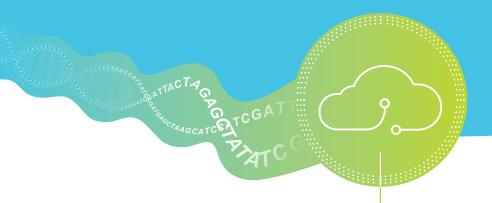


BIOMÉRIEUX EPISEQ®

NGS DATA ANALYSIS PLATFORM PROVIDING EASY-TO-USE APPLICATIONS FOR CLINICAL MICROBIOLOGISTS





# EPISEQ® ID FOR BACTERIAL AND FUNGAL IDENTIFICATION

Identification of bacterial and fungi through their respective 16S and ITS broad range PCR sequences.

In a single click, EPISEQ® ID assigns bacterial and fungal identification. EPISEQ® ID delivers a comprehensive list of detected bacteria and fungi at the most reliable taxonomical level or to the closest species level in case of upper identification level.

Multiple Quality Controls allow the user to rely on the delivered results.

A curated database leveraging the full power of ONT long reads sequencing, optimized for full length bacterial 16S and fungal ITS+D1D2 regions.

#### **EPISEQ® ID offers you:**

- Multiple Quality Controls including primers dimers content
- Identification of bacteria and fungi from the same dataset
- ✓ Multiple organism detection
- ✓ Validation page
- ✓ PDF report
- ✓ The ability to store and search all historical data.

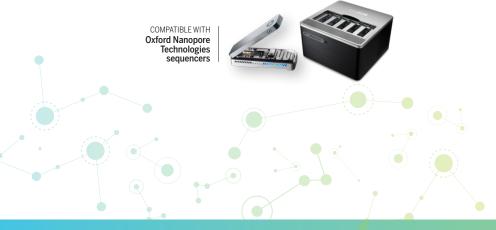
## CONFIDENCE

Allows determining the relevance of the identified organism. The confidence is based on the amount and quality of the sequences, enriched with a degree of similarity within the database.

## **COMPREHENSIVE**DATABASE

Identify more than 3000 bacteria and 1200 fungi ensuring to cover clinical species of concern, according to the WHO\*, FDA argos\*\* and publications.

\*World Health Organization \*\*U.S. Food and Drug Administration

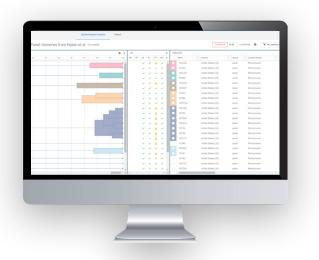


# ACCARDA TIACTA O PO TCGATI

## EPISEQ® CS

### FOR CLINICAL PATHOGENS OUTBREAK MONITORING

Easy bacterial typing & genome characterization on the 14 most common species involving Healthcare-Associated Infections (HAIs).



EPISEQ® CS performs Whole Genome Sequencing bacterial typing and antimicrobial gene characterization. It helps to confirm HAI outbreaks early and accurately.

It reports decisive data to further investigate a potential outbreak or cluster, thus triggering Infection Prevention and Control (IPC) protocols at an early stage.

#### **EPISEQ® CS offers you:**

- ✓ Quality control report
- ✓ Decision making tool
- ✓ Epidemiological analysis
- ✓ Virulome / resistome
- ✓ Typing results wgMLST, MLST, SPA, serotype, pathotype
- ✓ Plasmid identification
- ✓ Access to phylogenia<sup>(\*)</sup>
- Automatic alert about potential plasmid outbreak<sup>(\*)</sup>

<sup>(\*)</sup> Only available in the advanced subscription



#### **PHYLOGENIA**

Assess the phylogenetic relevance of your suspected bacterial outbreak thanks to a worldwide database of up to **80,000** bacterial genomes.

#### PLASMID OUTBREAK

Identify plasmids and their relatedness even across species<sup>1</sup>. Receive an automatic alert in case of a plasmid outbreak.

## >4000 RESISTANCE GENES 598 POINT MUTATION

Display all resistance genes or published genomic mutation(s) that could confer resistance.



# EPISEQ® 16S FOR MICROBIOME PROFILING STUDIES

Helps to investigate the role of the microbiome in patients' health.



The microbiology expertise of bioMérieux allows this solution to cover the full diversity of bacteria and archaea with alpha and beta diversity parameters.

This solution supports users to investigate the use of microbiome to define predictive biomarkers.

#### **EPISEQ® 16S offers you:**

- ✓ OTU assignment
- ✓ OTU abundance
- ✓ Alpha & beta diversity
- ✓ Clustering
- ✓ Statistical analyses
- ✓ Time-series analysis

## TRENDS SERIES

Your sample compared with others through time.

## **QIIME**

State-of-the-art pipeline.

#### **SILVA**

State-of-the-art database

#### **TRUST**

Your results with the embedded statistical analysis.





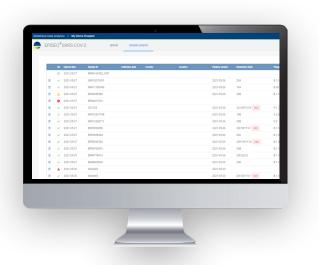
# EPISEQ® SARS-COV-2

FOR SARS-COV-2 VARIANT IDENTIFICATION

#### EPISEQ® SARS-COV-2 offers you:

- ✓ Quality control information
- ✓ Variant identification (based on Nextstrain & Pango)
- ✓ Genome assembly
- ✓ Sample report
- ✓ Mutation list
- Mapped alignment BAM

## With a WEEKLY UPDATE of the variant of concern (VOC) list issued by the WHO\* & CDC\*\*



The microbiology expertise of bioMérieux allows this solution, which identifies SARS-CoV-2 genomic variants from FASTQ files, to report the list of mutations detected in the spike gene and other genes of the variant sequenced.

A consensus sequence is created from the reads after alignment against the reference genome and solid results can be downloaded as BAM files.

## BATCH DOWNLOAD OF RESULTS

For easy submission to public health

## **COMPATIBLE**WITH THREE PLATFORMS

Illumina, Thermo Fisher Ion Torrent™ or Oxford Nanopore Technologies





## ACTIONABLE ANSWERS, FAST.

THE BIOMÉRIEUX EPISEQ® PLATFORM WORKS IN 3 EASY STEPS:



Import **raw data** directly from Next Generation Sequencing instruments.



Fast and intuitive workflow, in a few clicks, from data to actionable results.



A state-of-the-art bioinformatics pipeline to answer meaningful microbiological questions.



## **DISCOVER BIOMÉRIEUX VISION SUITE**

#### DATA-DRIVEN DECISION MAKING

BIOMÉRIEUX VISION SUITE turns laboratory and hospital data into insightful, actionable information to support diagnostic and clinical decisions at all stages to better support antimicrobial stewardship.

By providing a comprehensive suite of software solutions that collect, analyze, and merge various sources of data, BIOMÉRIEUX VISION SUITE empowers you to make the right decisions at the right time.

