

BIOMÉRIEUX EPISEQ®

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



PIONEERING DIAGNOSTICS

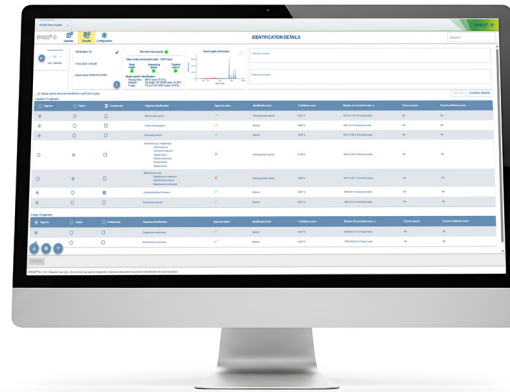
EPISEQ[®] ID

FOR BACTERIAL AND FUNGAL IDENTIFICATION

EPISEQ[®] ID offers you:

- Identification of bacteria and fungi from the same dataset
- Multiple Quality Controls including primers dimers content
- Multiple organism detection
- Validation page
- PDF report
- The ability to store and search all historical data
- Easy interpretation thanks to positive and negative control strategy

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.

COMPATIBLE WITH
Oxford Nanopore
Technologies
sequencers*



*Refer to product documentation for product requirements

CONFIDENCE SCORE

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

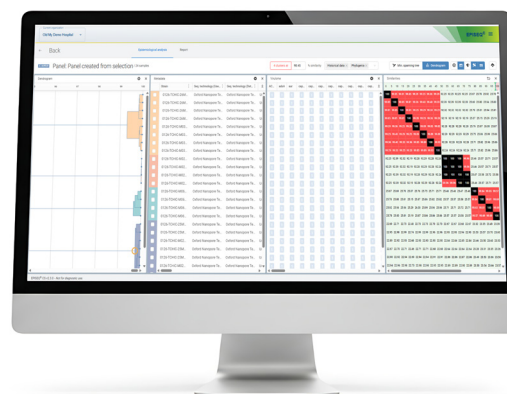
EPISEQ[®] CS

FOR CLINICAL PATHOGENS OUTBREAK MONITORING

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^(*)
- Automatic alert about potential plasmid outbreak^(*)
- *Candidozya Auris*

Easy bacterial and fungal typing & genome characterization on the 14 most common species and *Candidozya Auris* 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.

^(*) Only available in the advanced subscription

COMPATIBLE WITH THE
Illumina and Oxford
Nanopore Technologies
GridION sequencing
device*



*Refer to product documentation for product requirements

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 species¹. 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.

¹Evans, Daniel *et al.* eBioMedicine 2023;93:104681

EPISEQ[®] PLATFORM

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.**