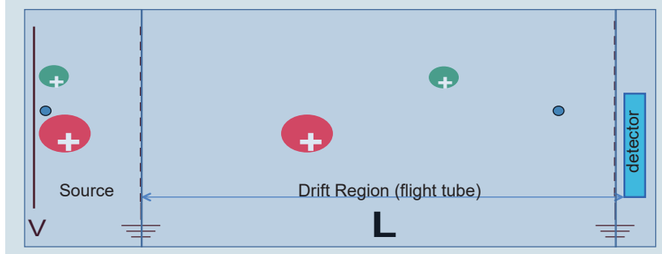
Stable Performance

Principle of Beyond 5000 **Mass spectrometry**

- Matrix assisted laser desorption ionization (MALDI): the analyte and matrix molecules form cocrystal on the target plate. After the laser energy is triggered, the matrix absorbs energy and transmits it to the analyte. Proton transfer occurs between them to ionize the analyte.

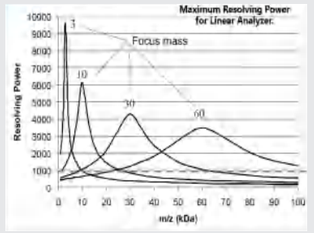
- Time of flight mass spectrometry (TOF-MS): after accelerating in the electric field, ions fly freely through the field free area and finally arrive at the detector. Its flight time is directly proportional to the mass charge ratio (M/z). Qualitative and quantitative analysis can be realized according to the time and quantity of ions arriving at the detector.



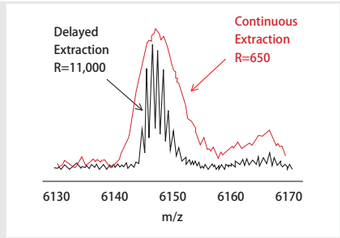


Innovate patented high-speed data acquisition and data processing technology to improve the reproducibility of spectrum

- Velocity and spatial synchronous focusing technology can achieve high resolution and sensitivity in a wide quality range.

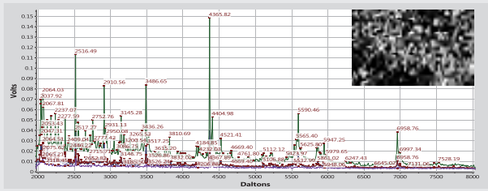


MALDI-TOF MS has different performance in the full quality detection range

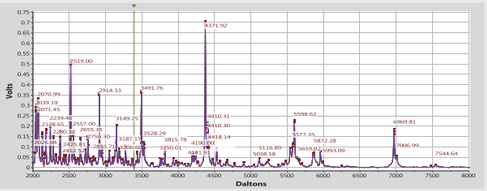


Innovation: speed and space synchronous focusing technology

- High frequency, long-life semiconductor laser, increase the sampling frequency, so that the reproducibility of the spectrum is high and can be quantified.

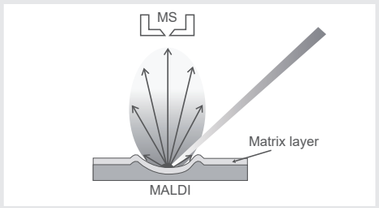


The reproducibility of mass spectrum is low under the traditional low laser emission times

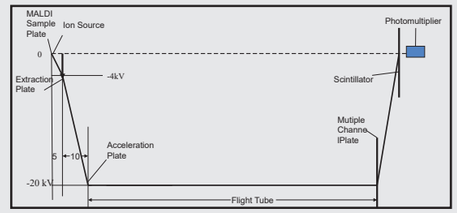


The spectrum has high reproducibility and can be quantified

- Patent: simultaneous grounding technology of target plate and ion detector eliminates the electric field effect at the edge of target plate and improves the reproducibility of spectrum.

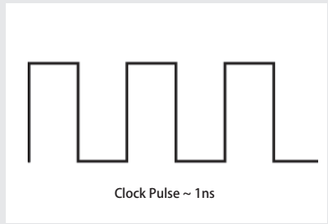


The results of mass spectrometry between traditional targets are different

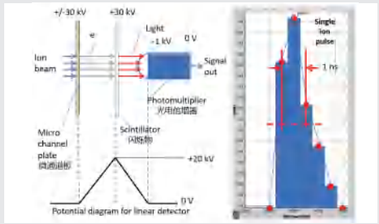


Eliminate the edge electric field effect through target plate grounding

- The new mixed ion detector has high-speed data acquisition and high spectral reproducibility.



The traditional pulse converter has blind spots in counting



The transient digital converter (TD) can accurately record all ion signals

QUENDA'S ORIGINAL DUAL DATABASE BUILDING METHOD

—MICROBIAL IDENTIFICATION TECHNOLOGY IS SUPERIOR

The specific protein fingerprints of microbial species and genera were constructed, and the microbial spectra to be tested were compared with the reference spectra in the database to complete the species and genus level identification.

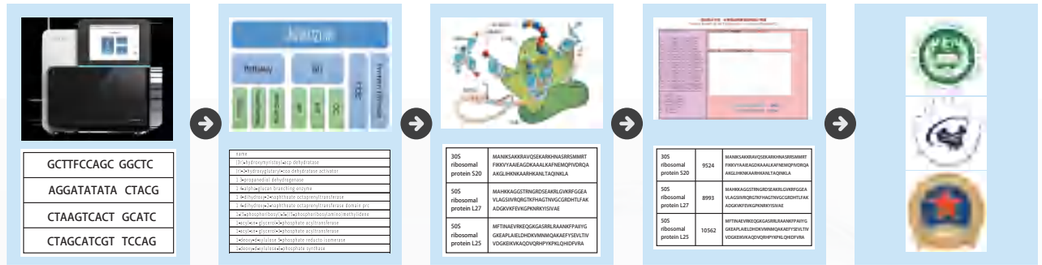
The more perfect the protein fingerprint in the database, the more scientific the comparison algorithm and the more accurate the identification results.

Method 1: Traditional microbial library building method

- Cooperate with many strain preservation institutions to collect rich strain information to construct species-specific protein fingerprints
- The disadvantage is that it is easy to be affected by bacterial culture conditions, and repeated exploration will spend much time and energy

Method 2: Quenda's original database building method combining genomics, proteomics and bioinformatics

- Ribosomal protein is recognized as the most efficient molecular marker for bacterial classification, and its conserved region has species and genus specificity
- Ribosomal proteins and species-specific structural proteins are selected, the molecular weight of proteins is calculated, and the fingerprint is constructed. Various modifications of proteins (such as methylation, acetylation, etc.) are considered in the process of building the library
- Cooperate with many strain preservation institutions to collect standard strains for database verification, which is scientific and rigorous



The gene sequence was obtained by sequencing

Gene annotation translation protein information

Select characteristic proteins

Build database

Strain verification

Advantages:

- Double insurance: scientific database construction and practical verification;
- More accurate information: the database is not affected by environmental factors such as training environment and training time;
- Great flexibility: there are two unique database building methods. When strains cannot be obtained, the database can be built through omics information, with high database building efficiency.

THREE DATABASES ENSURE MORE ACCURATE MICROBIAL IDENTIFICATIONC

Primary Database

- Support database upgrade;
- It supports users to build their own database, which can be added, deleted and maintained, and the operation is simple;
- It covers all kinds of common clinical bacteria and fungi;
- Including more than 1800 genera and 6600 strains.

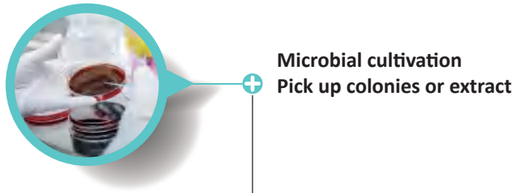
Fungal Database

- Support database upgrade and self built database expansion;
- Covering all kinds of common clinical fungi;
- Including more than 300 genera.

Secondary Database

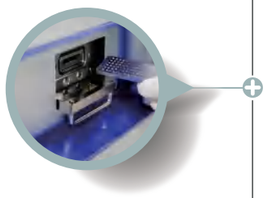
- The unique database of Rongzhi biology can effectively distinguish difficult to distinguish bacteria with similar genotypes;
- By improving the performance of the instrument, the reproducibility of mass spectrometry data is significantly improved, and small differences in similar spectra that cannot be identified by conventional microbial mass spectrometry can be identified;
- With the unique matching algorithm, the family and genus specific peak weight is low, while the strain specific peak weight is heavier;
- Including more than 100 kinds of Enterobacteriaceae, Citrobacter, Shigella, Raoul, Proteus and Salmonella.

TECHNOLOGY ROADMAP



Microbial cultivation
Pick up colonies or extract proteins

Put the sample on the target plate

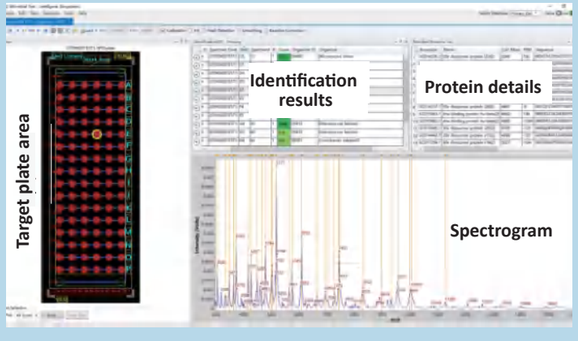


Testing

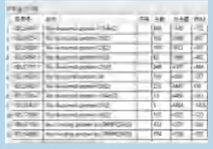
Obtain atlas and Identification Report

IDENTIFICATION RESULTS

- One click operation is simple and intuitive;
- Each peak of the map can trace protein information;
- Strong data processing and analysis capabilities, supporting atlas analysis, cluster analysis and traceability analysis.



Cluster heat map



Protein details

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APPLICATION IN CLINICAL MICROBIAL IDENTIFICATION

APPLICATION AREA

Microbial clinical diagnosis and prognosis;

Virus typing;

Study on bacterial drug resistance;

Virulence Analysis;

Molecular marker development;

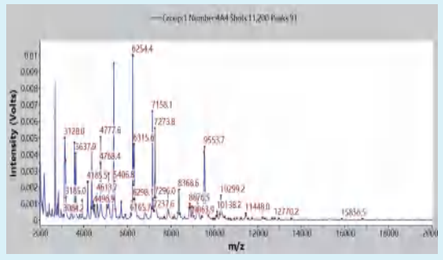
Epidemiological analysis;

Identification and prognosis of clinically difficult to detect

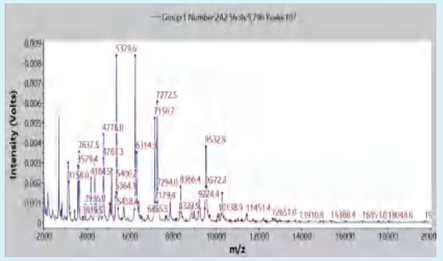
Unique secondary database and comparison algorithm can quickly distinguish various pathogens with highly similar genotypes

Identification of Shigella boydii

- Shigella is the most common pathogen of human bacillary dysentery. It is highly similar to Escherichia coli , and they are often wrongly detected;
- Mrobe MS's unique Shigella secondary database makes the identification results accurate and reliable.



Shigella flexneri



Escherichia coli

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APPLICATION IN CLINICAL MICROBIAL IDENTIFICATION

Identification of Filamentous fungi,Mycobacterium and Nocardia

Traditional identification methods are complex, time-consuming and inaccurate

- The database contains 150 species of mycobacteria, 195 species of filamentous fungi and 15 species of Nocardia;
- Patent sample pretreatment reagent;
- Inactivation, extraction and identification are completed in 30 minutes, which greatly shortens the identification time.

Type	Bacterium
Negative bacilli and Vibrio	Vibrio, Aeromonas, Campylobacter, Helicobacter, etc
Positive bacilli	Corynebacterium, bacillus, Lactobacillus, etc
Fastidious	Occult bacilli, Haemophilus, actinomycetes, HACEK group, Pasteurella, anaerobic bacteria, Streptococcus granulosus, etc
Bioterrorism bacteria	Brucella, Francisella, Burkholderia melioides, etc
Bacteria that are difficult to detect	Mycobacterium, Nocardia and other Actinomycetes, etc
Positive coccus	Aerococcus, Leuconostoc, Pediococcus, etc
Anaerobes	*Bacteroides fragilis, Clostridium perfringens, etc*
Filamentous	Mucor, biphasic fungi, skin fungi, dark fungi, Aspergillus, etc

- Filamentous fungi sample processing kit
- Class I Kit

- Mycobacterium and Nocardia sample processing kit
- Class I Kit

Multiple Virus Detection and Typing

Advantage：

- One device can complete the identification of viruses, bacteria and fungi;
- Single base resolution, accurate detection results;
- The sensitivity is as high as 10copies/ response, and it can also accurately screen patients with low viral load in the early stage;
- Low reagent cost and high cost performance.

Combined detection of 20 respiratory viruses including novel coronavirus

Types of Viruses	Test Content
Coronavirus	Novel coronavirus (sars-cov-2), SARS, mers
Other common respiratory	Respiratory syncytial virus (types A and B), human Boca virus (types 1 and 2), adenovirus, human rhinovirus Influenza A virus (and H1N1 subtype, 2009h1n1 subtype, H3N2 subtype)

HPV Typing

Types of Viruses	Test Content
High-risk HPV	16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68, 81
Medium-risk HPV	53，66，73，82
Low-risk HPV	6, 11, 67, 70, 34, 42

- Nucleic acid detection kit
- Class I Kit

- Special matrix kit for virus detection
- Class I Kit

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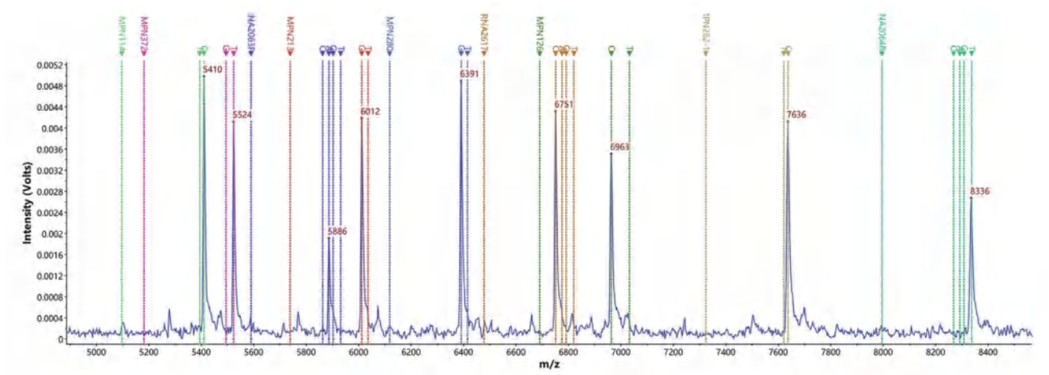
APPLICATION IN CLINICAL RESEARCH

Multiple Virus Typing and Drug Resistance Gene Detection

Typing and drug resistance gene detection of Mycoplasma pneumoniae

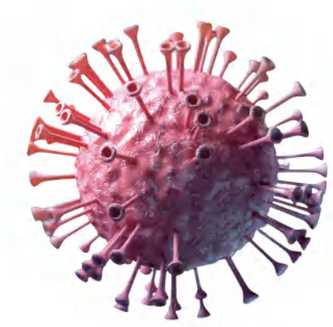
- The Chinese Center for Disease Control and Prevention (CDC) has established a method to simultaneously detect 6 Mycoplasma pneumoniae typing targets and 3 macrolide antibiotic (ML) resistance gene targets by using the Rongzhi biological mass spectrometry platform, which is low-cost and efficient, and has important clinical and scientific research value
  Fei Zhao, Jianzhong Zhang, et al. A multisite SNP genotyping and macrolide susceptibility gene method for Mycoplasma pneumoniae based on MALDI-TOF MS. iScience. 2021 Apr 16;24(5):102447



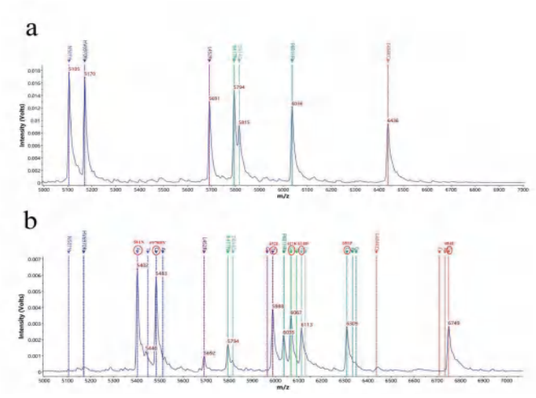
Test Type	Test Object
Typing target	N114[1461], N126[470], N213[47], N262[192], N280[1641] , N372[1112]
Drug resistance gene target	23S rRNA[2063], [a]23S rRNA[2064], 23S rRNA[2617]

Detection of Novel Coronavirus Variants

- The Chinese Center for Disease Control and Prevention (CDC) has established a method for joint detection of multiple novel coronavirus variants using the bio mass spectrometry platform, which has important clinical and scientific research value.
- Novel coronavirus variants, including alpha, beta, gamma, Delta, etc
  Fei Zhao, Jianzhong Zhang et al.A novel strategy for the detection of SARS-CoV-2 variants based on multiplex PCR-MALDI-TOF MS. (2021 submitted)



Coronavirus(SARS-CoV-2)



ABOUT QUENDA

Since its establishment, Quenda has relied on the resources and technology of XGZY group in laboratory instruments to provide supreme-quality products and one-stop laboratory solutions for global users.

The biggest advantage of Quenda is that it has an experienced R & D and service team, who can provide personalized services to support the whole process of product procurement.To understand the real situation and needs of each customer, develop professional laboratory solutions, flexibly and safely deliver products according to the import policy of various countries and offer instrument debugging and training.

Quenda pays great attention to every customer and maintains a permanent cooperative relationship with them by providing reliable service and equipment.