ABRomics analyses platform

A *One Health* Antimicrobial Resistance Analysis Facility

User Manual (UM)

2025-12-11
Version 1.2.1

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VERSION HISTORY

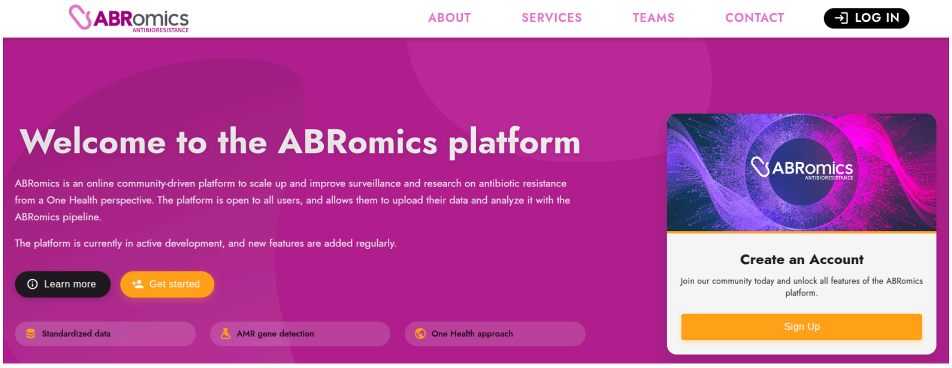
VERSION (of ABRomics analyses)	UPDATES	DATE
1.0.0	Document creation	2024-12-10
1.1.0	Addition of a tutorial on how to use demo files (FASTQ), Removed publishing feature, Updated analysis report section	2025-01-17
1.1.7	Addition of the new landing and home page information. Update of the “EXPLORE RESULTS OF THE COMMUNITY USING THE ABROMICS DATABASE” section and screenshots	2025-06-20
1.2.0	Update of the information based on the readdition of the FastA template, the new Quality Control feature and the interactive tour.	2025-09-18
1.2.1	Update of screenshots (for the 1.2.1 update of the platform) and content clarification.	2025-12-11

REGISTRATION & ACCOUNT MANAGEMENT

Landing page, register, and login

Create your account

To use ABRomics, you have to register and create an account. Click on "Sign Up" in the "Create an account" card or on the button "Get started", complete the form (First Name, Last Name, E-mail address, Password, Password confirmation, ORCID ID, Institution), and accept the privacy policy and the terms and conditions.



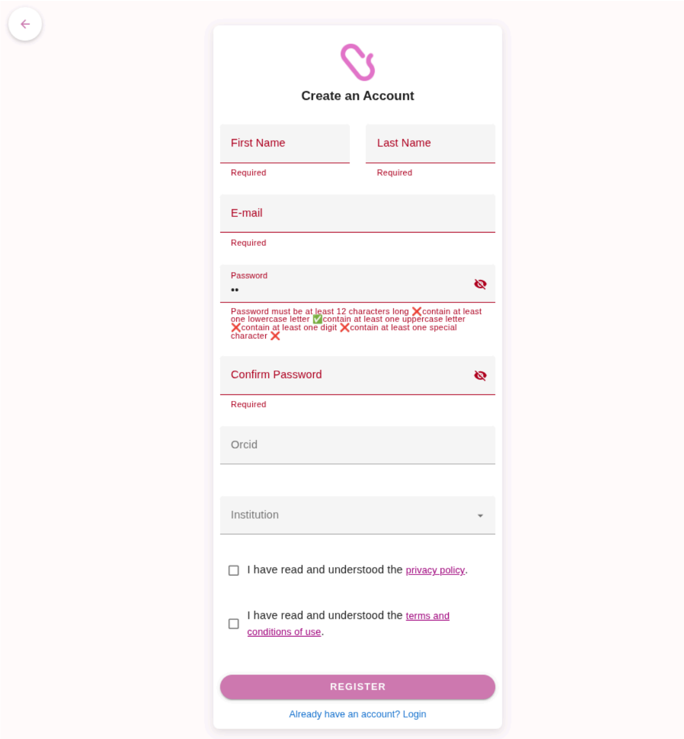
Welcome to the ABRomics platform

ABRomics is an online community-driven platform to scale up and improve surveillance and research on antibiotic resistance from a One Health perspective. The platform is open to all users, and allows them to upload their data and analyze it with the ABRomics pipeline.

The platform is currently in active development, and new features are added regularly.

Create an Account

Join our community today and unlock all features of the ABRomics platform.



Create an Account

Required

Password must be at least 12 characters long ❌contain at least one lowercase letter ✅contain at least one uppercase letter ❌contain at least one digit ❌contain at least one special character ❌

☐ I have read and understood the privacy policy.

☐ I have read and understood the terms and conditions of use.

Already have an account? Login

Once all required fields have been filled in, you should read the **ABRomics user charter** (the first page summarizes its key points) and the "terms and conditions of use". After checking the two boxes to accept them, you will be able to click the "Register" button.

Activate your account

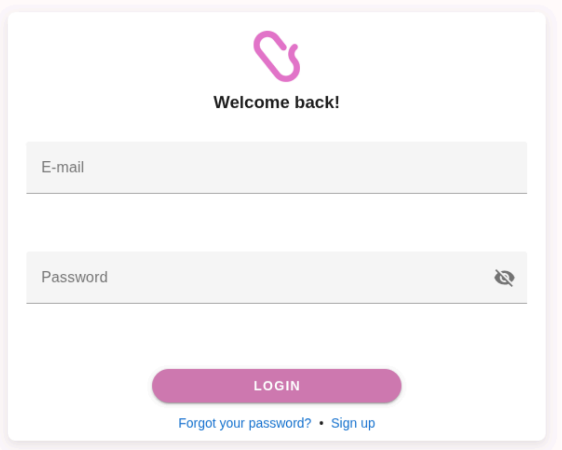
An account confirmation email will be sent to you: follow the link in the email to activate your account.

Important:

- *The email address must be a professional one and included in the ABRomics' whitelist.*
- *The password must be at least 12 characters long and comply with ISO 27001 standards and CNIL recommendations.*

Please contact an admin at abromics-support@groupes.france-bioinformatique.fr in case of difficulty while creating or activating an account.

The ABRomics platform "Login" page asks you for an email address and a password.



If you are registered, you can log in to your account by clicking on the "Log in" tab in the navigation menu. Once you have successfully authenticated yourself on the platform, you will be redirected to the ABRomics analysis Homepage.

If you try to log in too many times, you will need to wait before attempting again.

The limit is currently set at 20 requests/min to avoid spam.

On the ABRomics landing page, call-to-action buttons enable you to:

- Learn more about the ABRomics project ("Learn more" in the "Welcome to the ABRomics platform" section).
- Access and download the demo files ("Get demo files" in the "Upload" card).
- Learn more about the workflows used for our analyses ("Learn more" in the "Analysis" card).

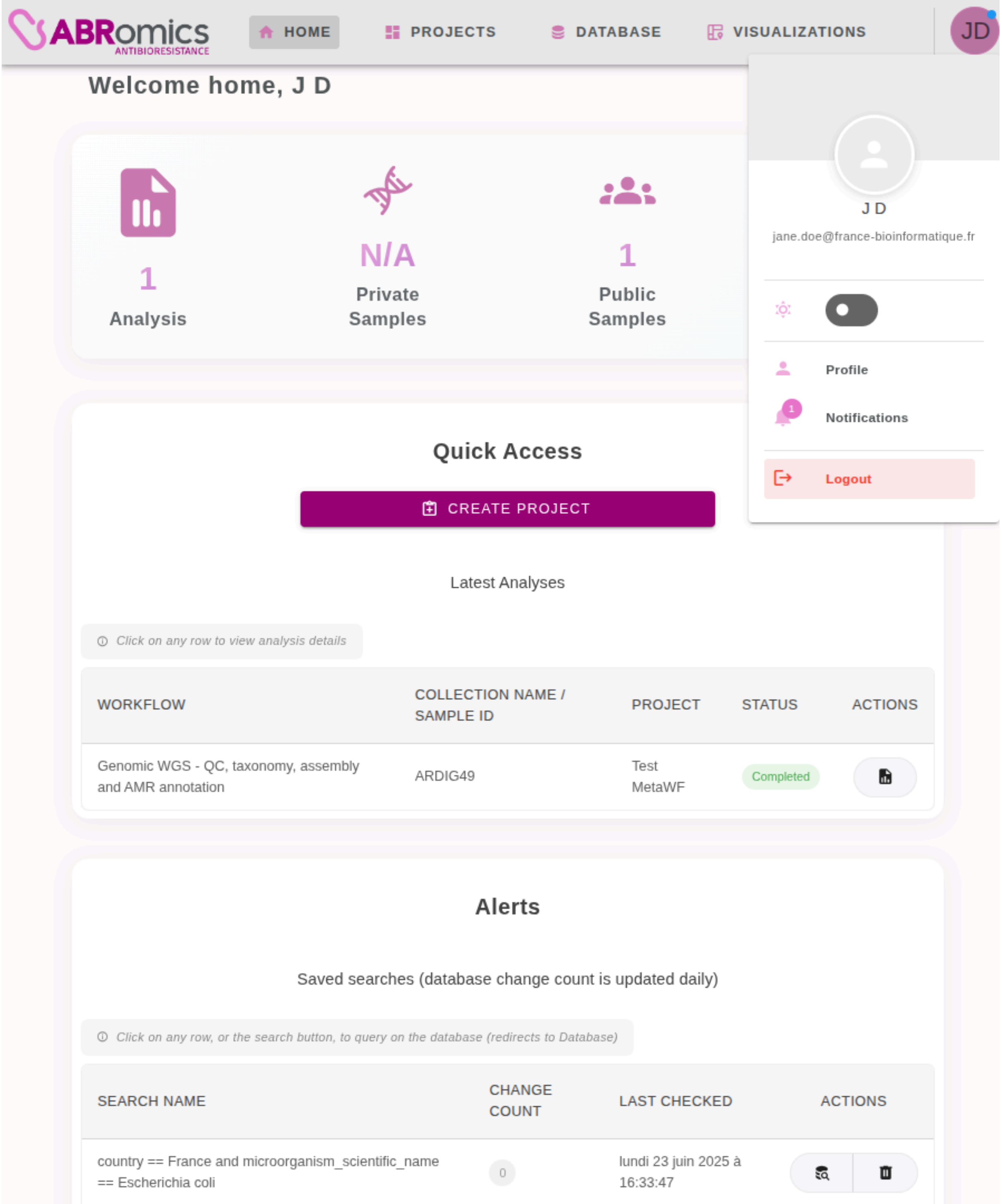
- Learn more about our *One Health* approach (“Learn more” in the “Collaborate” card).

You can find a tutorial on using the demo files in **Appendix 1**.

User profile

Once logged in, you arrive on your personal homepage, where you can view metrics of the projects you own or participate in. You will also find Information about the last 10 analyses you have launched. Finally, you can manage the alerts you saved during your searches in the ABRomics community Database.

If this is your first time using ABRomics, an optional interactive tour will start to showcase the platform’s features.



Welcome home, J D

jane.doe@france-bioinformatique.fr

Quick Access

Latest Analyses

ⓘ *Click on any row to view analysis details*

WORKFLOW	COLLECTION NAME / SAMPLE ID	PROJECT	STATUS	ACTIONS
Genomic WGS - QC, taxonomy, assembly and AMR annotation	ARDIG49	Test MetaWF	Completed	

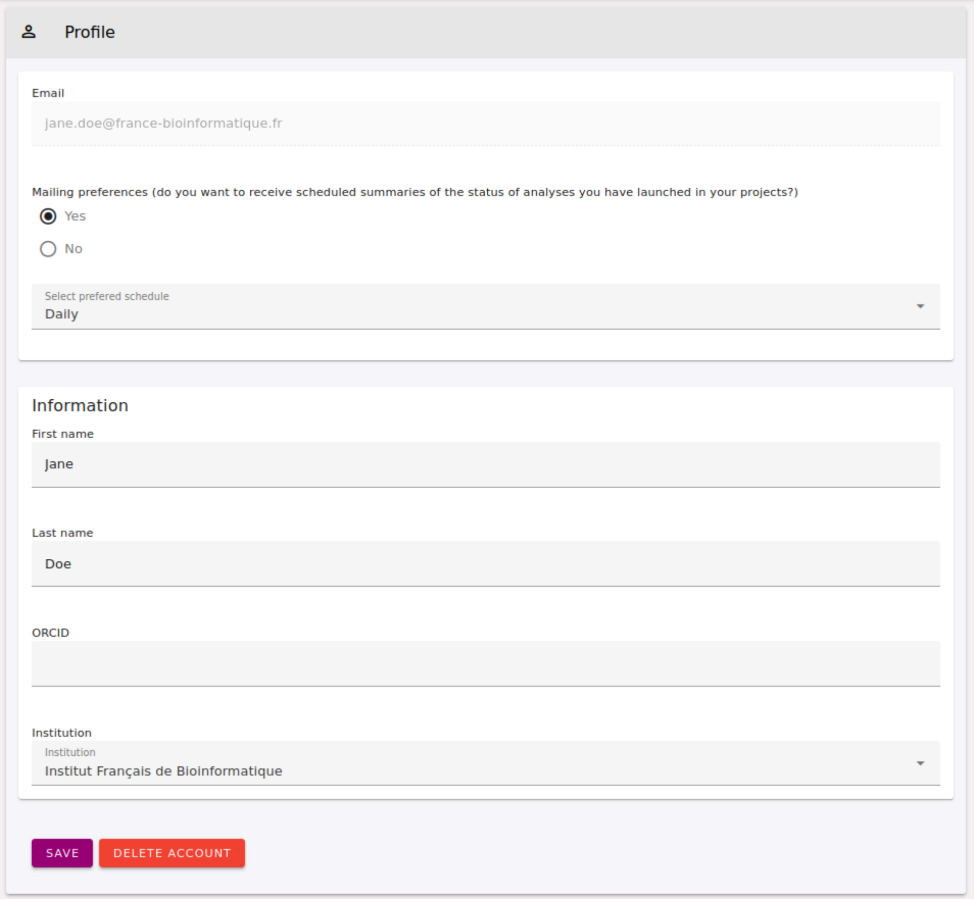
Alerts

Saved searches (database change count is updated daily)

ⓘ *Click on any row, or the search button, to query on the database (redirects to Database)*

SEARCH NAME	CHANGE COUNT	LAST CHECKED	ACTIONS
country == France and microorganism_scientific_name == Escherichia coli	0	lundi 23 juin 2025 à 16:33:47	

The User menu allows you to access your profile, view your notifications, and log out. You can open it by clicking on the thumbnail in the upper-right corner of the page. The “Profile” section is used to update the personal information you provided during registration (except for your email address) and to set your mailing preferences — specifically, whether you want to receive scheduled summaries of the status of your analyses, and if so, how often (Daily, Weekly, or Monthly).



Email: jane.doe@france-bioinformatique.fr

Mailing preferences (do you want to receive scheduled summaries of the status of analyses you have launched in your projects?)

● Yes
○ No

Select prefered schedule: Daily

Information

First name: Jane

Last name: Doe

ORCID:

Institution: Institut Français de Bioinformatique

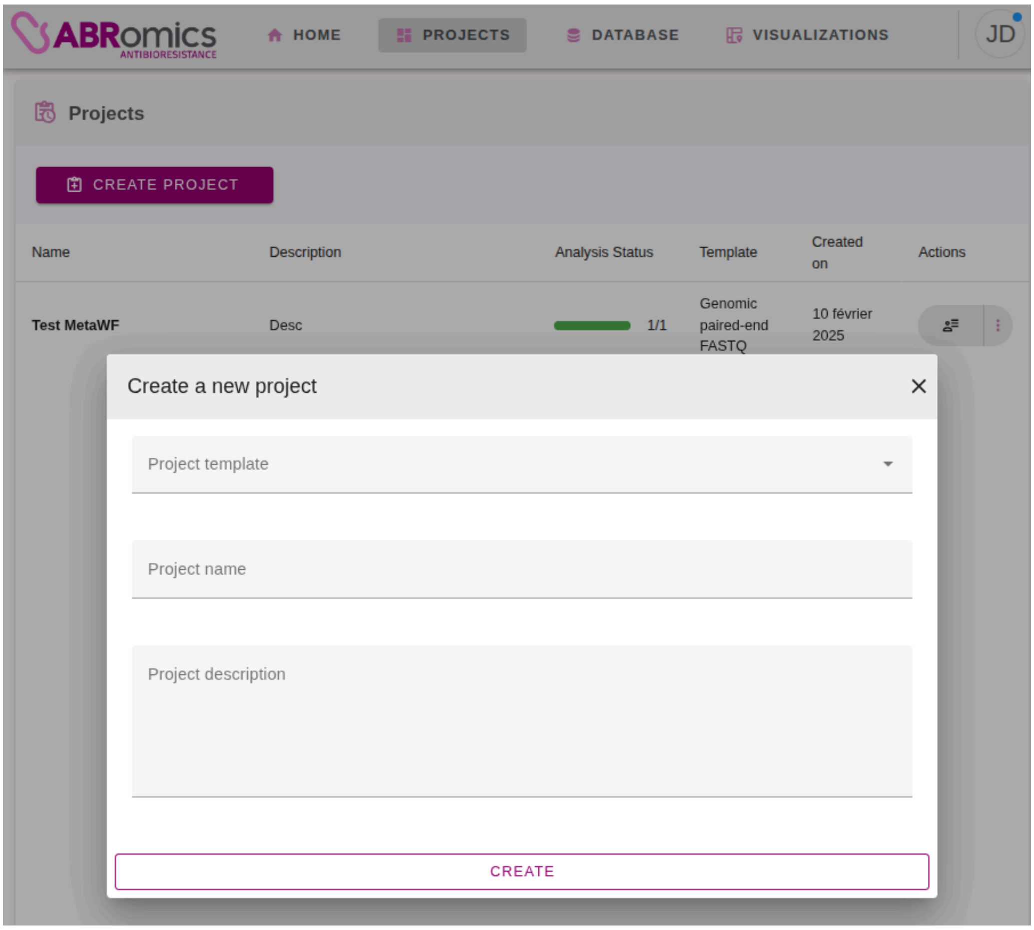
You can also choose to delete your account. A confirmation pop-up will appear, as this action will permanently delete all the projects you are supervising.

According to the **ABRomics user charter**, projects containing public data will only have their private data removed (samples, analyses, results). Collaborators will also lose access to these projects. All public results will remain available on the "Database" page, and other users will still be able to add the public samples from these projects to their own.

PROJECTS & PROJECT MANAGEMENT

You can access your projects and create new ones by clicking the "PROJECTS" menu. The page displays a list of all projects you have created or been added to, along with key information such as the project name, description, template, and creation date.

You can create a new project by clicking the pink "Create Project" button. A quick-access "Create Project" button is also available on your Home page.



Name	Description	Analysis Status	Template	Created on	Actions
Test MetaWF	Desc	1/1	Genomic paired-end FASTQ	10 février 2025	

To create a project, you must select a template and provide a project name and a short description.

A template defines several essential features of a project, including:

1. The type of metadata linked to the input files, which determines data structure and organization.
2. The types of analysis workflows that can be run, along with the results they produce.

In other words, a template determines the format of the results collection table for a project, influencing both the inputs (metadata, file types) and the outputs (analysis results). It provides the framework for managing input data and defines the range of analytical processes available in the project.

ABRomics V1.2.1 supports the analysis of sequencing data (FastQ) and assembly data (FastA).

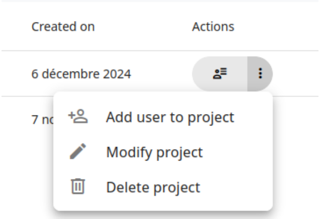
The expected inputs and metadata template to choose are described in this table:

Data	Expected data inputs	Template to choose
Sequencing data	● R1 fastq file (.fastq.gz, .fq.gz, fastqsanger.gz) ● R2 fastq file (.fastq.gz, .fq.gz, fastqsanger.gz)	Genomic paired-end FASTQ
Assembly data	● .fasta files	Genomic FASTA

After creating a project, you become the supervisor of that project. As a supervisor, you can:

- Add other users[1] to the project (you must know the email address associated with their ABRomics account);
- Change the project name or description;
- Delete the project.

Important: Deleting a project will permanently remove all private samples and analyses associated with the project.



The details of a project can be seen by clicking on the corresponding row (example below with "ABRomics DEMO"). A status bar shows you how many analyses in your project were successful, are running, or have failed.

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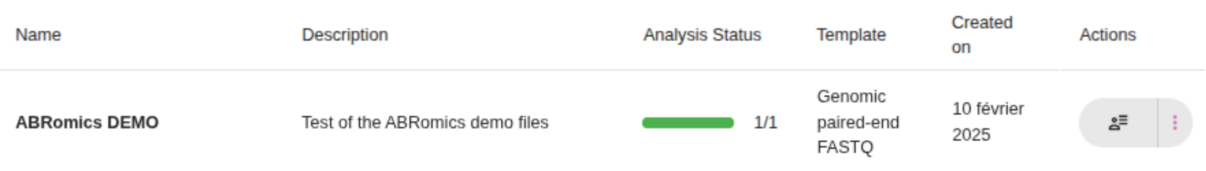
[1] Users added to a project are assigned the role of coworker by default. See the "Table of Roles and Permissions" in the Appendix for more details.

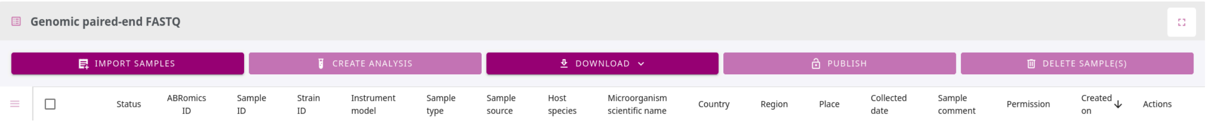


Name	Description	Analysis Status	Template	Created on	Actions
ABRomics DEMO	Test of the ABRomics demo files	1/1	Genomic paired-end FASTQ	10 février 2025	

The corresponding web page is split into three sections to allow data and results management of a given project:

1 – ***Action Buttons***: Directly below the project's template name (e.g., "Genomic paired-end FASTQ"), five pink buttons allow you to manage batches of samples:

- IMPORT SAMPLES
- CREATE ANALYSIS
- DOWNLOAD
- PUBLISH
- DELETE SAMPLE(S)



☐	Status	ABRomics ID	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country	Region	Place	Collected date	Sample comment	Permission	Created on	Actions

2 – ***Samples Table***: Below the action buttons, the table lists all samples in the project. Each row corresponds to a sample and includes 16 metadata columns:

> "Status", "ABRomics ID", "Sample ID", "Strain ID", "Instrument model", "Sample type", "Sample source", "Host species", "Microorganism scientific name", "Country", "Region", "Place", "Collected date", "Sample comment", "Permission", "Created on".

The displayed metadata may vary depending on the project template. Detailed information on these metadata is available in the appendix **"Table of Templates & metadata"**.

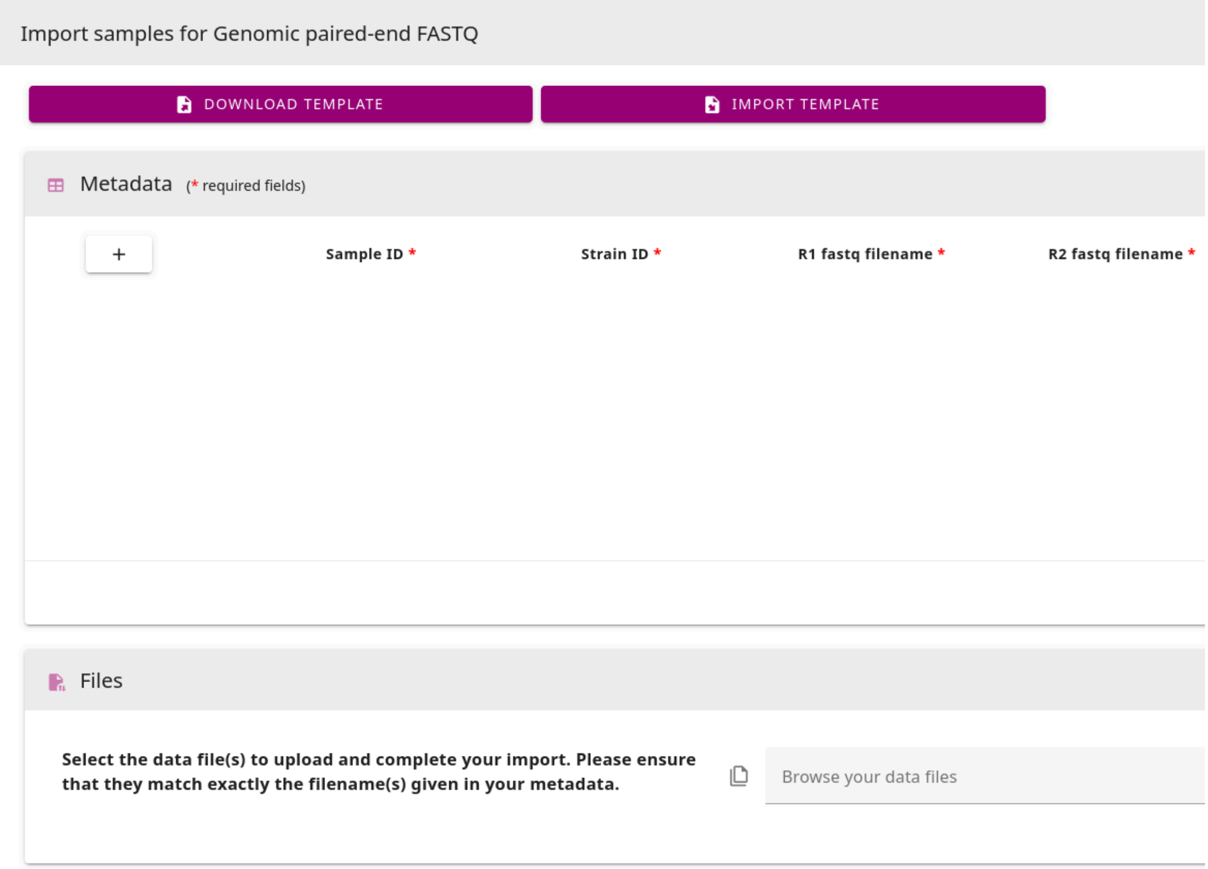
Specific actions for each sample can be accessed via the "Actions" button at the right end of the row.

3 – ***Filters menu sidebar***: To facilitate the management of samples, you can use the filters menu sidebar at the very left side of the table. The filter menu can be enlarged if you click on any of the icons. Filtering will be further explained in the **"Explore results"** sections.

GENOMIC WORKFLOWS ANALYSES

Upload a sample & metadata validation

To add a sample to a project, you must be the **project supervisor** (i.e., the project's creator). By clicking on the "IMPORT SAMPLES" button, the following pop-up appears:

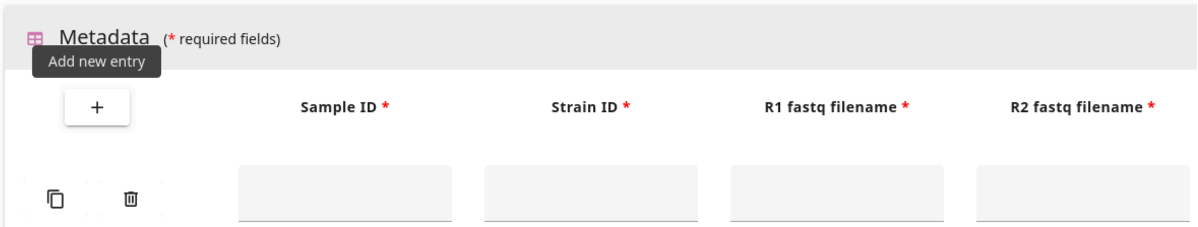


Select the data file(s) to upload and complete your import. Please ensure that they match exactly the filename(s) given in your metadata.

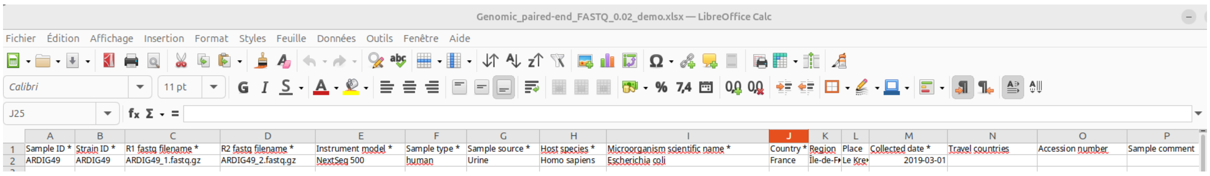
Entering metadata information

All mandatory metadata fields are indicated with an asterisk (*). You can enter the information in two ways:

1 – **Manual Entry**: Click the "**+**" button to add a new entry (i.e., a new sample). A new row will appear with empty fields for each metadata column. This method is recommended only if you have a small number of samples to add.



2 – **Using the Excel Template**: You can download and Excel file template by clicking the pink "DOWNLOAD TEMPLATE" button. This template contains the 16 metadata columns required for each sample. Like the interface, the .xlsx file provides guidance through selectable lists and tooltips. The demo file "Genomic_paired-end_FASTQ_0.02_demo.xlsx" contains one example row:



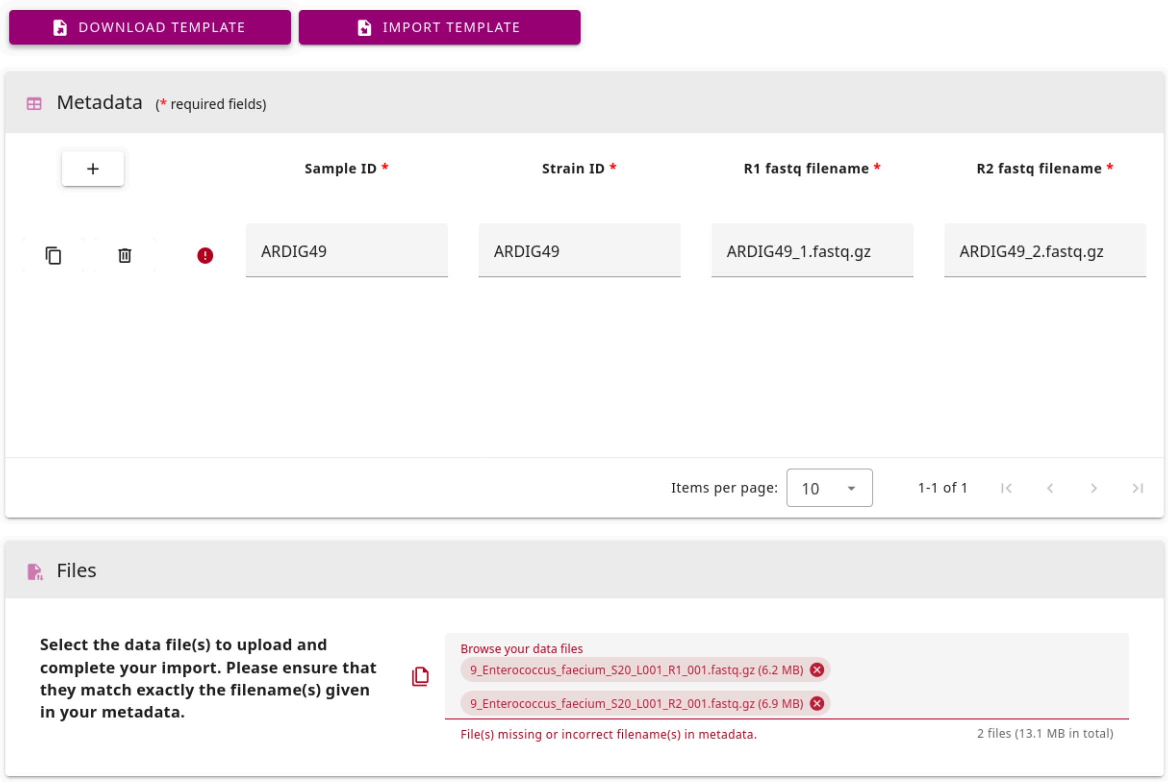
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Sample ID *	Strain ID *	R1 fastq filename *	R2 fastq filename *	Instrument model *	Sample type *	Sample source *	Host species *	Microorganism scientific name *	Country *	Region	Place	Collected date *	Travel countries	Accession number	Sample comment
2	ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-F	Le Kre	2019-03-01			

After you complete all mandatory metadata for your samples, click "IMPORT TEMPLATE" to select the .xlsx file and upload it into ABRomics.

Important: *The worksheet name in the .xlsx file must match the current template version used in ABRomics (e.g., "Genomic WGS 0.02"). If the version differs from the one expected by the platform, an error will appear. More details are available in the* ***"Tables of Templates and Metadata"*** *section.*

Uploading Sequence Files

You must then upload the sequence files (R1 and R2) associated with each sample. The filenames entered in the "**R1 fastq filename**" and "**R2 fastq filename**" metadata fields must exactly match the filenames of the uploaded files.



Metadata (* required fields)

Sample ID *	Strain ID *	R1 fastq filename *	R2 fastq filename *
ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz

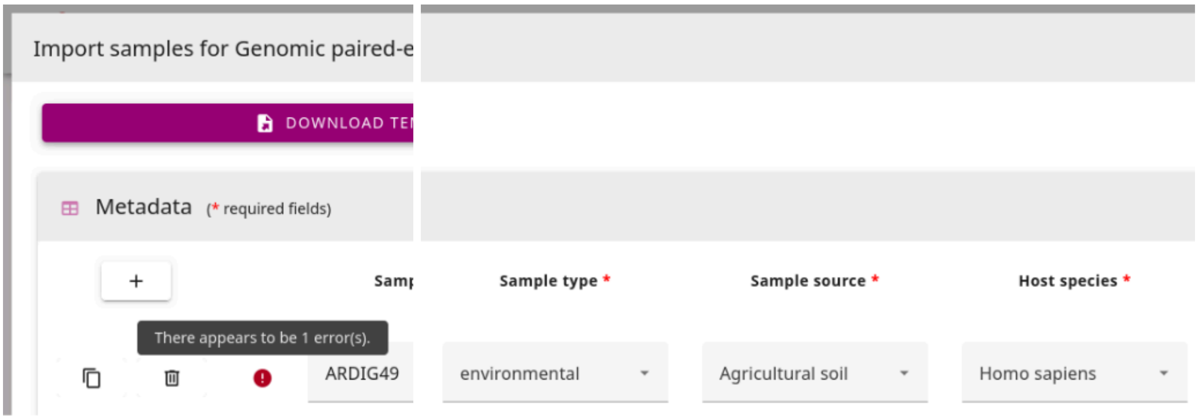
Files

Select the data file(s) to upload and complete your import. Please ensure that they match exactly the filename(s) given in your metadata.

Browse your data files
9_Enterococcus_faecium_S20_L001_R1_001.fastq.gz (6.2 MB)
9_Enterococcus_faecium_S20_L001_R2_001.fastq.gz (6.9 MB)
File(s) missing or incorrect filename(s) in metadata.
2 files (13.1 MB in total)

In the example above, the uploaded files do not match the expected names “ARDIG49_1.fastq.gz” and “ARDIG49_2.fastq.gz,”, leading to the following error message: “incorrect filename(s) in metadata”.

If metadata errors occur, the interface will point them out so you can correct them. In the example below, there is a wrong association between the sample type “environmental” and the host species “*Homo sapiens*”.



Import samples for Genomic paired-e

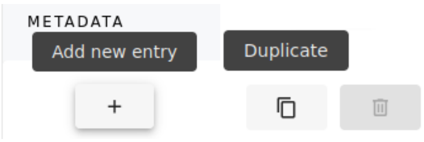
Metadata (* required fields)

There appears to be 1 error(s).

Samp	Sample type *	Sample source *	Host species *
ARDIG49	environmental	Agricultural soil	Homo sapiens

Managing Metadata Rows

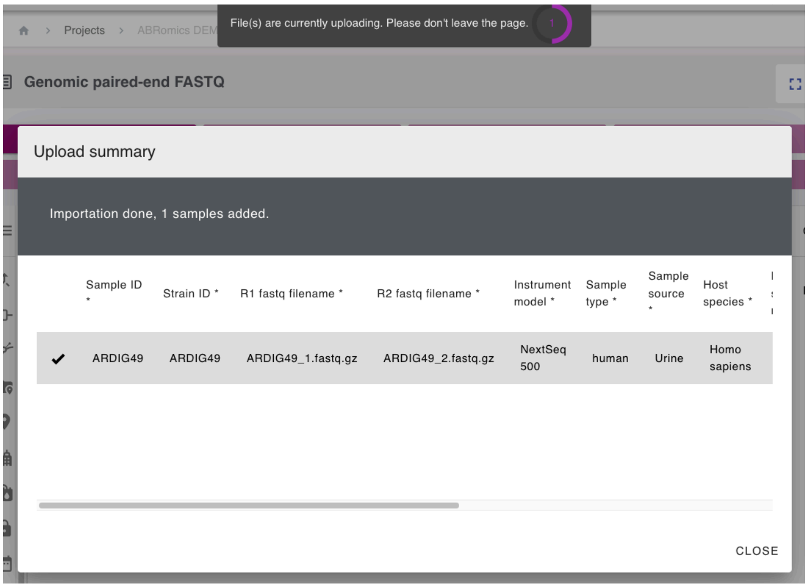
In the interface, you can duplicate existing rows or add new ones using the available buttons:



You may also fill in multiple rows directly in the .xlsx file before importing it, or import several .xlsx files if needed.

Final Step

If all rows are correctly filled in, a summary pop-up will appear, along with a warning advising you to stay on the page until the server finishes processing the input files. Once a sample has been added, the project supervisor can edit or delete it at any time using the **“Actions”** button located in the rightmost column of the table.



File(s) are currently uploading. Please don't leave the page.

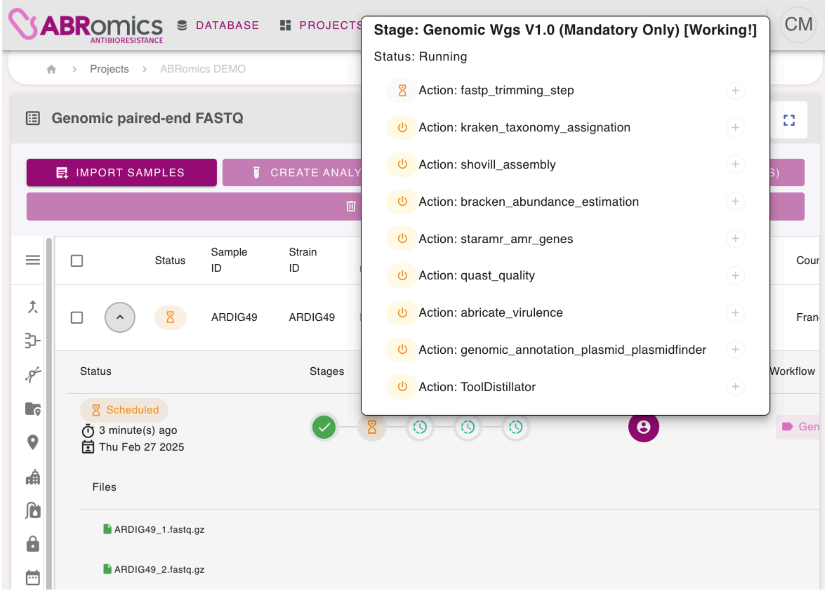
Importation done, 1 samples added.

	Sample ID *	Strain ID *	R1 fastq filename *	R2 fastq filename *	Instrument model *	Sample type *	Sample source *	Host species *
✓	ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz	NextSeq 500	human	Urine	Homo sapiens

Run an Analysis

Automatic Launch

After uploading a sample, the default analysis **automatically starts**. It may take a few seconds for the workflow to begin.



Stage: Genomic Wgs V1.0 (Mandatory Only) [Working!]

Status: Running

Action: fastp_trimming_step
Action: kraken_taxonomy_assignation
Action: shovill_assembly
Action: bracken_abundance_estimation
Action: staramr_amr_genes
Action: quast_quality
Action: abricate_virulence
Action: genomic_annotation_plasmid_plasmidfinder
Action: ToolDistillator

Genomic paired-end FASTQ

Status	Sample ID	Strain ID
	ARDIG49	ARDIG49

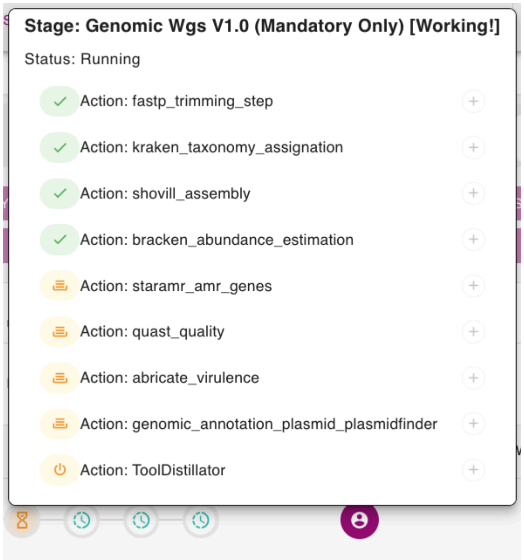
Status: Scheduled
3 minute(s) ago
Thu Feb 27 2025

Stages

Files
ARDIG49_1.fastq.gz
ARDIG49_2.fastq.gz

This screenshot shows that the FASTQ files (R1 and R2 in green) were successfully uploaded, and the genomic pipeline is currently running. Each step of the workflow is listed in the pop-up window. Detailed explanations of all analysis steps are available on the ABRomics portal: https://www.abromics.fr/home/abromics-platform/workflows-and-analyses/.

As each step completes, a **green checkmark** appears next to it.



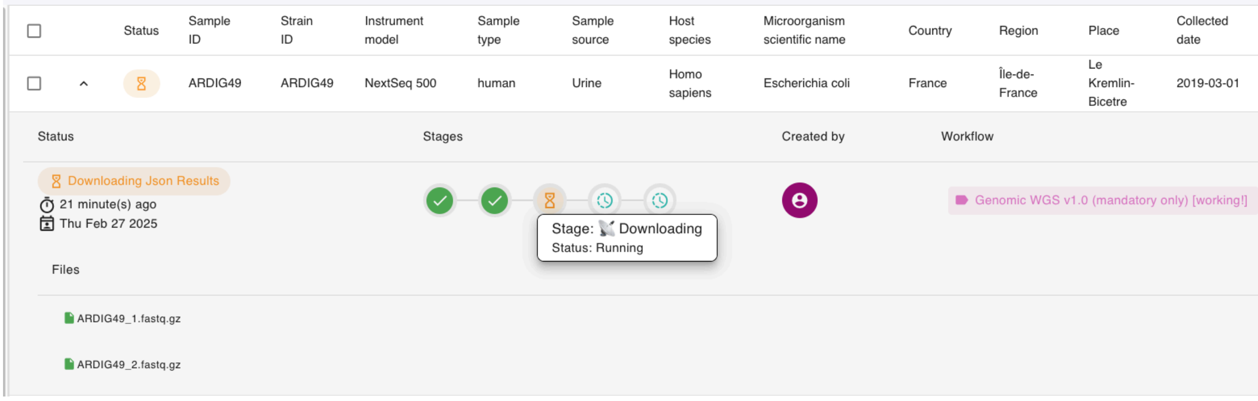
Stage: Genomic Wgs V1.0 (Mandatory Only) [Working!]

Status: Running

✓ Action: fastp_trimming_step
✓ Action: kraken_taxonomy_assignation
✓ Action: shovill_assembly
✓ Action: bracken_abundance_estimation
Action: staramr_amr_genes
Action: quast_quality
Action: abricate_virulence
Action: genomic_annotation_plasmid_plasmidfinder
Action: ToolDistillator

Example Timeline

- Around 30 minutes to 1 hour after uploading the demo sequence and metadata, the workflow reaches the “Downloading” stage:



☐		Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country	Region	Place	Collected date
☐	^	⌛	ARDIG49	ARDIG49	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-France	Le Kremlin-Bicetre	2019-03-01

Status	Stages	Created by	Workflow
⌛ Downloading Json Results ⏱ 21 minute(s) ago 📅 Thu Feb 27 2025	✓ ✓ ⌛ ◷ ◷ Stage: Downloading Status: Running	●	Genomic WGS v1.0 (mandatory only) [working!]

Files

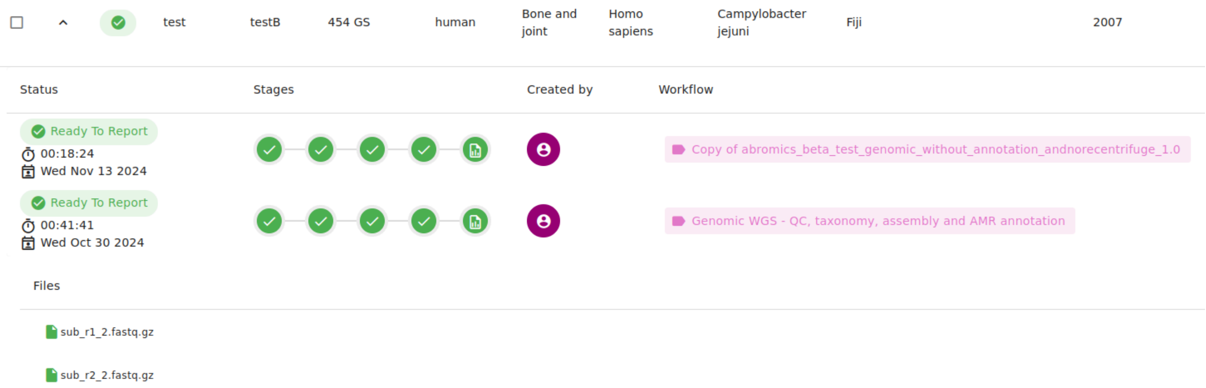
ARDIG49_1.fastq.gz

ARDIG49_2.fastq.gz

- About 3 minutes later, the whole workflow is completed.

Running Additional Analyses

Different analysis workflows can be run on a single sample. However, duplicate analyses of the same type are not allowed. To re-run an analysis, the previous one must first be deleted.



☐	^	✓	test	testB	454 GS	human	Bone and joint	Homo sapiens	Campylobacter jejuni	Fiji	2007

Status	Stages	Created by	Workflow
✓ Ready To Report ⏱ 00:18:24 📅 Wed Nov 13 2024	✓ ✓ ✓ ✓ 🗎	●	Copy of abromics_beta_test_genomic_without_annotation_andnorecentrifuge_1.0
✓ Ready To Report ⏱ 00:41:41 📅 Wed Oct 30 2024	✓ ✓ ✓ ✓ 🗎	●	Genomic WGS - QC, taxonomy, assembly and AMR annotation

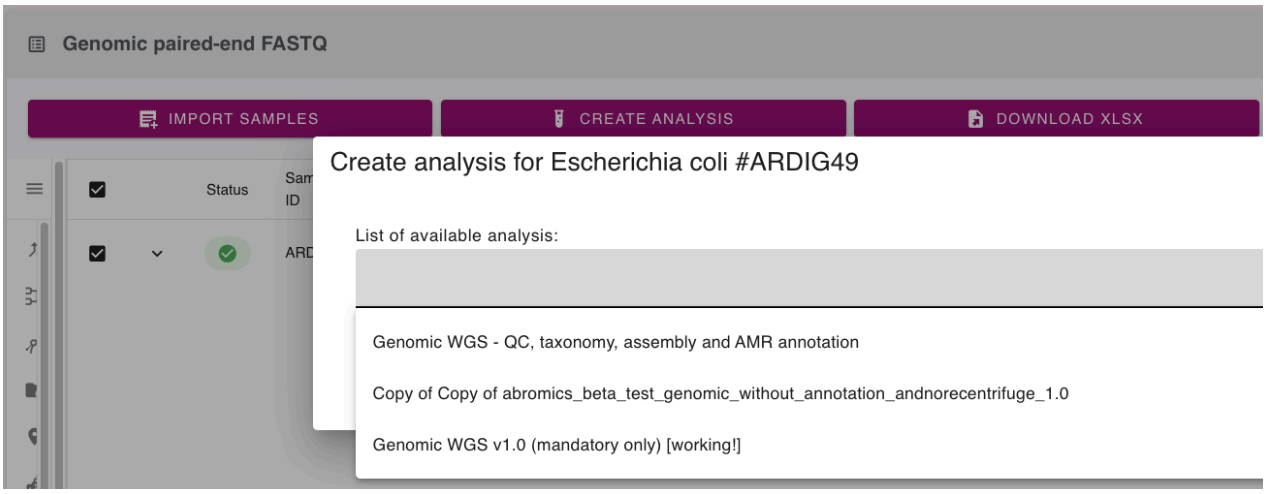
Files

sub_r1_2.fastq.gz

sub_r2_2.fastq.gz

Any project member (**supervisor** of the project or **coworker**) can run analyses on any sample in the project:

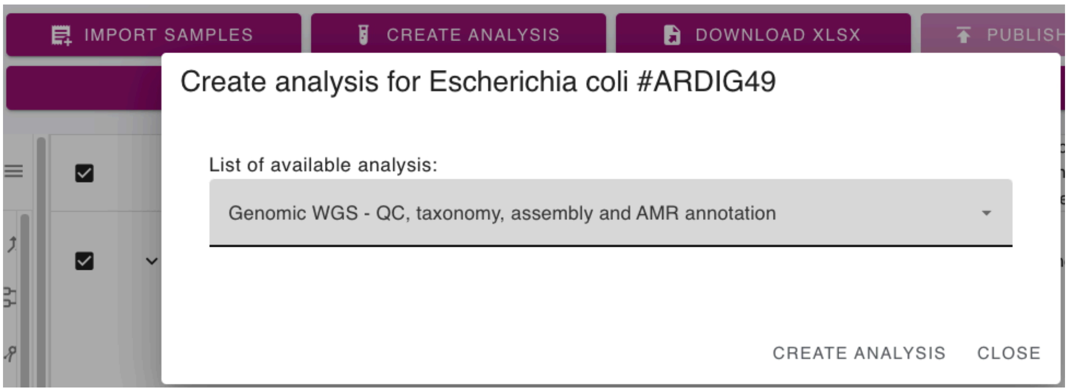
1. Select one or more samples using the checkboxes.
2. Click “Create Analysis”.
3. Choose an analysis from the dropdown menu.



Create analysis for Escherichia coli #ARDIG49

List of available analysis:

4. Click “Create Analysis” in the pop-up window.



Create analysis for Escherichia coli #ARDIG49

List of available analysis: Genomic WGS - QC, taxonomy, assembly and AMR annotation

Monitoring an Analysis

Project members can follow the progress of each analysis. The interface displays:

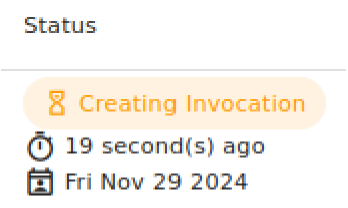
- ***Stages***: The global state of the analysis.
  - A successful analysis will go through these stages in the following order: **Ready** → **Scheduled** → **Downloading** → **Saving** → **Quality Control** → **Ready to report**.
  - If the analysis fails, the stage is shown as **Error**.
- ***Status***: The specific status within the current stage. Status descriptions for each stage are provided in the table below.
- ***Created by***: The user who launched the analysis.
- ***Workflow***: The type of analysis being run.
- ***Elapsed time***: Time since the analysis was created (shown below the status).
- ***Created date***: Displayed below the elapsed time.

Project members can cancel an analysis at any time before it reaches a final stage (“Ready to report” for a successful analysis or “Error” for a failed analysis).

Here is a table of analysis stages and statuses:

Analysis Stages	**Analysis Statuses**
1 - Ready	Not ready (default analysis will start soon), Ready, Retrying (analysis failed once and the automatic retry started)
2 - Scheduled	Creating invocation, Scheduled
3 - Downloading	Downloading json results, Ready to download, Downloading, Downloaded
4 - Saving	Saving (saving results in the ABRomics database)
5 - Quality control	Quality control (flags on the analysis results are generated for the report)
6 - Ready to report	Ready to report (report was generated and is accessible on ABRomics)
Error	Error (analysis failed)

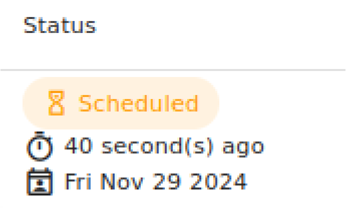
Here are some examples of stages and statuses displayed:


Status

Creating Invocation

19 second(s) ago

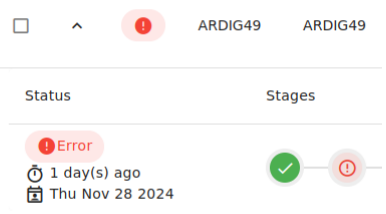
Fri Nov 29 2024


Status

Scheduled

40 second(s) ago

Fri Nov 29 2024


ARDIG49

ARDIG49

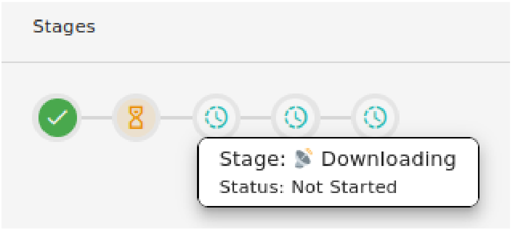
Status

Stages

Error

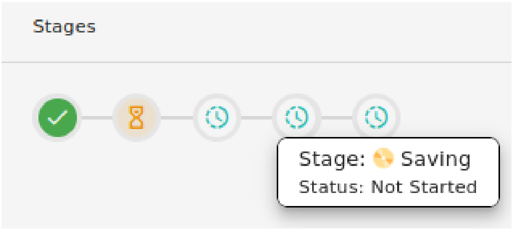
1 day(s) ago

Thu Nov 28 2024


Stages

Stage: Downloading

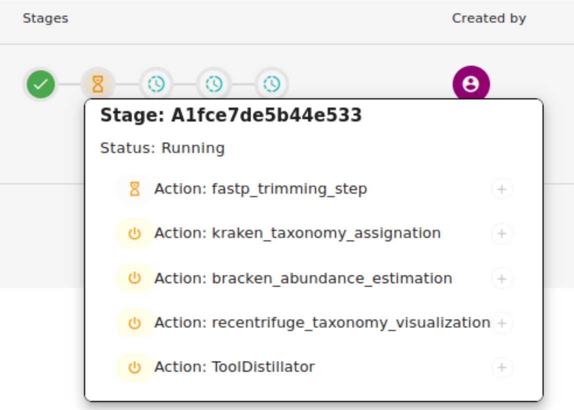
Status: Not Started


Stages

Stage: Saving

Status: Not Started

Under the scheduled stage, additional technical details about running jobs and tools are displayed.

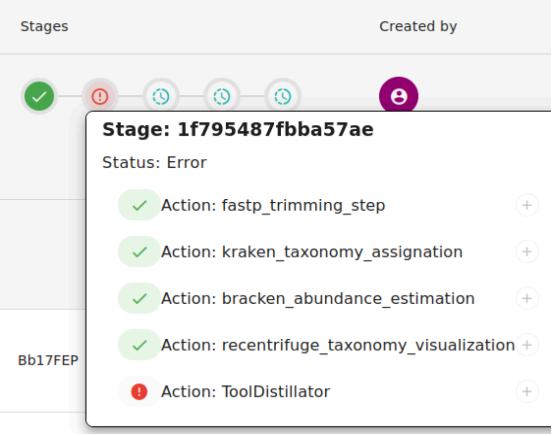


Stages | Created by

Stage: A1fce7de5b44e533

Status: Running

- Action: fastp_trimming_step
- Action: kraken_taxonomy_assignation
- Action: bracken_abundance_estimation
- Action: recentrifuge_taxonomy_visualization
- Action: ToolDistillator



Stages | Created by

Bb17FEP

Stage: 1f795487fbba57ae

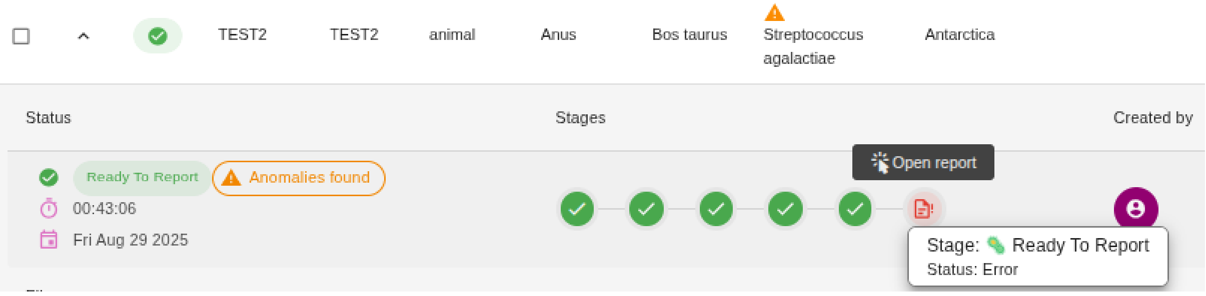
Status: Error

- ✓ Action: fastp_trimming_step
- ✓ Action: kraken_taxonomy_assignation
- ✓ Action: bracken_abundance_estimation
- ✓ Action: recentrifuge_taxonomy_visualization
- Action: ToolDistillator

If an analysis fails during the Scheduled phase, **one automatic retry** is performed. If the retry also fails, a project member may **manually retry** or **delete** the analysis.

Quality Control and Warnings

If issues are detected during Quality Control (QC), **warnings** appear.



☐ ✓ TEST2 TEST2 animal Anus Bos taurus ⚠ Streptococcus agalactiae Antarctica

Status | Stages | Created by

✓ Ready To Report ⚠ Anomalies found

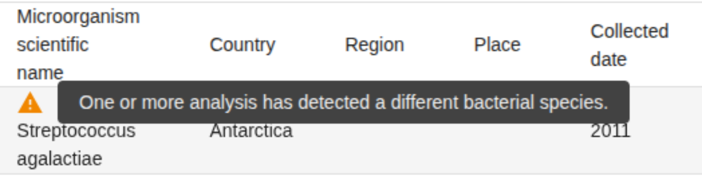
00:43:06

Fri Aug 29 2025

Stage: Ready To Report

Status: Error

For example, if the workflow detects a bacterial species different from the one provided in the metadata, a warning will suggest updating the metadata.

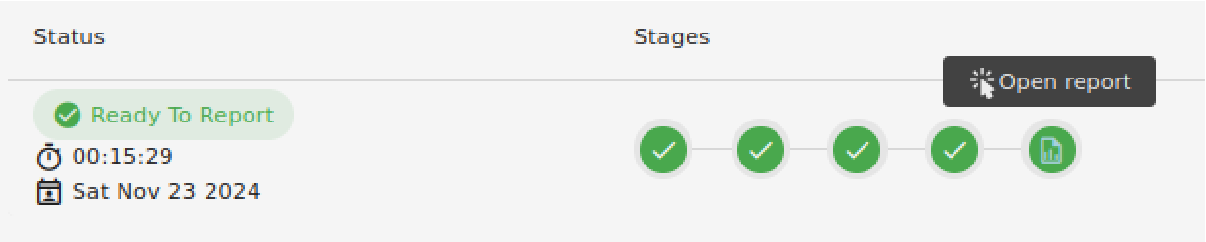


Microorganism scientific name	Country	Region	Place	Collected date
⚠ Streptococcus agalactiae	Antarctica			2011

One or more analysis has detected a different bacterial species.

Important: Changing the taxonomy metadata **does not relaunch the analysis**.

When an analysis succeeds, project members can **open the generated report** or **delete the analysis**.



Publishing an Analysis

A project supervisor may publish a sample and its analyses once **at least one analysis for that sample is successful**. Publishing makes the sample and its results **publicly accessible** to all ABRomics users.

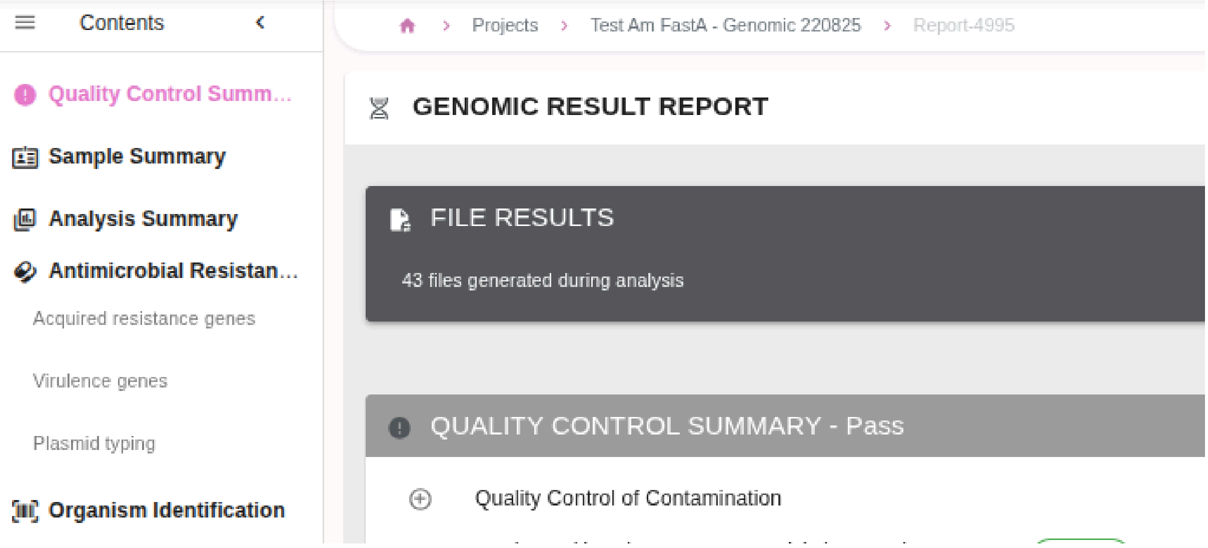
However, a sample **cannot** be published if:

- Quality control flagged a **failure**,
- Quality control raised **warnings that prevent publication**, or
- The analysis **has no quality control step** completed.

If QC raised only **warnings (no failures)**, the analysis will still appear in the **community database**.

View a report

When you click the Open report" button, you are redirected to the analysis report pages. A *Table of Contents* is displayed on the left side of the page, allowing you to quickly navigate to any section without scrolling through the entire report:



Contents

Quality Control Summ...

Sample Summary

Analysis Summary

Antimicrobial Resistan...

Acquired resistance genes

Virulence genes

Plasmid typing

Organism Identification

Projects > Test Am FastA - Genomic 220825 > Report-4995

GENOMIC RESULT REPORT

FILE RESULTS

43 files generated during analysis

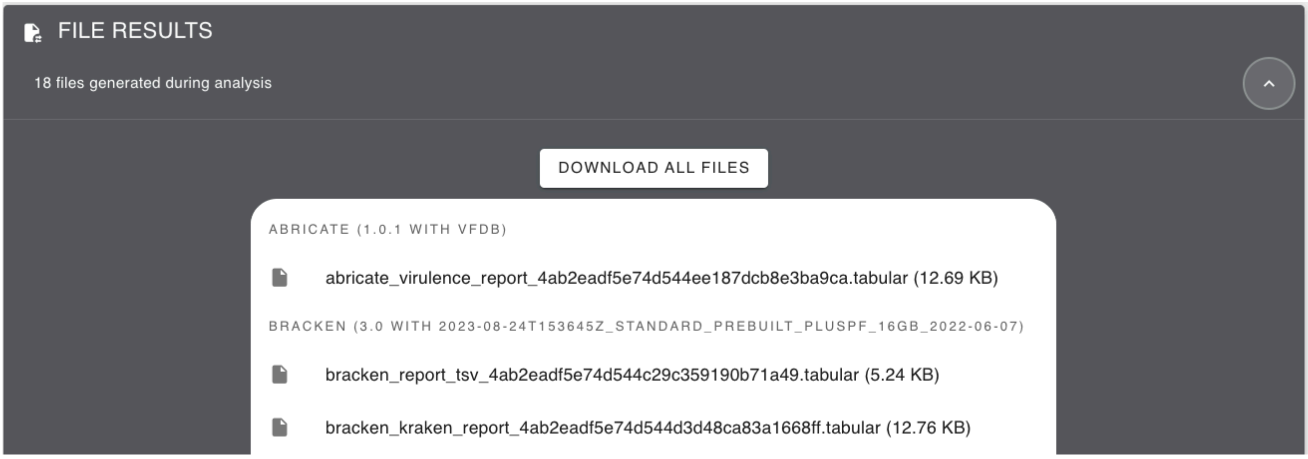
QUALITY CONTROL SUMMARY - Pass

Quality Control of Contamination

Each analysis report on the ABRomics platform is titled "Genomic result report". A brief description of the analyses used to generate the report appears directly below the title (e.g., "*Short paired-end read analysis to provide assembly, typing, genome annotation, and AMR gene detection*").

The report includes the following sections:

- **FILE RESULTS**: Contains the output files from all tools used in the analysis. Files can be downloaded individually or as a compressed archive (zip file).



FILE RESULTS

18 files generated during analysis

DOWNLOAD ALL FILES

ABRICATE (1.0.1 WITH VFDB)

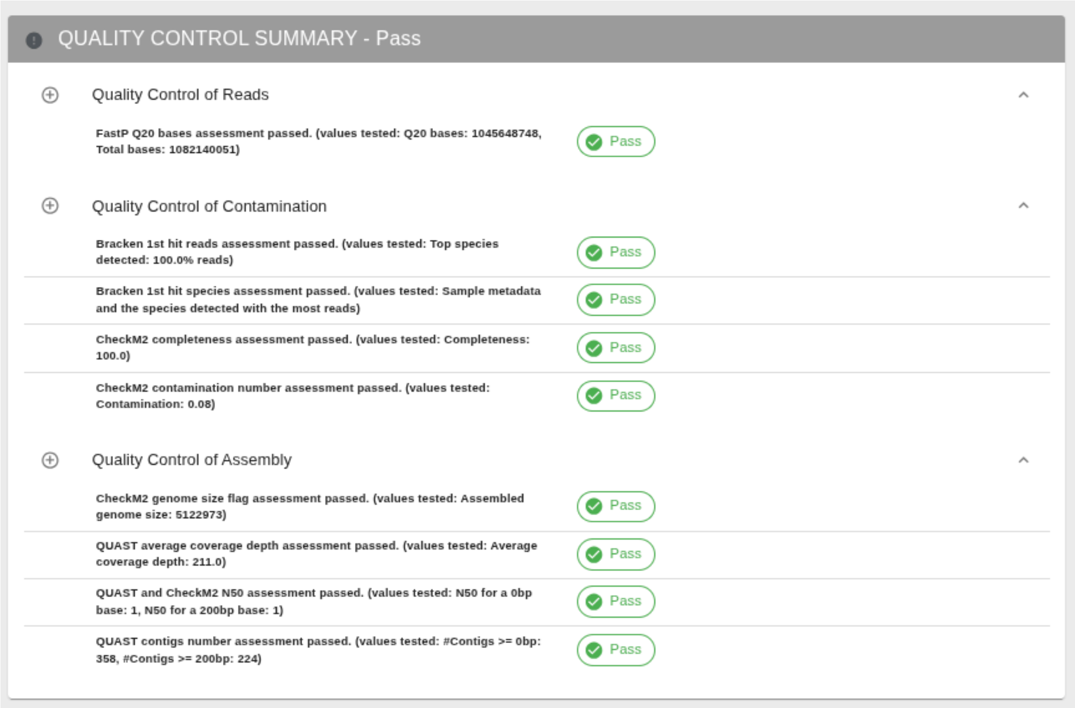
abricate_virulence_report_4ab2eadf5e74d544ee187dcb8e3ba9ca.tabular (12.69 KB)

BRACKEN (3.0 WITH 2023-08-24T153645Z_STANDARD_PREBUILT_PLUSPF_16GB_2022-06-07)

bracken_report_tsv_4ab2eadf5e74d544c29c359190b71a49.tabular (5.24 KB)

bracken_kraken_report_4ab2eadf5e74d544d3d48ca83a1668ff.tabular (12.76 KB)

- **QUALITY CONTROL SUMMARY**: Divided into subsections: “Quality Control of Reads” (only for Genomic FastQ), “Quality Control of Contamination”, and “Quality Control of Assembly”. These subsections display flags that alert users to any issues detected during the workflow.



QUALITY CONTROL SUMMARY - Pass

Quality Control of Reads

FastP Q20 bases assessment passed. (values tested: Q20 bases: 1045648748, Total bases: 1082140051)	✓ Pass

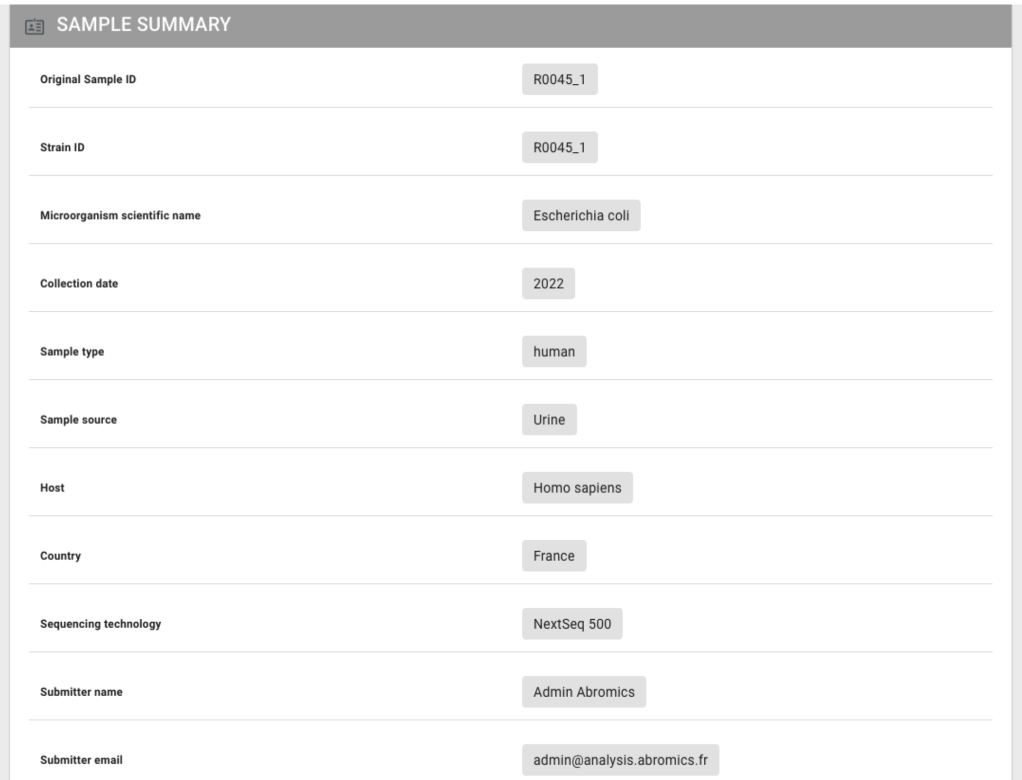
Quality Control of Contamination

Bracken 1st hit reads assessment passed. (values tested: Top species detected: 100.0% reads)	✓ Pass
Bracken 1st hit species assessment passed. (values tested: Sample metadata and the species detected with the most reads)	✓ Pass
CheckM2 completeness assessment passed. (values tested: Completeness: 100.0)	✓ Pass
CheckM2 contamination number assessment passed. (values tested: Contamination: 0.08)	✓ Pass

Quality Control of Assembly

CheckM2 genome size flag assessment passed. (values tested: Assembled genome size: 5122973)	✓ Pass
QUAST average coverage depth assessment passed. (values tested: Average coverage depth: 211.0)	✓ Pass
QUAST and CheckM2 N50 assessment passed. (values tested: N50 for a 0bp base: 1, N50 for a 200bp base: 1)	✓ Pass
QUAST contigs number assessment passed. (values tested: #Contigs >= 0bp: 358, #Contigs >= 200bp: 224)	✓ Pass

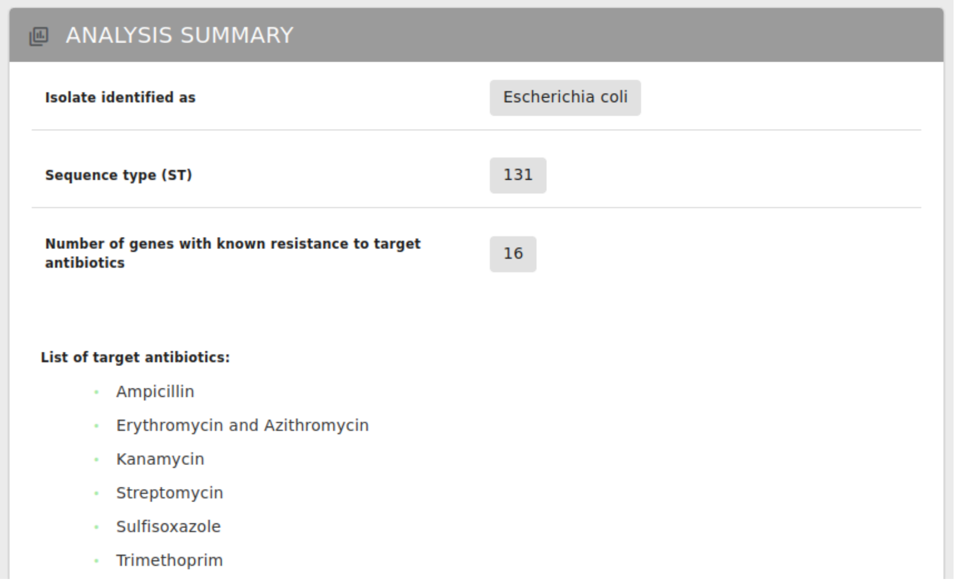
- **SAMPLE SUMMARY**: Provides an overview of the sample metadata submitted by the sample owner.



SAMPLE SUMMARY

Original Sample ID	R0045_1
Strain ID	R0045_1
Microorganism scientific name	Escherichia coli
Collection date	2022
Sample type	human
Sample source	Urine
Host	Homo sapiens
Country	France
Sequencing technology	NextSeq 500
Submitter name	Admin Abromics
Submitter email	admin@analysis.abromics.fr

- **ANALYSIS SUMMARY**: Presents the key results of the analysis, including: the isolate identified, the number of genes with known resistance to target antibiotics, and the list of these target antibiotics.



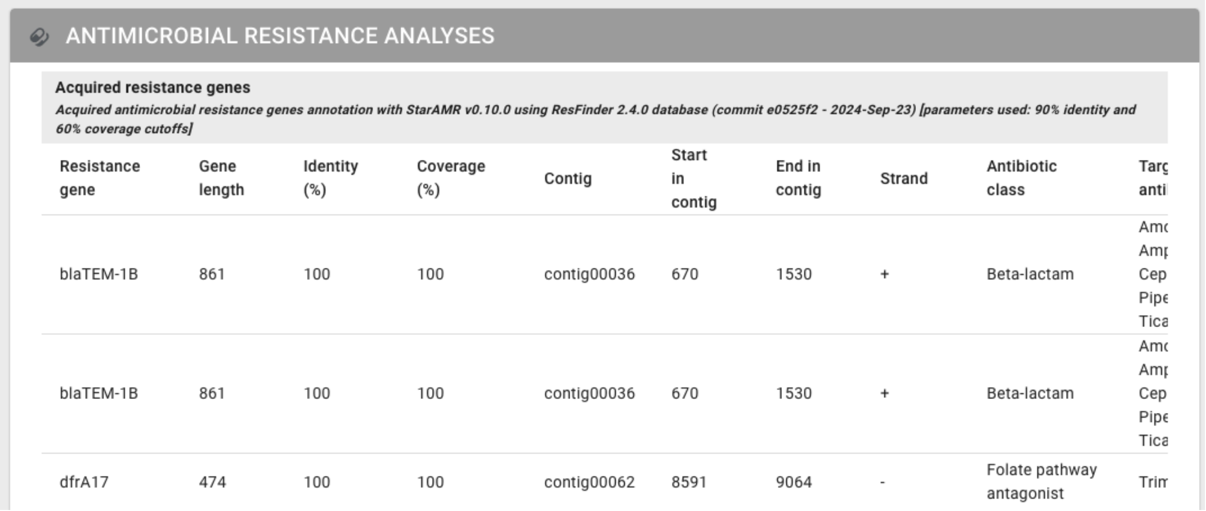
ANALYSIS SUMMARY

Isolate identified as	Escherichia coli
Sequence type (ST)	131
Number of genes with known resistance to target antibiotics	16

List of target antibiotics:

- Ampicillin
- Erythromycin and Azithromycin
- Kanamycin
- Streptomycin
- Sulfisoxazole
- Trimethoprim

- **ANTIMICROBIAL RESISTANCE ANALYSES**: Includes three subsections: acquired resistance genes, virulence genes, and plasmid typing. This section also lists the tools used and their versions.

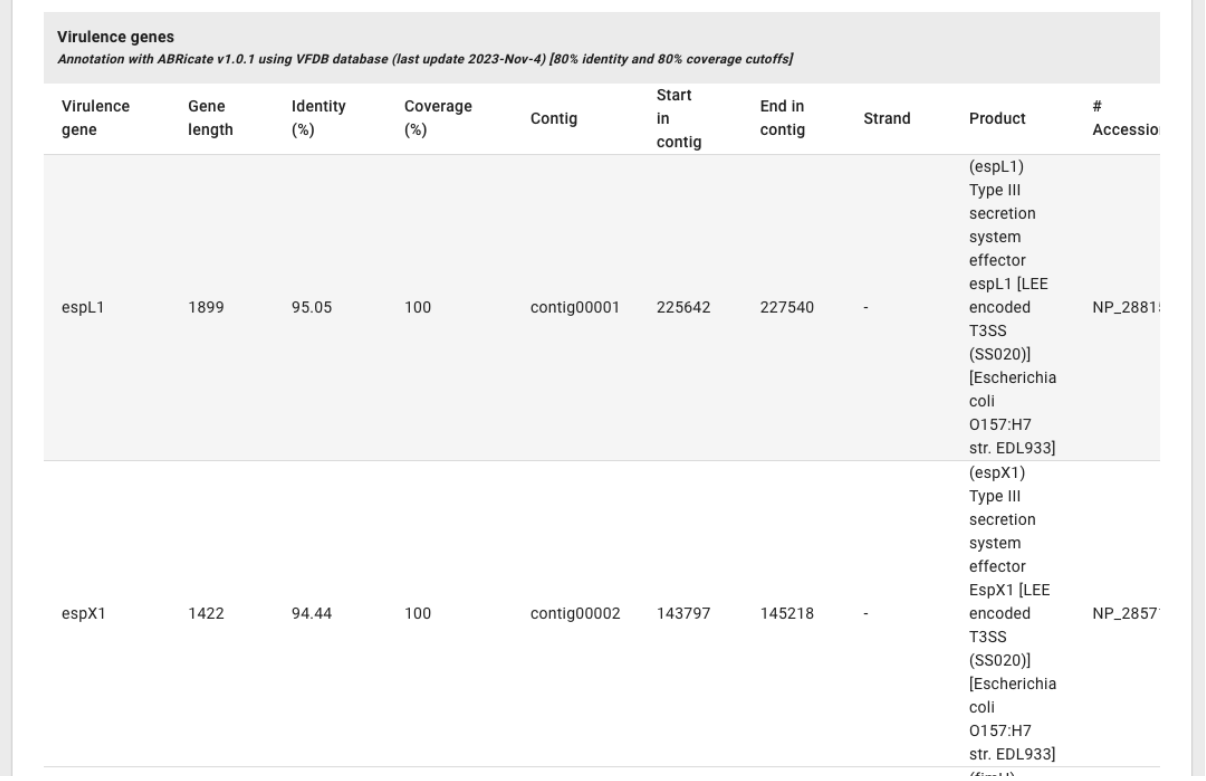


ANTIMICROBIAL RESISTANCE ANALYSES

Acquired resistance genes

Acquired antimicrobial resistance genes annotation with StarAMR v0.10.0 using ResFinder 2.4.0 database (commit e0525f2 - 2024-Sep-23) [parameters used: 90% identity and 60% coverage cutoffs]

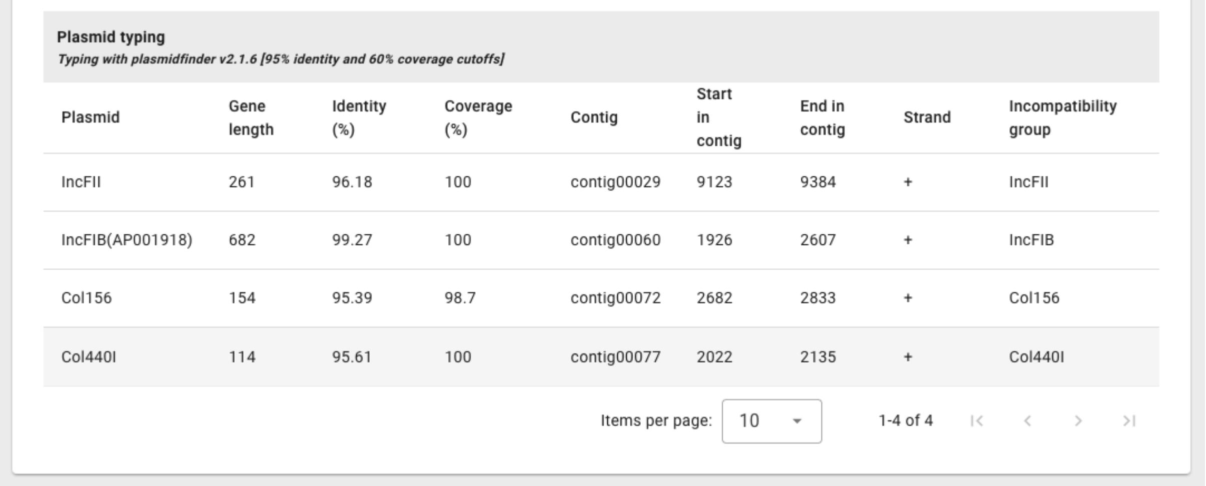
Resistance gene	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Antibiotic class	Targ anti
blaTEM-1B	861	100	100	contig00036	670	1530	+	Beta-lactam	Amc Amp Cep Pipe Tica
blaTEM-1B	861	100	100	contig00036	670	1530	+	Beta-lactam	Amc Amp Cep Pipe Tica
dfrA17	474	100	100	contig00062	8591	9064	-	Folate pathway antagonist	Trim



Virulence genes

Annotation with ABRicate v1.0.1 using VFDB database (last update 2023-Nov-4) [80% identity and 80% coverage cutoffs]

Virulence gene	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Product	# Accessio
espL1	1899	95.05	100	contig00001	225642	227540	-	(espL1) Type III secretion system effector espL1 [LEE encoded T3SS (SS020)] [Escherichia coli O157:H7 str. EDL933]	NP_2881
espX1	1422	94.44	100	contig00002	143797	145218	-	(espX1) Type III secretion system effector EspX1 [LEE encoded T3SS (SS020)] [Escherichia coli O157:H7 str. EDL933]	NP_2857

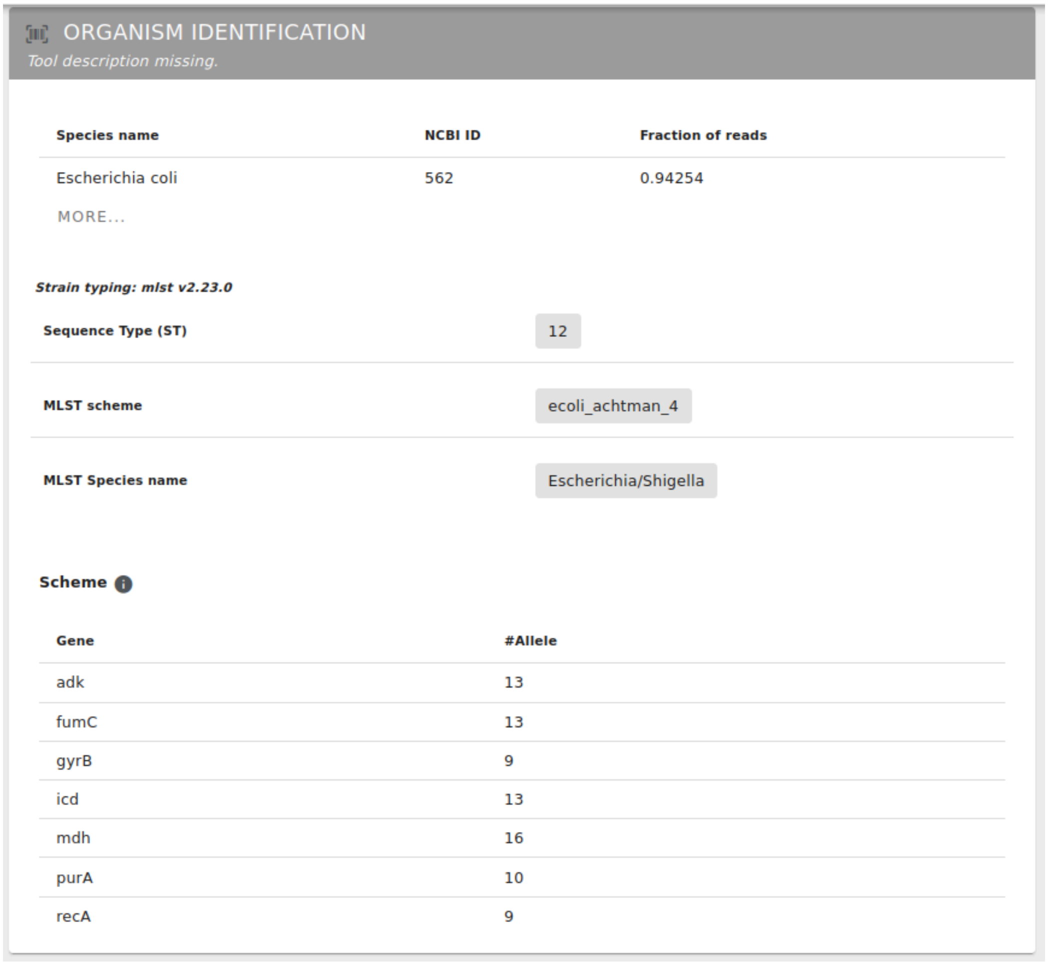


Plasmid typing

Typing with plasmidfinder v2.1.6 [95% identity and 60% coverage cutoffs]

Plasmid	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Incompatibility group
IncFII	261	96.18	100	contig00029	9123	9384	+	IncFII
IncFIB(AP001918)	682	99.27	100	contig00060	1926	2607	+	IncFIB
Col156	154	95.39	98.7	contig00072	2682	2833	+	Col156
Col440I	114	95.61	100	contig00077	2022	2135	+	Col440I

- **ORGANISM IDENTIFICATION:** Displays the results of the taxonomic assignment with the Kraken2 tool, along with the detected Sequence Type, and the corresponding MLST scheme and species found.



Tool description missing.

Species name	NCBI ID	Fraction of reads
Escherichia coli	562	0.94254

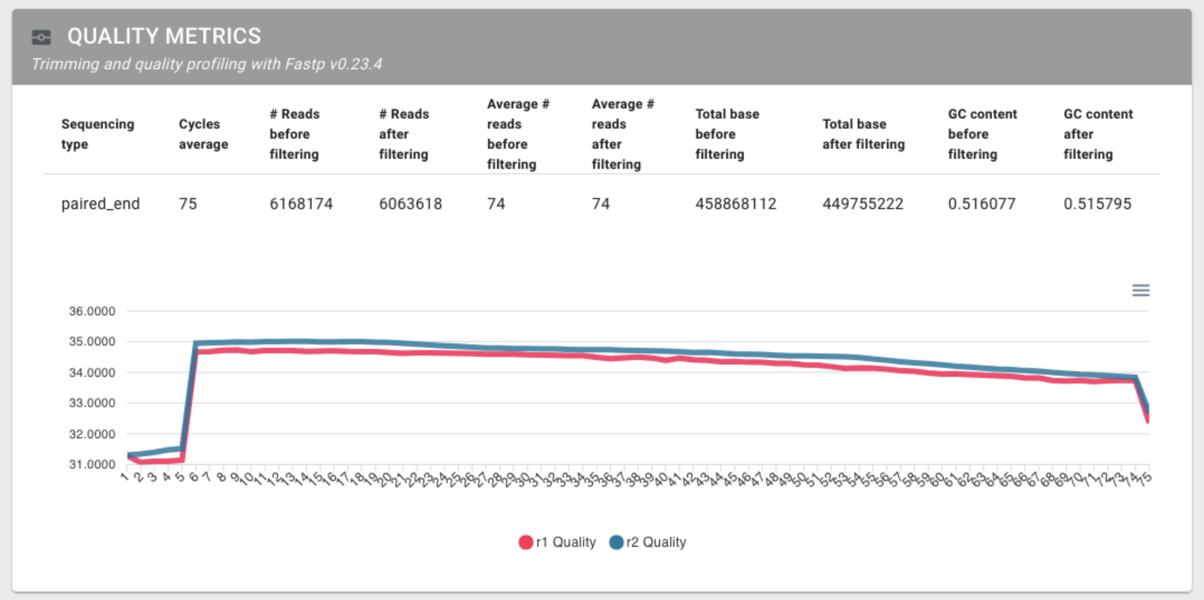
Strain typing: mlst v2.23.0

Sequence Type (ST)	12
MLST scheme	ecoli_achtman_4
MLST Species name	Escherichia/Shigella

Scheme

Gene	#Allele
adk	13
fumC	13
gyrB	9
icd	13
mdh	16
purA	10
recA	9

- **QUALITY METRICS**: Available only for genomic paired-end FASTQ template. Shows FASTQ quality control results from the Fastp tool, including quality metrics before and after trimming for R1 and R2 files:



QUALITY METRICS

Trimming and quality profiling with Fastp v0.23.4

Sequencing type	Cycles average	# Reads before filtering	# Reads after filtering	Average # reads before filtering	Average # reads after filtering	Total base before filtering	Total base after filtering	GC content before filtering	GC content after filtering
paired_end	75	6168174	6063618	74	74	458868112	449755222	0.516077	0.515795

- **QUALITY ASSEMBLY**: Shows the results of quality control of the assembled sequences with the Shovill tool.

QUALITY ASSEMBLY

Assembly with Shovill v1.1.0 + Assembly quality with Quast v5.3.0

# Contigs	Largest contig	GC (%)	N50	Mapped (%)	Properly paired (%)	Average coverage depth	# Pseudogene
134	308280	50.71	114182	99.7	98.41	84	

Contig lengths (bp) distribution

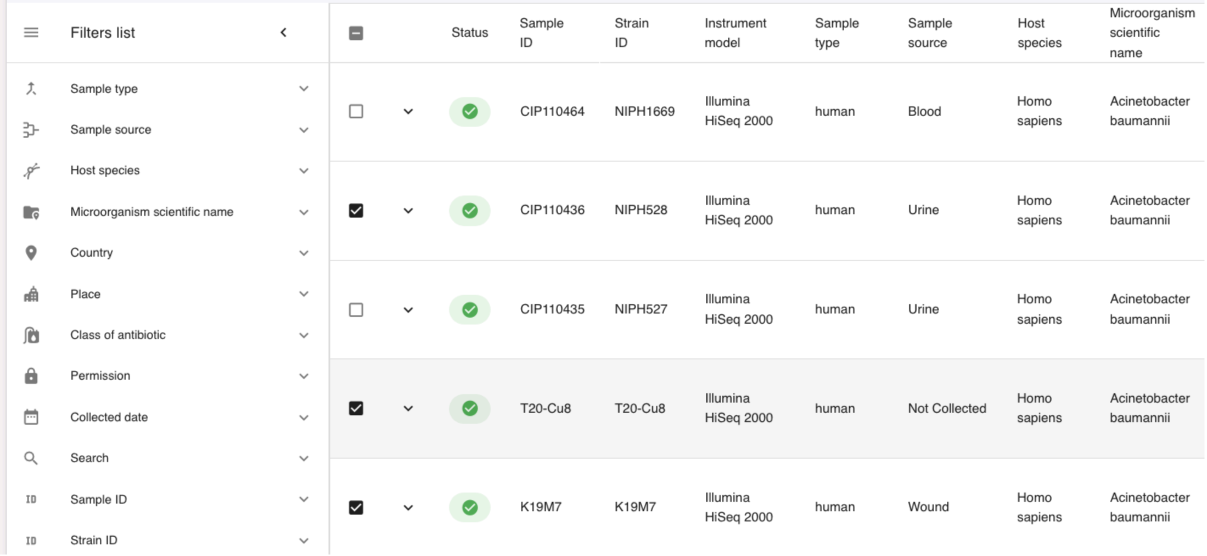
Contig mean coverages

EXPLORE RESULTS IN A PROJECT

Filter, download, or delete data

Within a project, several additional actions are available:

- Any project member can create analyses in a batch;
- Any project member can download a .xlsx results file for selected samples. As of ABRomics v1.2.1, the .xlsx contains eleven sheets:
    1. **Sheet Info**: Describes each sheet in the file.
    2. **Metadatas**: Contains the biological metadata and ABRomics analysis metadata.
    3. **MLST**: Contains the MLST results.
    4. **Taxonomy Detected**: Contains the results of the organism identification step.
    5. **Resfinder:** Contains the resistance genes results from Resfinder.
    6. **Virulence**: Contains the virulence genes results.
    7. **Plasmidfinder**: Contains the plasmid typing results from Plasmidfinder.
    8. **Functional Annotation**: Contains metrics on the functional annotation done with Bakta (Not shown on the analysis report).
    9. **Read QC**: Contains metrics on the quality control step of the raw reads.
    10. **Assembly QC**: Contains metrics on the quality control step of the assembly.
    11. **Quality Control Flags**: Contains all the quality control flags used by ABRomics for the whole workflow.
- Only the project supervisor can publish or delete samples.



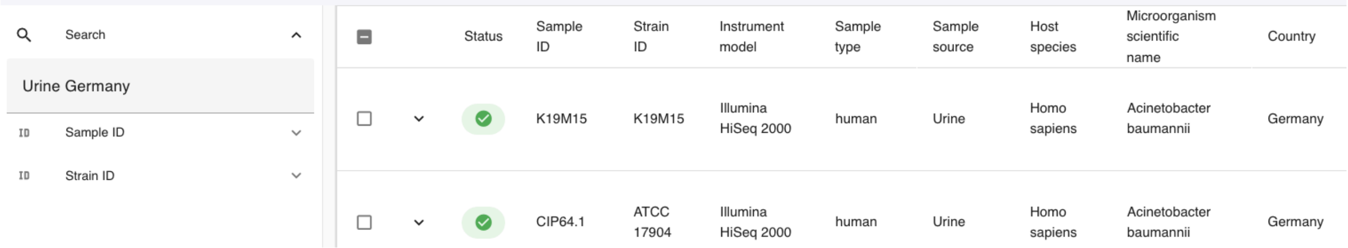
▬		Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name
☐	⌄	✓	CIP110464	NIPH1669	Illumina HiSeq 2000	human	Blood	Homo sapiens	Acinetobacter baumannii
☑	⌄	✓	CIP110436	NIPH528	Illumina HiSeq 2000	human	Urine	Homo sapiens	Acinetobacter baumannii
☐	⌄	✓	CIP110435	NIPH527	Illumina HiSeq 2000	human	Urine	Homo sapiens	Acinetobacter baumannii
☑	⌄	✓	T20-Cu8	T20-Cu8	Illumina HiSeq 2000	human	Not Collected	Homo sapiens	Acinetobacter baumannii
☑	⌄	✓	K19M7	K19M7	Illumina HiSeq 2000	human	Wound	Homo sapiens	Acinetobacter baumannii

You can select samples either one by one by clicking on the checkbox at the beginning of a row in the sample collection table, or by selecting all samples shown on the page by clicking on the checkbox at the left of the column titles.

You can filter out samples in the sample collection table by using the filter menu ("Filter list" on the left).

This can be done:

- according to sample metadata: "Sample type", "Sample source", "Host species", "Country", "Place", "Permission", "Collected date", "Sample ID", "Strain ID";
- or according to analyses results: "Microorganism scientific name"[2], MLST result "Sequence type"[3], "Class of antibiotic", "Analysis status".



Urine Germany

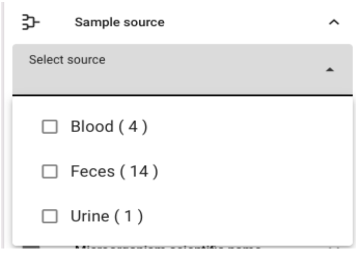
▬		Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country
☐	⌄	✓	K19M15	K19M15	Illumina HiSeq 2000	human	Urine	Homo sapiens	Acinetobacter baumannii	Germany
☐	⌄	✓	CIP64.1	ATCC 17904	Illumina HiSeq 2000	human	Urine	Homo sapiens	Acinetobacter baumannii	Germany

---

[2] The filter "Microorganism scientific name", in this case, corresponds to the name of the taxonomy detected with the highest percentage of reads.

[3] The filter "Sequence type" can only be used if a "Microorganism scientific name" is selected.

For each filter, the possible values are shown in a drop-down list. Each value is followed by the corresponding number of analyses matching the selected filter criterion.



In the case of the « **Class of antibiotic** » filter, there are 2 types of possible values in the drop-down list:

- **A single class of antibiotic** (for example: Aminoglycoside)
- **A set of multiple antibiotic classes** (for example: Aminoglycoside, Quinolone)

For example, if you want to retrieve analyses with the following results:

« Resistance genes known to target Aminoglycoside class antibiotics and Quinolone class antibiotics »

you need to filter by selecting only this single value:

« Aminoglycoside, Quinolone »

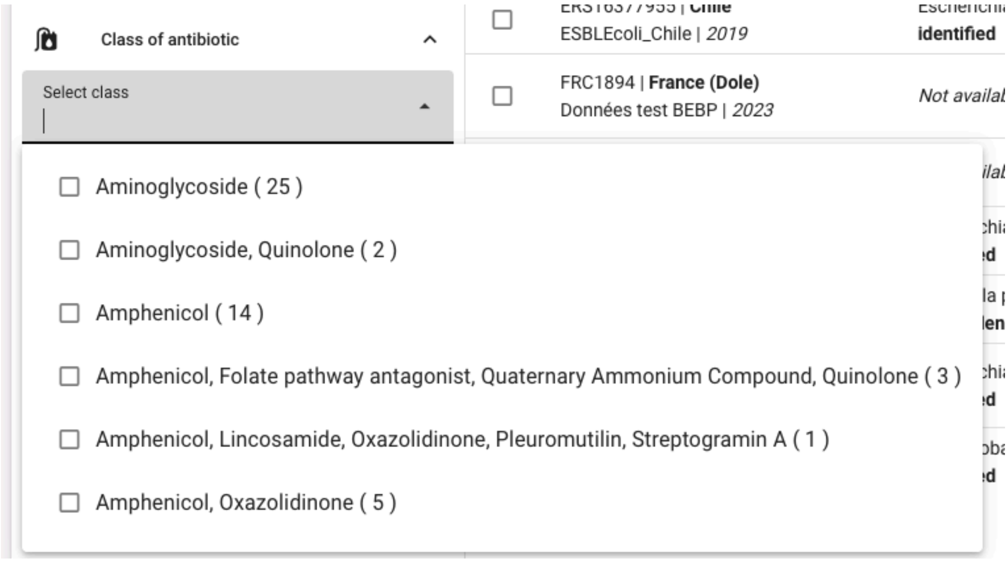
If you filter by selecting the 2 values independently (check box behind « Aminoglycoside » and check box behind « Quinolone »), this will return these results:

« Resistance genes known to target Aminoglycoside class antibiotics only »

and

« Resistance genes known to target Quinolone class antibiotics only »

To illustrate this, the following example shows that 2 results match the filter criterion « Aminoglycoside, Quinolone». These 2 results are not part of the 25 results matching the « Aminoglycoside » filter criterion. In total, the database contains 27 results with at least one resistance gene known to target Aminoglycoside class antibiotics.



Class of antibiotic

Select class

- ☐ Aminoglycoside (25)
- ☐ Aminoglycoside, Quinolone (2)
- ☐ Amphenicol (14)
- ☐ Amphenicol, Folate pathway antagonist, Quaternary Ammonium Compound, Quinolone (3)
- ☐ Amphenicol, Lincosamide, Oxazolidinone, Pleuromutilin, Streptogramin A (1)
- ☐ Amphenicol, Oxazolidinone (5)

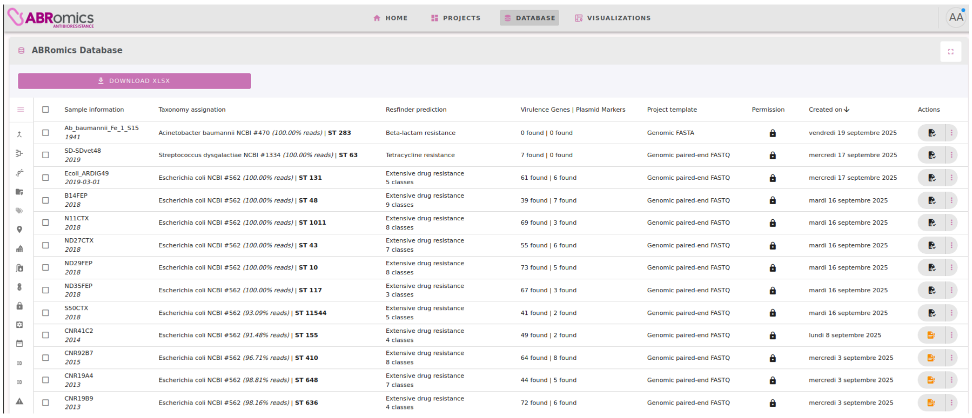
☐ ESBLEcoli_Chile | *2019* **identified**

☐ FRC1894 | **France (Dole)** Données test BEBP | *2023* *Not availal*

EXPLORE RESULTS OF THE COMMUNITY USING THE ABROMICS DATABASE

Filter, download, and visualize data

The second main page on ABRomics is “DATABASE”. Any connected ABRomics user can access this page and look up analysis results saved in the ABRomics database.



☐	Sample information	Taxonomy assignation	Resfinder prediction	Virulence Genes | Plasmid Markers	Project template	Permission	Created on ↓	Actions
☐	Ab_baumannii_Fe_1_S15 *1941*	Acinetobacter baumannii NCBI #470 *(100.00% reads)* | **ST 283**	Beta-lactam resistance	0 found | 0 found	Genomic FASTA	🔒	vendredi 19 septembre 2025	
☐	SD-SDvet48 *2019*	Streptococcus dysgalactiae NCBI #1334 *(100.00% reads)* | **ST 63**	Tetracycline resistance	7 found | 0 found	Genomic paired-end FASTQ	🔒	mercredi 17 septembre 2025	
☐	Ecoli_ARDIG49 *2019-03-01*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 131**	Extensive drug resistance 5 classes	61 found | 6 found	Genomic paired-end FASTQ	🔒	mercredi 17 septembre 2025	
☐	B14FEP *2018*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 48**	Extensive drug resistance 9 classes	39 found | 7 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	N11CTX *2018*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 1011**	Extensive drug resistance 8 classes	69 found | 3 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	ND27CTX *2018*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 43**	Extensive drug resistance 7 classes	55 found | 6 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	ND29FEP *2018*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 10**	Extensive drug resistance 8 classes	73 found | 5 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	ND35FEP *2018*	Escherichia coli NCBI #562 *(100.00% reads)* | **ST 117**	Extensive drug resistance 3 classes	67 found | 3 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	S50CTX *2018*	Escherichia coli NCBI #562 *(93.09% reads)* | **ST 11544**	Extensive drug resistance 5 classes	41 found | 2 found	Genomic paired-end FASTQ	🔒	mardi 16 septembre 2025	
☐	CNR41C2 *2014*	Escherichia coli NCBI #562 *(91.48% reads)* | **ST 155**	Extensive drug resistance 4 classes	49 found | 2 found	Genomic paired-end FASTQ	🔒	lundi 8 septembre 2025	
☐	CNR92B7 *2015*	Escherichia coli NCBI #562 *(96.71% reads)* | **ST 410**	Extensive drug resistance 8 classes	64 found | 8 found	Genomic paired-end FASTQ	🔒	mercredi 3 septembre 2025	
☐	CNR19A4 *2013*	Escherichia coli NCBI #562 *(98.81% reads)* | **ST 648**	Extensive drug resistance 7 classes	44 found | 5 found	Genomic paired-end FASTQ	🔒	mercredi 3 septembre 2025	
☐	CNR19B9 *2013*	Escherichia coli NCBI #562 *(98.16% reads)* | **ST 636**	Extensive drug resistance 4 classes	72 found | 6 found	Genomic paired-end FASTQ	🔒	mercredi 3 septembre 2025	

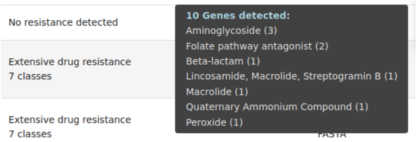
There are currently two different ways of seeing results on ABRomics, either a “List” view on the current “DATABASE” page or a “Map” view accessible on the “VISUALIZATIONS” page. The extend button “[ ]” at the very far right enables you to maximize and minimize the results table.

Here, each result (row in the table) is described with 6 columns:

1 – **Sample information**: information about the sample on which the analysis was made (Sample ID, date of collection (YYYY, YYYY-MM, or YYYY-MM-DD));

2 – **Taxonomy assignation**: information about the taxonomy detected (scientific name of the microorganism found after analyzing the sample, corresponding NCBI ID, percentage of reads, MLST sequence type if any);

3 – **Resfinder prediction**: information about the level of resistance detected (“No resistance detected” if none were detected. If a mono-resistance was predicted, “‘Antibiotic class name’ resistance” will be displayed. If 2 resistances were predicted, then “Multi-drug resistance predicted” will be displayed, and if more than 2 resistances were predicted, then “Extensive drug resistance” will be displayed). Hovering above the displayed text will show a tooltip detailing the resistance genes found;

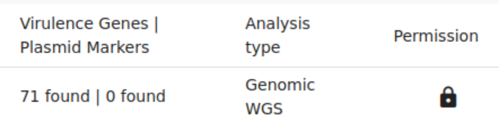


No resistance detected

Extensive drug resistance
7 classes

Extensive drug resistance
7 classes

10 Genes detected:
Aminoglycoside (3)
Folate pathway antagonist (2)
Beta-lactam (1)
Lincosamide, Macrolide, Streptogramin B (1)
Macrolide (1)
Quaternary Ammonium Compound (1)
Peroxide (1)



Virulence Genes | Plasmid Markers	Analysis type	Permission
71 found | 0 found	Genomic WGS	🔒

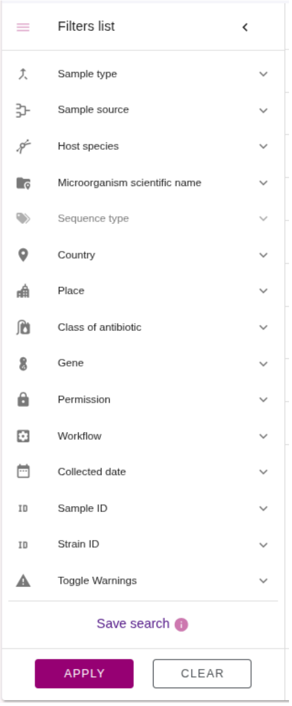
4 – **Virulence genes | Plasmid markers**: information about the number of virulence genes detected and the number of plasmid markers found. Hovering above the displayed text on the left side of the vertical bar " | " will show a tooltip detailing the virulence genes found. Similarly, hovering above the displayed text on the right side of the vertical bar " | " will show a tooltip detailing the plasmid markers found;

5 – **Analysis type**: indicates the type of template associated with the project from which the sample was uploaded;

6 – **Permission**: indicates whether the results of the analysis were made public or not. This status impacts the level of information shown in the report.

Specific actions can be done with the "**Actions**" button at the right end of the row. These actions will be further detailed in the next subsection "Access reports, join a project, add a public sample to a project".

Similarly to the detailed project view, you can use a filter menu to filter according to the specific results you are searching for:



- You can filter out according to sample metadata: "Sample type", "Sample source", "Host species", "Country", "Place", "Collected date", "Sample ID", "Strain ID";
- Or according to analyses results: "Microorganism scientific name"[4],, MLST result "Sequence type"[5], "Class of antibiotic", "Gene" (i.e, resistance genes found), "Workflow" used or "Permission".

You can save your query as an alert by clicking on "Save search" **after** applying filters. These alerts are displayed on your Home page to inform you of new analyses added to the community database.

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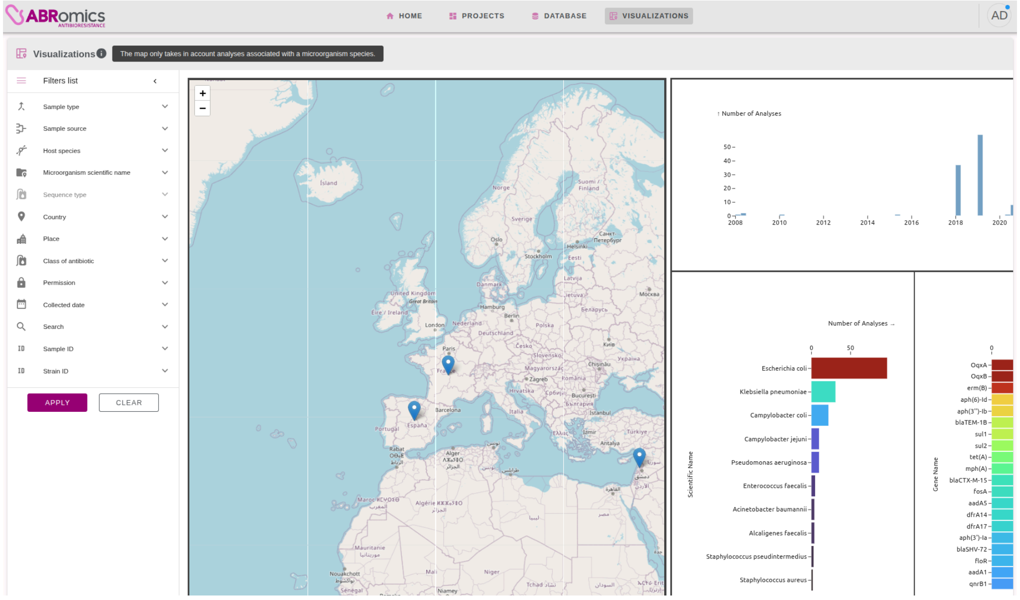
[4] The filter "Microorganism scientific name", in this case, corresponds to the name of the taxonomy chosen by the user who completed metadata information and uploaded the sample.

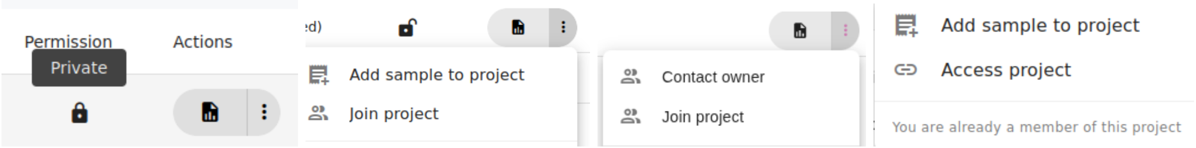
[5] The filter "Sequence type" can only be used if a "Microorganism scientific name" is selected.



The map only takes in account analyses associated with a microorganism species.

The “map” view in “VISUALIZATIONS”, the third main page of ABRomics, shows the locations of samples according to their “country” metadata. Hovering over a country will highlight the corresponding number of samples and the three most represented antibiotic classes in the detected AMR genes of these samples based on ABRomics analyses. You can filter values on the map either with the filter menu or by dragging your mouse across the statistical graphics.

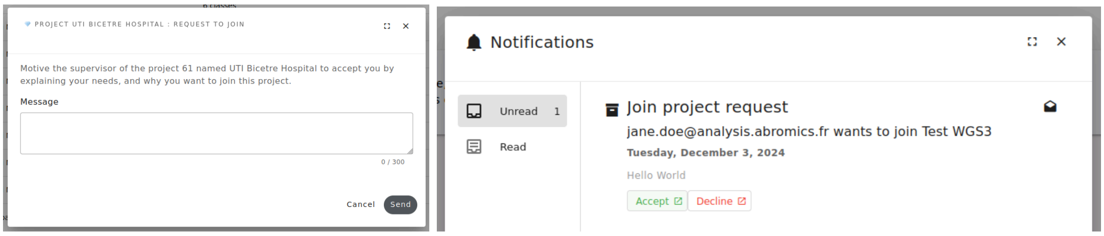
Access reports, contact owner / request to join a project and add a public sample to a project



You are already a member of this project

Any logged-in user can access a "light" version of an analysis report (for privacy, these light reports do not show any information about the provider of the sample). If a sample was made public by the supervisor of the project the sample was imported in, then other users can access the "full" report of the analysis. Section "View a report" details the information given in a report.

You can also use the ABRomics analyses "Database" page to request access to a project. By clicking on the kebab menu icon (3 dots) in the "Actions" column and then clicking on "Join project", a pop-up enables you to write a message to the project supervisor. The supervisor will then receive a notification and can choose to either accept the request and add you as a coworker in the project or refuse. If you are already part of the project, you will see an "Access project" button instead, and if you have already sent a request, you will not be able to spam messages.



PROJECT UTI BICETRE HOSPITAL : REQUEST TO JOIN

Motive the supervisor of the project 61 named UTI Bicetre Hospital to accept you by explaining your needs, and why you want to join this project.

Message:

Join project request

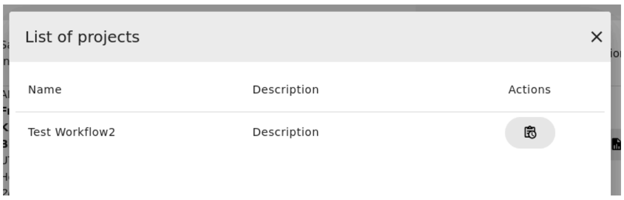
jane.doe@analysis.abromics.fr wants to join Test WGS3

Tuesday, December 3, 2024

Hello World

The first user writes a message, then the second User (project supervisor) receives a notification and chooses whether to "Accept" or "Decline" the request.

You can also send them a message without a request, and the project supervisor might contact you back by email.



List of projects

Name	Description	Actions
Test Workflow2	Description	

You can add any public sample (samples made public in ABRomics) to your own projects, as long as you have at least one project with a template that is compatible with that public sample. To do this, click "Add sample to project", then click the icon button in the "Actions" column.

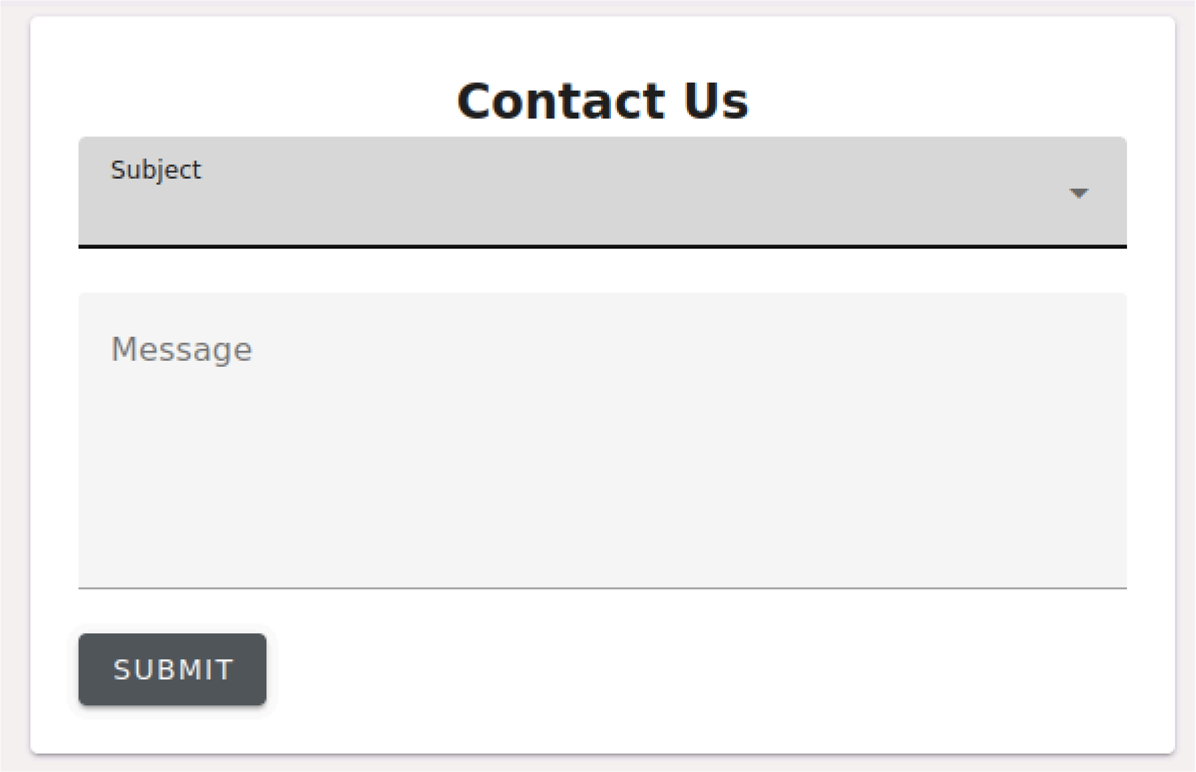
CONTACT US

As mentioned previously, if any issues arise or if you want to give us feedback, you can contact the support team at:

abromics-support@groupes.france-bioinformatique.fr.

When logged in, you can also send a message directly on the platform through the "**Contact Us**" page, available in the footer. The footer is visible on every page of ABRomics.

If you are logged out, you can access the contact page by clicking the "CONTACT" button in the navigation menu.

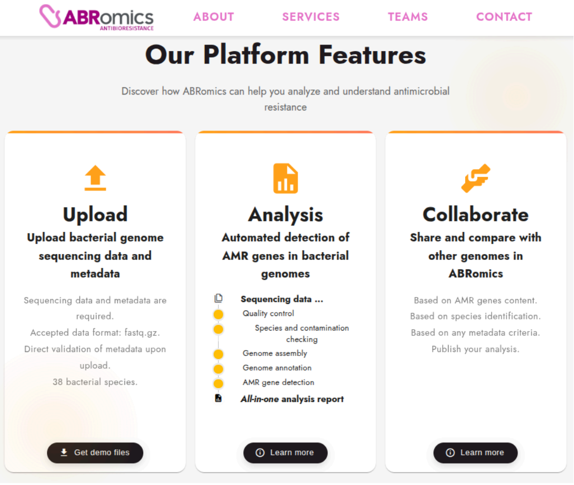
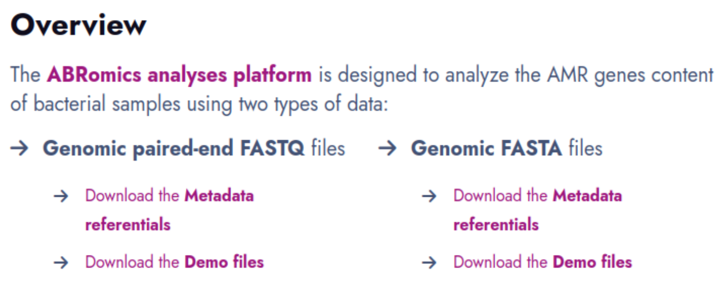
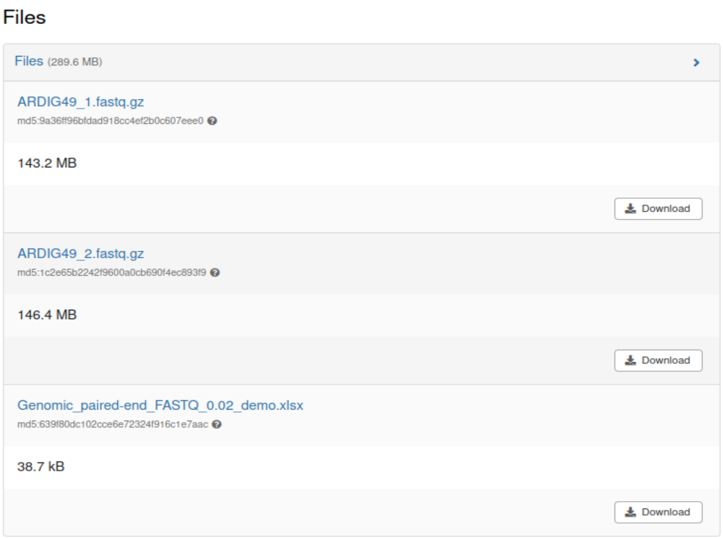


You can select a subject between four choices: "Bug", "Feature" (any feature you would like to see on ABRomics), "Account creation" (if you have any issues when creating your account) and "Other".

APPENDIX

How to use demo files

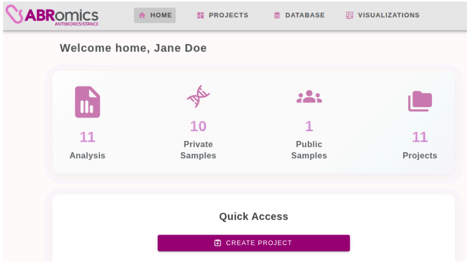
Appendix 1: Use the demo files available on Zenodo to create your first project 🥳

You can find the demo files on the ABRomics analysis homepage (https://analysis.abromics.fr/) by clicking on the **“GET THE DEMO FILES” button**.	 **Our Platform Features** Discover how ABRomics can help you analyze and understand antimicrobial resistance **Upload** **Upload bacterial genome sequencing data and metadata** Sequencing data and metadata are required. Accepted data format: fastq.gz. Direct validation of metadata upon upload. 38 bacterial species. **Analysis** **Automated detection of AMR genes in bacterial genomes** **Sequencing data ...** Quality control Species and contamination checking Genome assembly Genome annotation AMR gene detection ***All-in-one* analysis report** **Collaborate** **Share and compare with other genomes in ABRomics** Based on AMR genes content. Based on species identification. Based on any metadata criteria. Publish your analysis.
You will be redirected to https://www.abromics.fr/abromics-platform/metadata-referential/ web page, where you can find FASTQ or FASTA demo files* : Click on “**Download the Demo files**” on the left (fastQ file format)	 **Overview** The **ABRomics analyses platform** is designed to analyze the AMR genes content of bacterial samples using two types of data: → **Genomic paired-end FASTQ** files → Download the **Metadata referentials** → Download the **Demo files** → **Genomic FASTA** files → Download the **Metadata referentials** → Download the **Demo files**
You will be redirected to https://zenodo.org/records/14366711 where you can find a description of the files and the **download links under the “Files” section** of the page. ARDIG49_1.fastq.gz is the **R1 input file** and ARDIG49_2.fastq.gz is the **R2 input file**. Genomic_paired-end_FASTQ_0.02_demo.xlsx is the demo **metadata template**.	 Files Files (289.6 MB) ARDIG49_1.fastq.gz md5:9a36ff96bfdad918cc4ef2b0c607eee0 143.2 MB ARDIG49_2.fastq.gz md5:1c2e65b2242f9600a0cb690f4ec893f9 146.4 MB Genomic_paired-end_FASTQ_0.02_demo.xlsx md5:639f80dc102cce6e72324f916c1e7aac 38.7 kB

Follow the steps described in section **"PROJECTS & PROJECT MANAGEMENT"** to create your demo project*

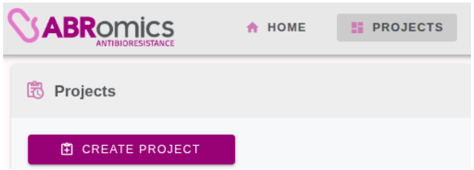
**Select a template associated with the type of demo files (ex: a WGS template for fastq.gz demo files).*

1



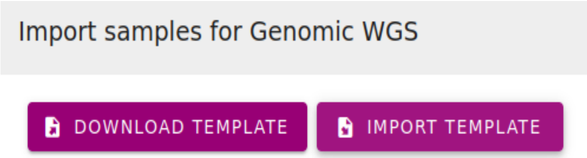
OR

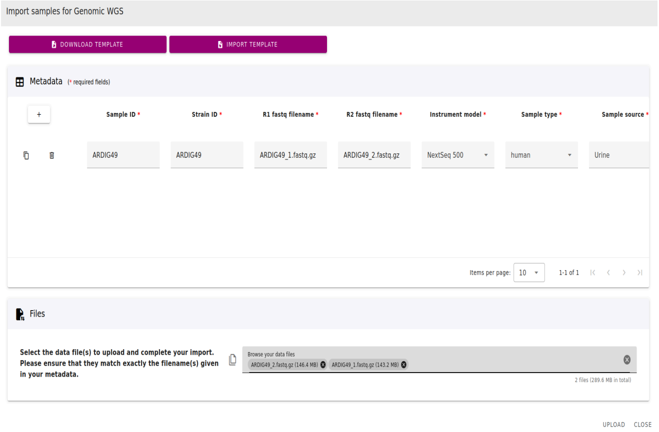
2



Follow the steps described in section **"Upload a sample & metadata validation"** and upload the demo sample by importing the demo metadata template and the demo raw data files.

If everything went smoothly, you should have something similar to the screenshot on the right. After clicking on "Upload", a pop-up should appear with a summary of the data uploaded to the platform.





Metadata (* required fields)

Sample ID *	Strain ID *	R1 fastq filename *	R2 fastq filename *	Instrument model *	Sample type *	Sample source *
ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz	NextSeq 500	human	Urine

Items per page: 10 1-1 of 1

Files

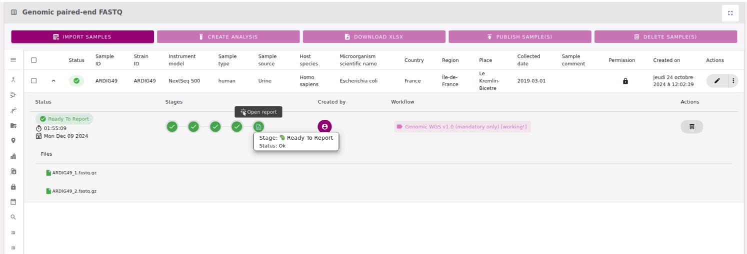
Select the data file(s) to upload and complete your import. Please ensure that they match exactly the filename(s) given in your metadata.

Browse your data files: ARDIG49_2.fastq.gz (146.4 MB) ARDIG49_1.fastq.gz (143.2 MB)

2 files (289.6 MB in total)

fig.: Example with FASTQ demo files.

The default analysis starts automatically and after about 30' you can access the results of the analysis by clicking on "Open report" in the report bullet.
Tada 🎉



Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country	Region	Place	Collected date	Sample comment	Permission	Created on	Actions
✓	ARDIG49	ARDIG49	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-France	Le Kremlin-Bicetre	2019-03-01		🔒	jeudi 24 octobre 2024 à 12:02:39	

Status	Stages	Created by	Workflow	Actions
Ready To Report 01:55:09 Mon Dec 09 2024	✓ ✓ ✓ ✓		Genomic WGS v1.0 (mandatory only) [working!]	

Stage: Ready To Report
Status: Ok

Files
ARDIG49_1.fastq.gz
ARDIG49_2.fastq.gz

Table of “Roles in a project & permissions”

Appendix 2: Possible actions of the ABRomics analyses platform depending on the user’s role in a project

	Supervisor	Coworker
Add user	x (add a coworker)	
Remove user	x	
Change user role	x	
Edit project metadata	x	
Delete project	x	
Add sample (upload input files)	x	
Edit sample metadata	x	
Create new analysis	x	x
Retry analysis in error	x	x
Delete analysis	x	x (only his/her own analysis)
Download input files	x	
View report	x	x
Download result files	x	x
Publish sample	x	

Table of “Templates & metadata”

Appendix 3: Metadata referential of the ABRomics « Genomic paired-end FASTQ » template (short-reads paired-end FASTQ files as inputs)

Field name	Description/guidelines for ABRomics users	ABRomics status	Validation	Accepted values
Sample ID	ID of the sample	mandatory	Sample ID must be unique in the whole document	Free text
Strain ID	Name of the isolated strain	mandatory	Strain ID must be unique in the whole document	Free text
R1 fastq filename	Name of the fastq forward file	mandatory	The filename must end by ".fastq.gz"	Free text
R2 fastq filename	Name of the fastq reverse file	mandatory	The filename must end by ".fastq.gz"	Free text
Instrument model	The sequencing instrument model used in the experiment	mandatory	One of the accepted values	See "Fields values" (*)
Sample type	Indicate if the sample is collected on human, on animal or in an environment	mandatory	One of the accepted values	See "Fields values" (*)
Sample source	Site of isolation of the sample	mandatory	One of the accepted values	See "Fields values" (*)
Host species	Species of the host	mandatory	One of the accepted values	See "Fields values" (*)
Microorganism scientific name	Scientific name of the isolated microorganism	mandatory	One of the accepted values	See "Fields values" (*)
Country	Name of the country in which the sample has been collected	mandatory	Country english full name	See "Fields values" (*)
Region	Region where the sample has been collected	optional	**These 2 fields cannot be completed with the excel template. You first need to upload the excel template with the "IMPORT TEMPLATE" button first. Then select in the drop-down list the "Region" first and finally the "Place".**	
Place	Place where the sample has been collected	optional		
Collected date	The date of sampling	mandatory	Must be a valid full date. For example: 07/10/2024	Must be a valid full date
Travel countries	Countries where the host traveled to in the last 3 months prior to the sampling	optional	Country english full name. If multiple countries, separate each by comma	See "Fields values" (*)
Accession number	Accession numbers associated with the sample	optional	Multiple values should be split by ';'	Free text
Sample comment	Any comments on the sample.	optional	Free text	Free text

* Fields values are listed here: https://www.abromics.fr/abromics-platform/metadata-referential/

Appendix 4: Metadata referential of the ABRomics « Genomic FASTA » template (FASTA files as inputs)

Field name	Description/guidelines for ABRomics users	ABRomics status	Validation	Accepted values
Sample ID	ID of the sample	**mandatory**	Sample ID must be unique in the whole document	Free text
Strain ID	Name of the isolated strain	**mandatory**	Strain ID must be unique in the whole document	Free text
Fasta filename	Name of the fasta file	**mandatory**	The filename must end by ".fasta"	Free text
Instrument model	The sequencing instrument model used in the experiment	optional	One of the accepted values	See "Fields values" (*)
Assembly method	Method used to assembly raw reads to a final fasta file	optional	Free text	Free text
Sample type	Indicate if the sample is collected on human, on animal or in an environment	**mandatory**	One of the accepted values	See "Fields values" (*)
Sample source	Site of isolation of the sample	**mandatory**	One of the accepted values	See "Fields values" (*)
Host species	Species of the host	**mandatory**	One of the accepted values	See "Fields values" (*)
Microorganism scientific name	Scientific name of the isolated microorganism	**mandatory**	One of the accepted values	See "Fields values" (*)
Country	Name of the country in which the sample has been collected	**mandatory**	Country english full name	See "Fields values" (*)
Region	Region where the sample has been collected	optional	**These 2 fields cannot be completed with the excel template. You first need to upload the excel template with the "IMPORT TEMPLATE" button first. Then select in the drop-down list the "Region" first and finally the "Place".**	
Place	Place where the sample has been collected	optional		
Collected date	The date of sampling	**mandatory**	Must be a valid full date. For example: 07/10/2024	Must be a valid full date
Travel countries	Countries where the host travelled to in the last 3 months prior to the sampling	optional	Country english full name. If multiple countries, separate each by comma	See "Fields values" (*)
Accession number	Accession numbers associated with the sample	optional	Multiple values should be split by ';'	Free text
Sample comment	Any comments on the sample.	optional	Free text	Free text

* Fields values are listed here: https://www.abromics.fr/abromics-platform/metadata-referential/