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**NATIONAL STANDARD OF THE
PEOPLE'S REPUBLIC OF CHINA**

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**Method for identification of airborne pathogenic microorganism
based on metagenomics sequencing**

空气中病原微生物宏基因组测序鉴定方法

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Table of Contents

Preface	III
Introduction	IV
1 Scope	1
2 Normative references	1
3 Terms and Definitions	1
4 Abbreviations	2
5 Principle	2
6 Reagents	2
7 Instruments and Equipment	2
8 Test step	3
9 Quality Control	4
10 Identification of airborne pathogenic microorganisms	4
Appendix A (informative) Nucleic acid extraction method	6
Appendix B (informative) Sequencing process	7
Appendix C (informative) Reference genome database and selection of pathogenic microorganisms	8
Appendix D (informative) Example 10 of comparative analysis of Yersinia pestis and SARS virus sequencing data Reference	12

Foreword

This document complies with the provisions of GB/T 1:1-2020 "Standardization Work Guidelines Part 1: Structure and Drafting Rules of Standardization Documents" Drafting:

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Introduction

Detection and health safety of airborne pathogenic microorganisms in daily environments, public places, medical and health environments, and biosafety laboratories Environmental protection is closely related: Pathogenic microorganisms can spread in the air through bioaerosols and cause the spread of infectious diseases: airborne pathogens The accurate identification of microorganisms is of great significance for the prevention and control of infectious diseases and the monitoring and protection of the environment: due to airborne pathogens Microorganisms have characteristics such as lineage diversity, species complexity, and rapid variability, making Acer's high-throughput, fast, and accurate Gene sequencing methods have technical advantages in the identification of pathogenic microorganisms in the air:

In response to the need for standardization of metagenomic sequencing and identification methods for pathogenic microorganisms in the air, this document provides information on important pathogenic microorganisms in the air:

Detection and identification methods are carried out in key aspects such as air microbial aerosol sampling, pre-processing methods, library preparation, sequencing, and data result analysis:

Regulations have been formulated to meet the standardized use of metagenomic sequencing methods for airborne pathogenic microorganisms to improve China's monitoring of pathogenic microorganisms: ability:

Metagenomic sequencing and identification method of airborne pathogenic microorganisms

1 Scope

This document specifies the test conditions, test procedures, quality control and identification of metagenomic sequencing and identification methods for airborne pathogenic microorganisms:

This document is suitable for metagenomic sequencing identification and monitoring of pathogenic microorganisms such as bacteria, fungi, and viruses in the air:

2 Normative reference documents

GB/T 6682

GB/T 18204

GB 19489

GB/T 30989

GB/T 39990

GB/T 40974

GB 41918

3 Terms and definitions

The following terms and definitions apply to this document: 3:1 Microorganisms that invade organisms and cause infections or even infectious diseases, including bacteria, fungi, viruses, etc: 3:2 metagenome metagenome The sum of the genetic material of all microorganisms in a specific environment, including the genomes of cultivable and uncultivable microorganisms: [Source: JJF1265-2022,4:54] 3:3 Sequencing Determination of the order and composition of the nucleotide bases (adenine, guanine, cytosine, thymine or uracil) in nucleic acid molecules:

Note: Sequences are usually expressed from 5' end to 3' end:

[Source: ISO 20397-2:2021,3:19] 3:4 Library A group of nucleotide submolecules obtained from biological sources, artificial synthesis or cloning technology, such as genomic libraries and complementary DNA library: