

## The infectious disease genomics portal

AREScLOUD software hosts validated\* bioinformatics pipelines – powered by AI and the proprietary ARESdb – to comprehensively type and characterize pathogens, and to explore outbreaks and transmission events.

**SIGN UP**  
[www.ares-genetics.cloud](http://www.ares-genetics.cloud)

If you need sequencing capacity, the Ares NGS Service laboratory is fully equipped to help with data generation, too. Contact us at [services@ares-genetics.com](mailto:services@ares-genetics.com).

## How it works

Upload short or long read sequence data

Automated analysis and sample QC

Interpretation and reporting



Bioinformatic pipelines for

- Isolates
- Native specimen
- Environmental samples



ARESdb



**ID, type and characterize pathogens from genome data.**  
Generate interactive and static reports for clinical isolates.



**Predict antibiograms from genome data using AI.**  
Comprehensively detect genetic and mutational AMR markers.  
Detect and type plasmids.



**Analyze local bacterial outbreaks.**  
Explore transmission patterns for pathogens and AMR, assisted by metadata.

## Why AREScLOUD

### Validated analysis

Rely on accurate and reproducible data thanks to validated analytics, as demonstrated in multiple clinical validation studies\*:

1. Validation of Illumina isolate sequencing following CLIA guidelines.
2. Multicenter clinical validation of ONT isolate sequencing.
3. Multicenter clinical validation of antibiogram prediction from genome data.

### Predictable cost

Subscription models that combine predictable operational costs with the scalability of cloud software.

### Save valuable time

Save time through fully automated bioinformatics. Process entire outbreak datasets within hours of data upload.

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## Predict antibiograms from genome data

### AMR Testing

Predicted Antibiogram

Search

Compound Class <sup>1</sup>	Compound <sup>2</sup>	Result <sup>3</sup>	Clinical Breakpoints	Actions	Details
<input type="checkbox"/> Cephalosporins (1st)	<input type="checkbox"/> Cefazolin	Resistant	S ≤ 2 µg/ml (R > 4 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Macrolides	<input type="checkbox"/> Azithromycin	Resistant	S ≤ 8 µg/ml (R > 18 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Penicillins Combinations	<input type="checkbox"/> Amoxicillin / Sulbactam	Resistant	S ≤ 8 µg/ml (R > 18 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Penicillins	<input type="checkbox"/> Amoxicillin	Resistant	S ≤ 8 µg/ml (R > 18 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Short-acting beta-lactams	<input type="checkbox"/> Sulfafurazole	Resistant	S ≤ 256 µg/ml (R > 256 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Anticoagulants	<input type="checkbox"/> Dexamethasone	Susceptible	S ≤ 4 µg/ml (R > 8 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Aminoglycosides	<input type="checkbox"/> Tobramycin	Susceptible	S ≤ 4 µg/ml (R > 8 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Carbapenems	<input type="checkbox"/> Ertapenem	Susceptible	S ≤ 0.5 µg/ml (R > 1 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Carbapenems	<input type="checkbox"/> Imipenem	Susceptible	S ≤ 1 µg/ml (R > 2 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Carbapenems	<input type="checkbox"/> Meropenem	Susceptible	S ≤ 1 µg/ml (R > 2 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Cephalosporins (2nd)	<input type="checkbox"/> Cefuroxime	Susceptible	S ≤ 8 µg/ml (R > 18 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> Cephalosporins (3rd)	<input type="checkbox"/> Ceftriaxone	Susceptible	S ≤ 1 µg/ml (R > 2 µg/ml)	<input type="checkbox"/>	<input type="checkbox"/>

Model Type	Balanced Accuracy	Sensitivity	Specificity	PPV	NPV	Test Set Isolates
ML-based: 97126fd+rule(pcv_rfb)	95.3%	93.1%	97.5%	96.1%	85.5%	329

### Genes & Variants

Filter by Antimicrobial Compound

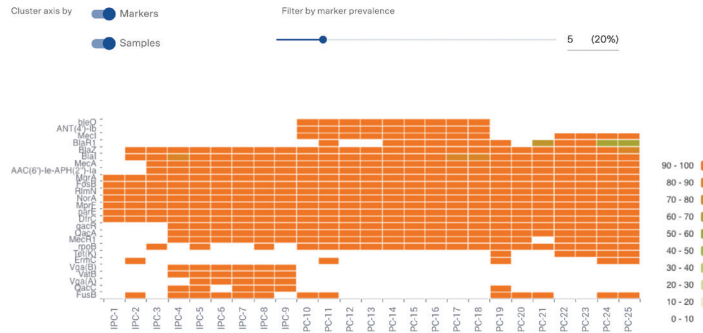
Marker Class <sup>1</sup>	Marker <sup>2</sup>	Variants	Alignment Length	Sequence Identity	Sequence Coverage	Details
<input type="checkbox"/> ABC efflux pump	<input type="checkbox"/> MibA	-	371 aa	98.9%	100%	<input type="checkbox"/>
<input type="checkbox"/> ABC efflux pump	<input type="checkbox"/> MibB	-	582 aa	99.7%	100%	<input type="checkbox"/>
<input type="checkbox"/> ABC efflux pump	<input type="checkbox"/> MibC	-	137 aa	100%	100%	<input type="checkbox"/>

## Compare AMR profiles and explore prevalent AMR markers

### AMR Annotation & Profiling

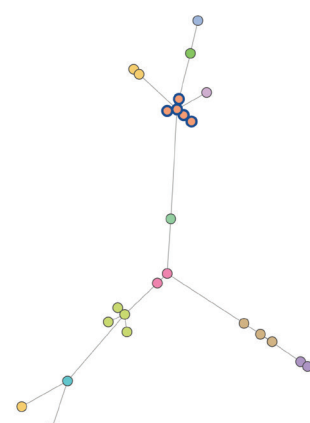
#### AMR Marker Annotations

Heatmap of antimicrobial resistance markers by sample. Marker coverage is colored from red (low) to green (high). Individual mutations are aggregated by gene/protein and not shown explicitly. Axes can be hierarchically clustered by markers (y-axis) or samples (x-axis); markers can be filtered by their minimum number of occurrences across samples.



## Cluster isolates based on genomic relatedness and study transmission events in the context of metadata

1 2 3 4 5 6 7 8 9 10 11 12 13



### Samples

Search

Sample ID	Laboratory ID	Sample Type	Microorganism	MLST Schema	cgMLST Cluster <sup>1</sup>	Quality Control
<input type="checkbox"/> 518	NCHL_00000001	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	1	<input type="checkbox"/> Passed
<input type="checkbox"/> 514	NCHL_00000001	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	1	<input type="checkbox"/> Passed
<input checked="" type="checkbox"/> 520	NCHL_00000008	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	2	<input type="checkbox"/> Passed
<input checked="" type="checkbox"/> 530	NCHL_00000002	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	2	<input type="checkbox"/> Passed
<input checked="" type="checkbox"/> 511	NCHL_00000004	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	2	<input type="checkbox"/> Passed
<input checked="" type="checkbox"/> 513	NCHL_00000001	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	2	<input type="checkbox"/> Passed
<input checked="" type="checkbox"/> 522	NCHL_00000008	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	2	<input type="checkbox"/> Passed
<input type="checkbox"/> 525	NCHL_00000004	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	3	<input type="checkbox"/> Passed
<input type="checkbox"/> 54	NCHL_00000002	Isolate	<i>Staphylococcus epidermidis</i>	ST-2   sepidermidis	4	<input type="checkbox"/> Passed



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\* For research use only and not for diagnostics purposes.

Request a Demo: [services@ares-genetics.com](mailto:services@ares-genetics.com)

### \* Validation studies:

- Lepuschitz, S. et al. Front Microbiol 11, 1883 (2020). <https://www.frontiersin.org/articles/10.3389/fmicb.2020.01883/full>
- Beisken, S. et al. Ares Genetics (2021) <https://arestech-public.s3.eu-central-1.amazonaws.com/resources/ARESSis+ONT+Validation.pdf>
- Ferreira, I. et al. Journal of clinical microbiology (2020) <https://journals.asm.org/doi/10.1128/JCM.00273-20>