

## Application of metagenomics next generation sequencing in infectious diseases

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In recent years, metagenomics next-generation sequencing (mNGS) has gradually been applied in clinical pathogen detection, particularly for cases where common tests fail to detect pathogens, in critically ill patients, or in immunocompromised individuals. mNGS provides timely and accurate diagnostic information. In cases of respiratory infections, central nervous system infections, bloodstream infections, bone and joint infections, and infections in immunocompromised patients, mNGS has shown to increase detection rates by 20-60% compared to traditional pathogen tests. It is especially advantageous for detecting difficult-to-identify pathogens (such as *Mycobacterium*, anaerobes, etc.) or in patients with multiple infections.

However, mNGS is a high-threshold testing technique, and thus the standardization of the process is crucial. Sterile sample collection and preservation environments are essential to avoid contamination from background microorganisms. Correct sample storage and transport temperatures are necessary to maintain the integrity of the specimens and prevent nucleic acid degradation. Only through validated testing processes, quality control-compliant testing steps, appropriate threshold evaluation in data analysis, and correct result interpretation can accurate detection results be provided.



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Finally, the report results should be interpreted by professional clinical doctors, who should combine clinical symptoms and routine tests to comprehensively assess and interpret the findings. This approach helps identify the most likely pathogens and determine the most appropriate treatment while safeguarding the patient's well-being.

