EBISA (Epidemiological Bacterial Identification Software Analysis)

Version: V1.0

### Software Overview

EBISA is an innovative bioinformatics tool designed to quickly identify and compare 18 important bacterial strains by uploading fasta-formatted gene sequence files. This software provides valuable support in the fields of public health, disease control, and biosecurity, enabling researchers to efficiently identify pathogens.

## **Function Description**

- Receives fasta-formatted gene sequence files and compares them against an integrated bacterial strain database.
- Identifies 18 bacterial strains, including Bacillus anthracis, Yersinia pestis, Brucella abortus, Brucella melitensis, Brucella ovis, Brucella suis, Brucella canis, Clostridium tetani, Bordetella pertussis, Mycobacterium leprae, Chlamydia trachomatis, Neisseria meningitidis, Mycobacterium ulcerans, Listeria monocytogenes, Mycoplasma pneumoniae, Vibrio vulnificus, Legionella pneumophila, and Streptococcus suis.
- Provides an export function to output comparison results as Excel files for easy data analysis and report preparation.

# **Technical Features**

- •Utilizes specialized electronic probes (e-probes) technology to ensure accurate and rapid comparison.
- •Supports a positive result upon detection of a single probe, with the reliability enhanced by increasing the number of detected probes.
- The user interface is intuitive and easy to use, requiring no specialized bioinformatics knowledge.

# **Operation Process**

- 1.Install and start the EBISA software.
- 2.Log in to your account and select the "Upload Sequence" feature.
- 3.Import the fasta-formatted gene sequence file.
- 4.Set the comparison parameters and start the comparison analysis.
- 5. View the comparison results and confirm the strain identification.
- 6.Export the results as an Excel file for saving or printing.

#### Installation and Deployment

1.Download the EBISA software installation package from the official website.

2.Follow the installation wizard to complete the installation process.

#### Cautions

- 1. Verify the file format before uploading the sequence file.
- 2.Regularly update the software and database to keep the latest strain information and comparison algorithms.
- 3.For positive results, it is recommended to perform laboratory validation to confirm the identification.
- 4.Strictly adhere to data protection regulations to ensure that the processed data complies with privacy protection requirements.
- 5.For technical issues, seek technical support through official channels.

EBISA software provides researchers with an efficient means for rapid identification of bacterial strains, which is of great significance for timely response to infectious disease outbreaks and biosecurity events.