

Société Française
de Microbiologie

MICROBES 2023

18^e CONGRÈS NATIONAL DE LA SFM

4-6
octobre

**LE COUVENT
DES JACOBINS**

CENTRE DES CONGRÈS DE
DE RENNES MÉTROPOLE



an integrated multi-omics platform for antibiotic resistance research and public health

Claudine Médigue, on behalf of the **ABRomics consortium**

CNRS, UAR3601 Institut Français de Bioinformatique & UMR8030

Génomique Métabolique, Evry



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Déclaration de conflit d'intérêt

Pour cette présentation,
je déclare n'avoir aucun conflit d'intérêt.

Rational for ABRomics

- Increasing access to sequencing for clinical laboratories, including outside university-teaching hospitals
- Genomics and metagenomics improve our knowledge about the (complex) circulation of antibiotic-resistant bacteria, mobile genetic elements (MGE) and antibiotic resistance genes (ARG)
- Investigations remain mostly siloed, while a global picture is needed
- To address this gap for the community in France, a simple tool which gives access to bioinformatic solutions is needed
=> **The French priority plan on AMR (2020-2030), AAP « structurants »**



Projects and actions supported

The PPR on Antimicrobial Resistance funds for €40M, 11 research projects, a meta-network of professionals, a multi-omics data platform, a digital observatory of social dimensions and research positions.

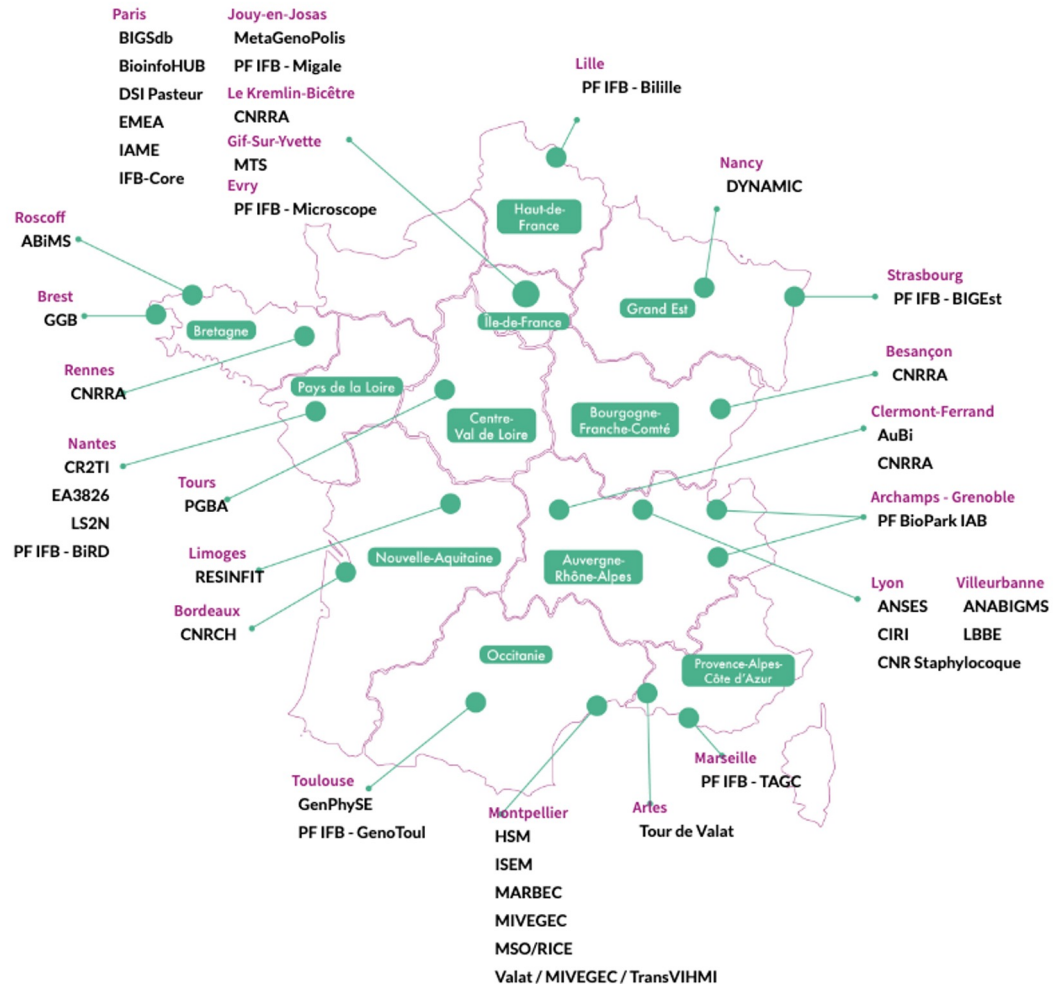
A multi-omics data platform, 2 M€ for 4 years



Start: 1-11-2021



The ABRomics consortium



Team effort at the national level (43 partners !)

Multidisciplinary consortium

Includes national reference centers for antibiotic resistance

Coordination by Claudine Médigue (French Institute of Bioinformatics) and Philippe Glaser (Institut Pasteur)

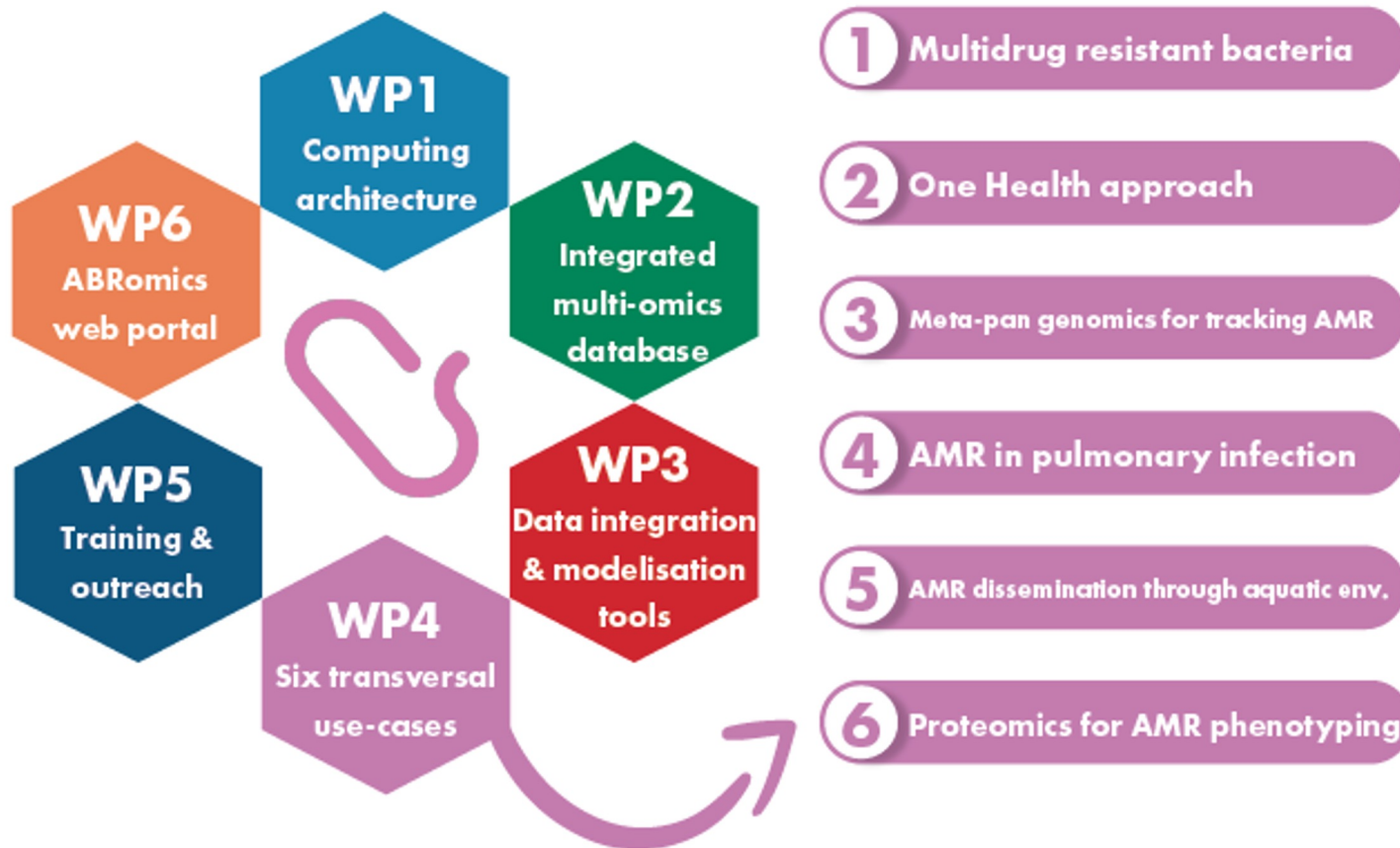


Objectives of ABRomics

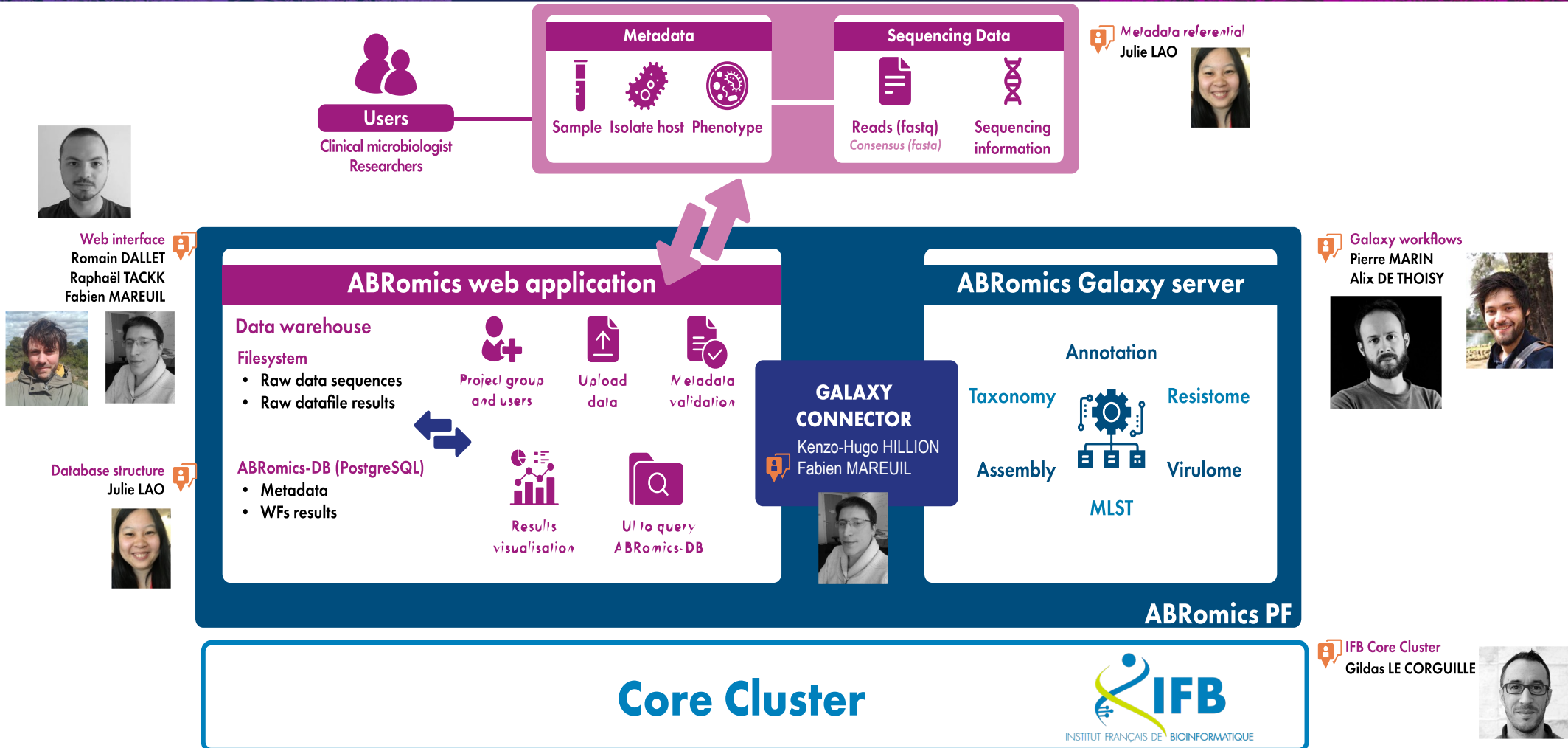
- Provide an open access to genomic and metagenomic analyses through **standardised and controlled pipelines** and an up-to-date set of **mathematical and bioinformatic tools**
- Built a repository of **structured, interoperable, standardized and well-annotated multi-omics microbiological data from human, animal and environmental origins**
- **Be easily usable** by non bio-informaticians and experts in AMR analysis
- Provide a **shared platform** to improve the **surveillance and research on antibiotic resistance**

Online community-driven platform to scale up and improve surveillance of antibiotic resistance

Work packages of ABRomics



The ABRomics ecosystem



Where are we today ?

- **The first version of ABRomics has been developed :**

- A standard Galaxy workflow for raw genomic data: assembly & QC metrics; ARG, ST, and virulence factors predictions.
- Sequences, metadata, and results of the WF feed the ABRomics database
- Report analysis downloadable and full API access to the database with authentication for private data

=> **Opened** for internal testing since October the 1st and **to all at the beginning of 2024**

- **Ongoing and next developments:**

- cgMLST
- Integration of reference genomes in the ABRomics DB
- Multiple pages for database visualization and exploration
- Metagenomic pipeline and integration of results in the ABRomics DB
- Option to data submission in international repository (ENA)

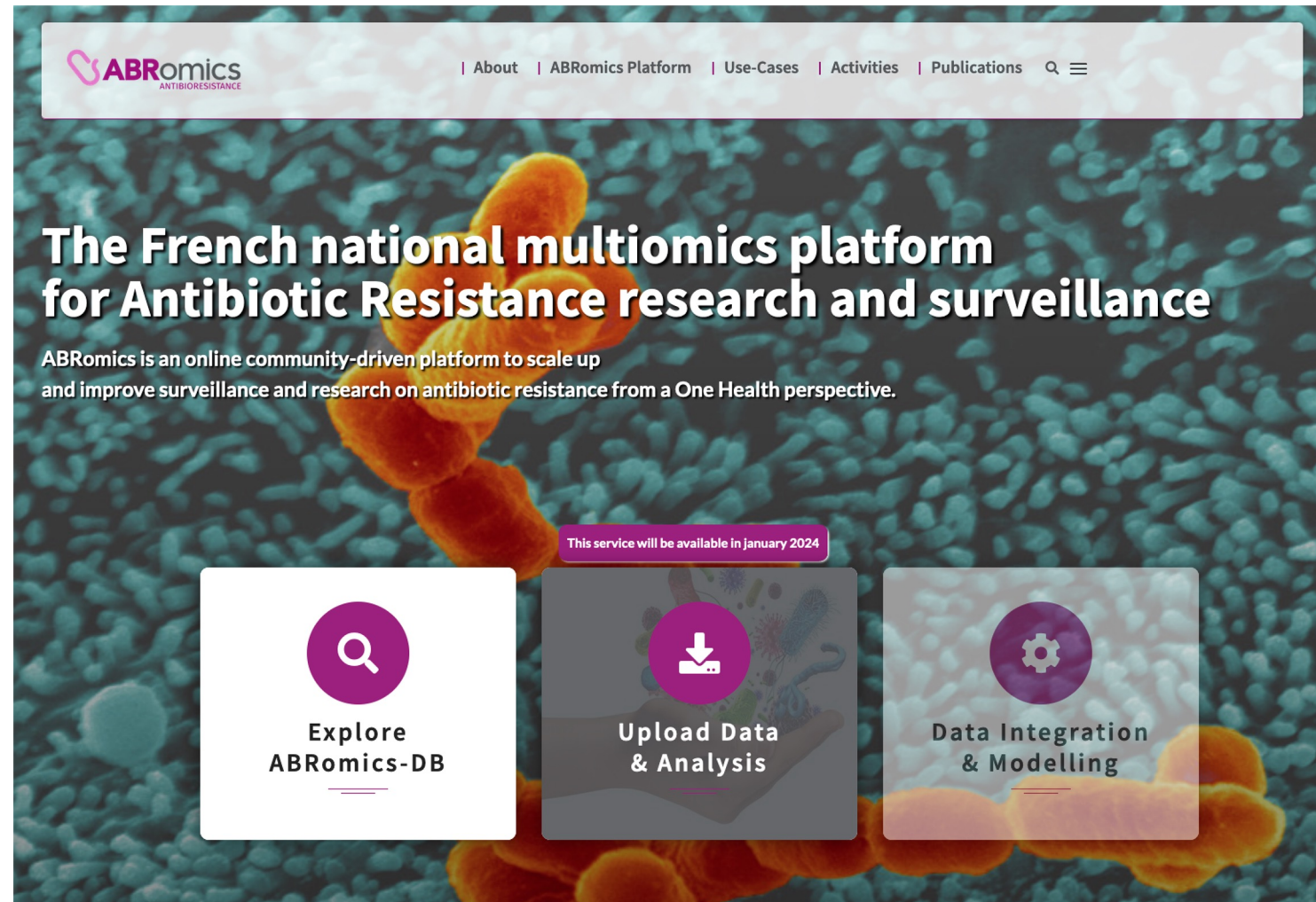
... and many others functionalities linked to WP3/WP4

More information on our ABRomics portal (ongoing dev.)

<https://www.abromics.fr>

Contact us:

abromics-support@groupe.france-bioinformatique.fr



ABRomics
ANTIBIORESISTANCE

| About | ABRomics Platform | Use-Cases | Activities | Publications

The French national multiomics platform for Antibiotic Resistance research and surveillance

ABRomics is an online community-driven platform to scale up and improve surveillance and research on antibiotic resistance from a One Health perspective.

This service will be available in January 2024

- Explore ABRomics-DB
- Upload Data & Analysis
- Data Integration & Modelling

Thanks for your attention !...



Beta version: genomic analysis

Bacterial species considered for the beta version:

- Enterobacterales : *Escherichia coli* (+*Shigella spp.*), *Klebsiella pneumoniae*, *Klebsiella aerogenes*, *Enterobacter cloacae* complex, *Citrobacter freundii*, *Citrobacter koseri*, *Morganella morganii*, *Salmonella enterica*
- *Staphylococcus aureus*
- *Pseudomonas aeruginosa*
- *Acinetobacter baumannii*
- *Enterococcus faecalis* and *Enterococcus faecium*

Then, other species from the WHO list of priority pathogens

- *Neisseria gonorrhoeae*
- *Campylobacter spp*
- *Helicobacter pylori*
- *Streptococcus pneumoniae*
- *Haemophilus influenzae*