

OMI  PathDx

# Pathogen Metagenomic Sequencing

Clinician Infopack



## Our Story

OMI Biomedics connects clinicians with advanced genetic tests to help guide diagnosis and treatment. We work with trusted laboratory partners to offer accurate and clinically useful tests, designed to fit into real-world practice.

## Our Mission

We aim to bring clarity and support to patients and families on their journey toward a definitive diagnosis and effective treatment by providing high-quality genetic tests that enable healthcare providers to deliver evidence based, personalized care for improved patient outcomes.

## Our Vision

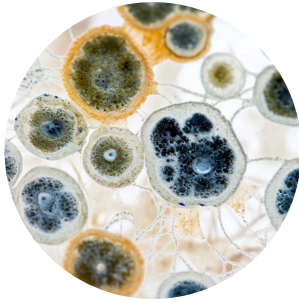
We envision a future where every patient who needs to can access clear answers to their most pressing health questions through the power of genetic testing. By partnering with healthcare professionals and empowering them with the tools and insights they need, we aspire to make genetic testing an integral part of modern medicine - streamlining diagnoses, improving treatment, and enhancing patient lives across the globe.



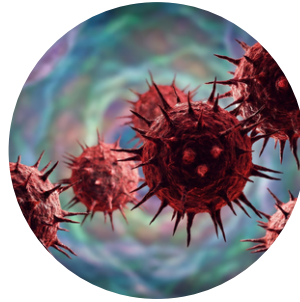
# Product overview

PMseq™ Pathogen Metagenomic Sequencing is based on metagenomics, which allows for the simultaneous detection of major microorganisms in a sample using next-generation sequencing without the need for prior knowledge of their identities. PMseq™ can detect more than 36,000 types of pathogens, including bacteria, fungi, viruses, parasites, and more, as well as representative drug resistance and virulence genes without bias. By using PMseq™, the positive rate of pathogen diagnosis can be significantly increased, guiding the clinical targeted use of antibiotics and assisting in the precise diagnosis and treatment of infections.

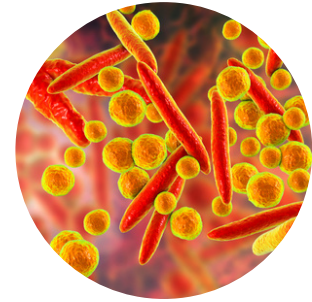
## Applicable Population



**Complicated or unexplained infectious patients**



**Severe infectious patients**



**Immunocompromised patients**

## Detection Scope

Detects over 36,000 pathogens and their representative resistance and virulence genes in a single test, and also supports analysis of human chromosomal copy number variations (CNV).

**16,343 Bacteria** (Including 226 Mycobacteria and 179 Mycoplasma/Chlamydia/Rickettsia)

**2,431 Fungi**

**16,679 Viruses** (Including 11,545 DNA viruses, 5,134 RNA viruses)

**718 Parasites**

**33 Drug-resistant genes**

Detects 67 types of antibiotic-resistant bacteria, including genes/sites such as CTX-M, KPC, OXA, MecA, NDM, and 23S rRNA.

**281 Virulence genes** (Including rmpA, rmpA2, iutA, hly, ctxA/ctxB, etc.)



# Test Advantages

## High Data Volume

High-throughput sequencing technology boosts data output, ensuring **ultra-sensitive** pathogen detection and robust support for precise diagnosis of complex infections.

## Comprehensive Testing

One-time detection of **36,000** pathogens, including drug-resistant and virulence genes (e.g., *Mycobacterium tuberculosis* resistance mutations), for full-spectrum pathogen analysis in complex infections.

## Precision Processing

Targeted sample pretreatment and optimized workflows enhance testing **sensitivity**, delivering **accurate, reliable** results for clinical decisions.

## Clinical-level database

Powered by a clinical-grade database and **intelligent algorithms**, ensuring **precise** report **outcomes** to **guide diagnosis** and **treatment** of complex infections.

## Fully Qualified

End-to-end process—from nucleic acid extraction to analysis software—holds clinical certifications, guaranteeing **quality**, authority, and **credibility** of results.

## Reliable Performance

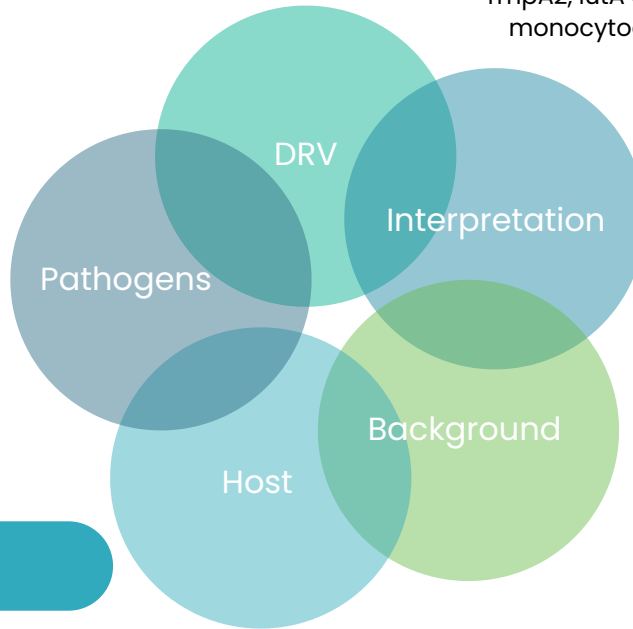
Standardized quality management ensures stable, consistent testing. Years of passing **NHC's mNGS external quality assessments** validate the **accuracy** and **reliability**

## Drug Resistance and Virulence Database

### Pathogen Database

- Over 36,000 kinds of pathogens, strictly control genome quality
- Independently integrate algorithms to screen representative reference sequences
- Comprehensive evaluation

- 32 representative drug resistance genes. Include CTX-M, KPC, OXA, MecA, NDM, etc. (CARD database).
- 281 representative virulence genes. Include rmpA, rmpA2, iutA of *Klebsiella pneumoniae*, hly of *Listeria monocytogenes*, and ctxA/ctxB of *Vibrio cholerae* (VFDB database).



### Interpretation Database

- Comprehensive and meticulous literature research
- Precisely extract pathogen interpretation information

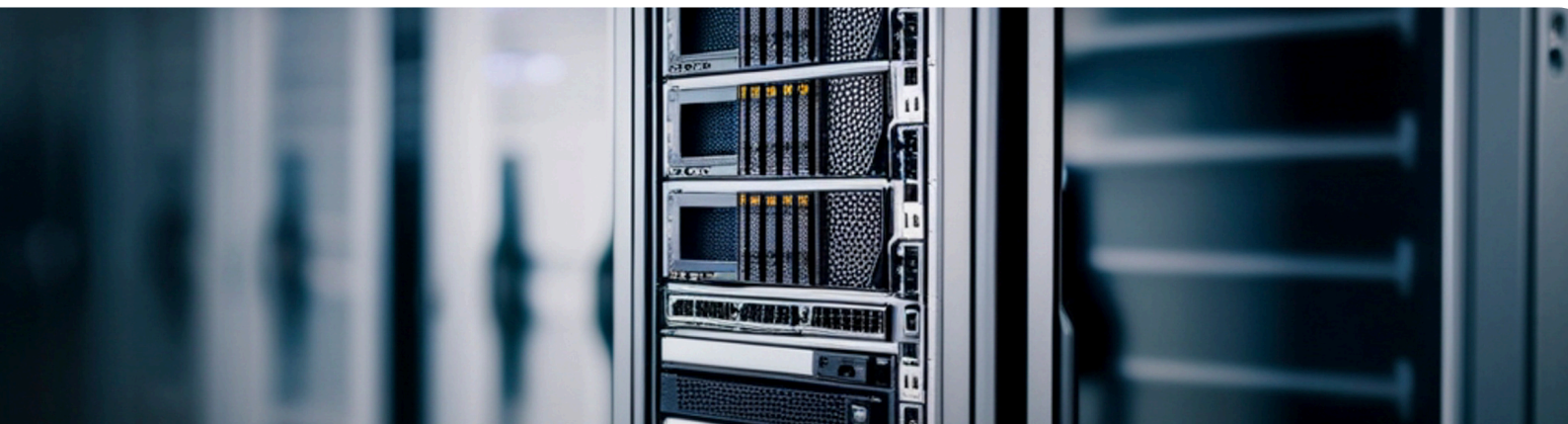
### Host Database

- Internationally common human reference genome
- Our partner's proprietary self-assembled genome database

### Detection Background Database

- Diversified background library for large-sample data analysis
- Constructed from 300,000 real samples
- Accumulated over many years of clinical practice

Clinical-level databases and a core intelligent algorithm ensure accurate results.

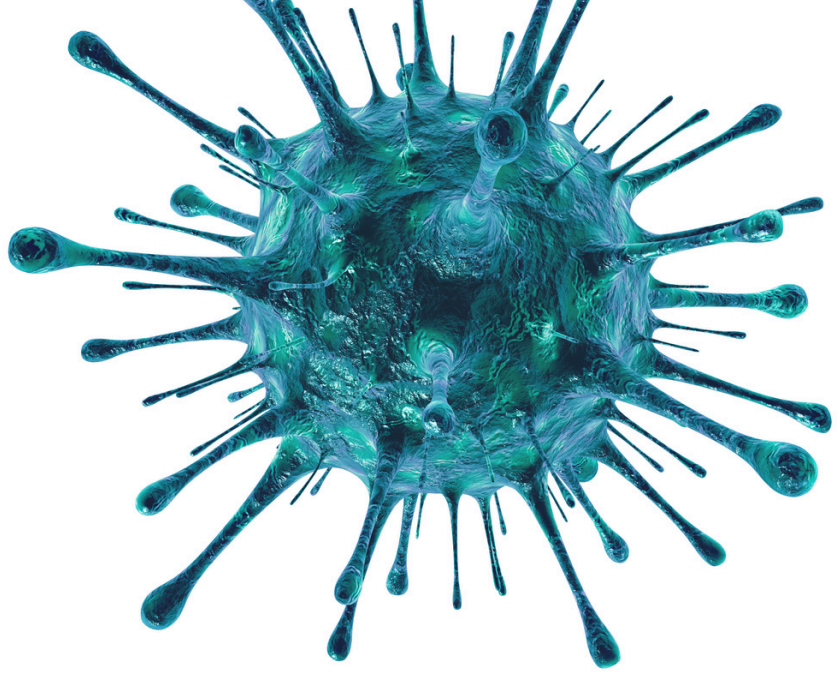




## Sample Types

Clinical Presentation	Sample Types
Bloodstream infections, sepsis	Peripheral blood
Encephalitis, meningitis, myelitis	Cerebrospinal fluid; brain abscess aspirate; spinal fluid; brain tissue
Upper respiratory tract infections	Nasopharyngeal swab (preferred); oropharyngeal swab
Lower respiratory tract infections	Protected brush sample (preferred); bronchoalveolar lavage fluid; lung tissue; endotracheal aspirate; deep sputum
Pleuritis	Pleural fluid; ascites
Joint infections, prosthetic infections	Synovial fluid; prosthetic sonicate fluid
Ocular infections	Vitreous humor; aqueous humor; corneal tissue; ocular discharge
Skin and soft tissue infections	Wound swab; wound tissue (junction of normal and necrotic tissue); abscess
Urinary tract infections	Urine (first morning urine preferred); bladder aspirate
Genitourinary infections	Urethral, vaginal, cervical, or endometrial secretions; pelvic abscess; prostatic fluid; semen; ulcer discharge
Deep and superficial abscesses	Purulent fluid; aspirate fluid
Tissue infection	Fresh tissue; biopsy tissue; paraffin-embedded tissue
Fever of unknown origin	Peripheral blood plus focal site samples (if available)
Patients intolerant to invasive surgery	Peripheral blood

For more information regarding sampling please request our **sampling guidelines**.



## Workflow

Consultation

Sample collection

Documentation

Shipment

Sequencing

Data analysis

Interpretation

Results

## TAT

**12-14 working days** from sample acceptance to report release.

## Request a Demo Report

Healthcare professionals interested in our service can request a demo report to evaluate the capabilities and insights provided by our genomic testing.



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