ABRomics
ANTIBIORESISTANCE

ABRomics analyses platform

A *One Health* Antimicrobial Resistance Analysis Service

User Manual (UM)

10/12/2024

Version 1.0

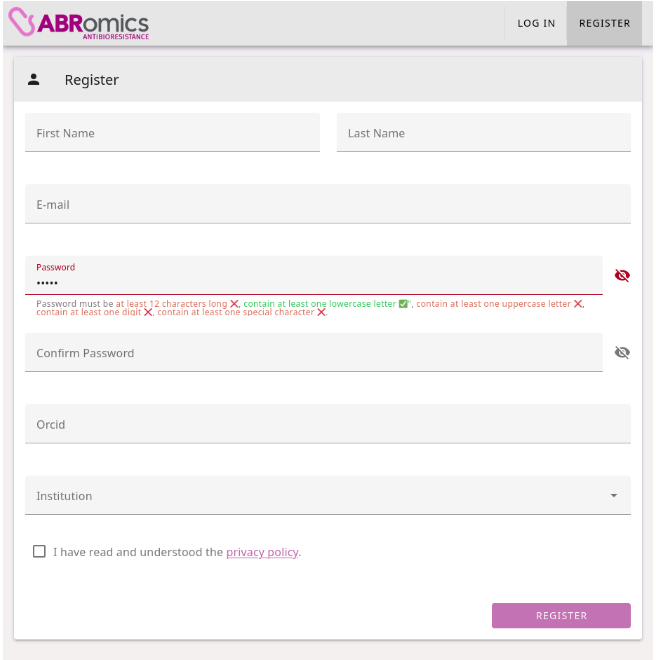
Table of Content

VERSION HISTORY

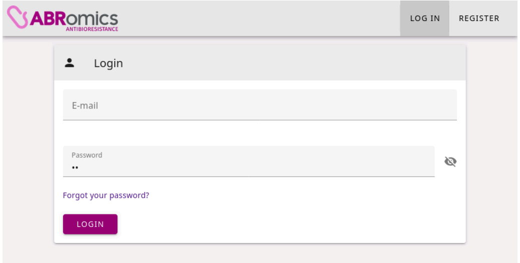
VERSION	UPDATES	DATE
1.0	Document creation	10/12/2024

REGISTRATION & ACCOUNT MANAGEMENT

Register and login



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 ✗.



To use the platform, you have to register and create an account. Click on “Register” on the upper right corner of the page, complete the form (First Name, Last Name, E-mail address*, Password**, Password confirmation, ORCID ID, Institution), and accept the privacy policy and user chart.

Only when all required fields are completed and the checkbox checked you will be able to click on the “Register” button.

You will then receive an account confirmation email and you need to click on the link in the email to activate your account.

*The email address has to be institutional and part of ABRomics’ whitelist.

**The password has to be at least 12 characters long and follow ISO 27001 norms and CNIL recommendations.

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

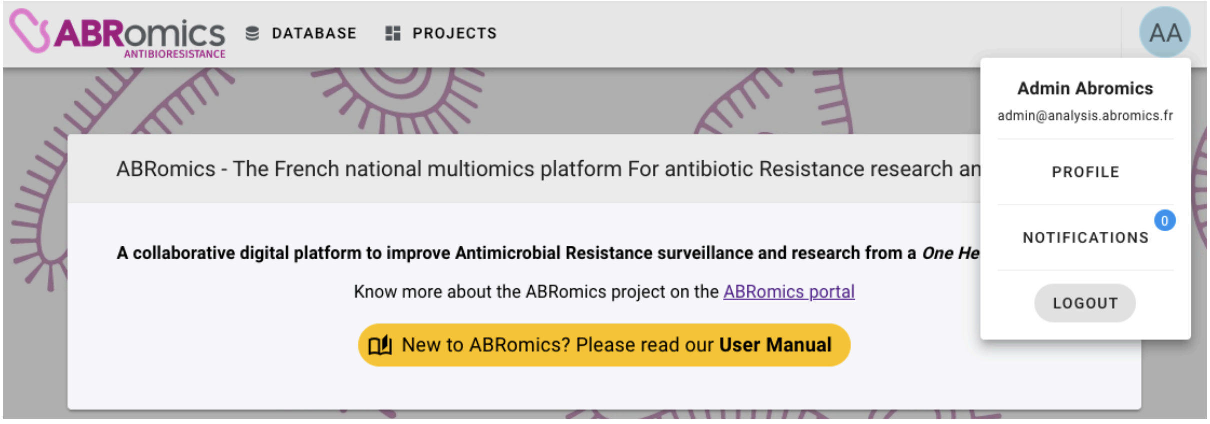
The “Login” page asks you for an email address and password.

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 on the platform, you will be redirected to the ABRomics analyses 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.

User profile



ABRomics - The French national multiomics platform For antibiotic Resistance research an

A collaborative digital platform to improve Antimicrobial Resistance surveillance and research from a *One He*

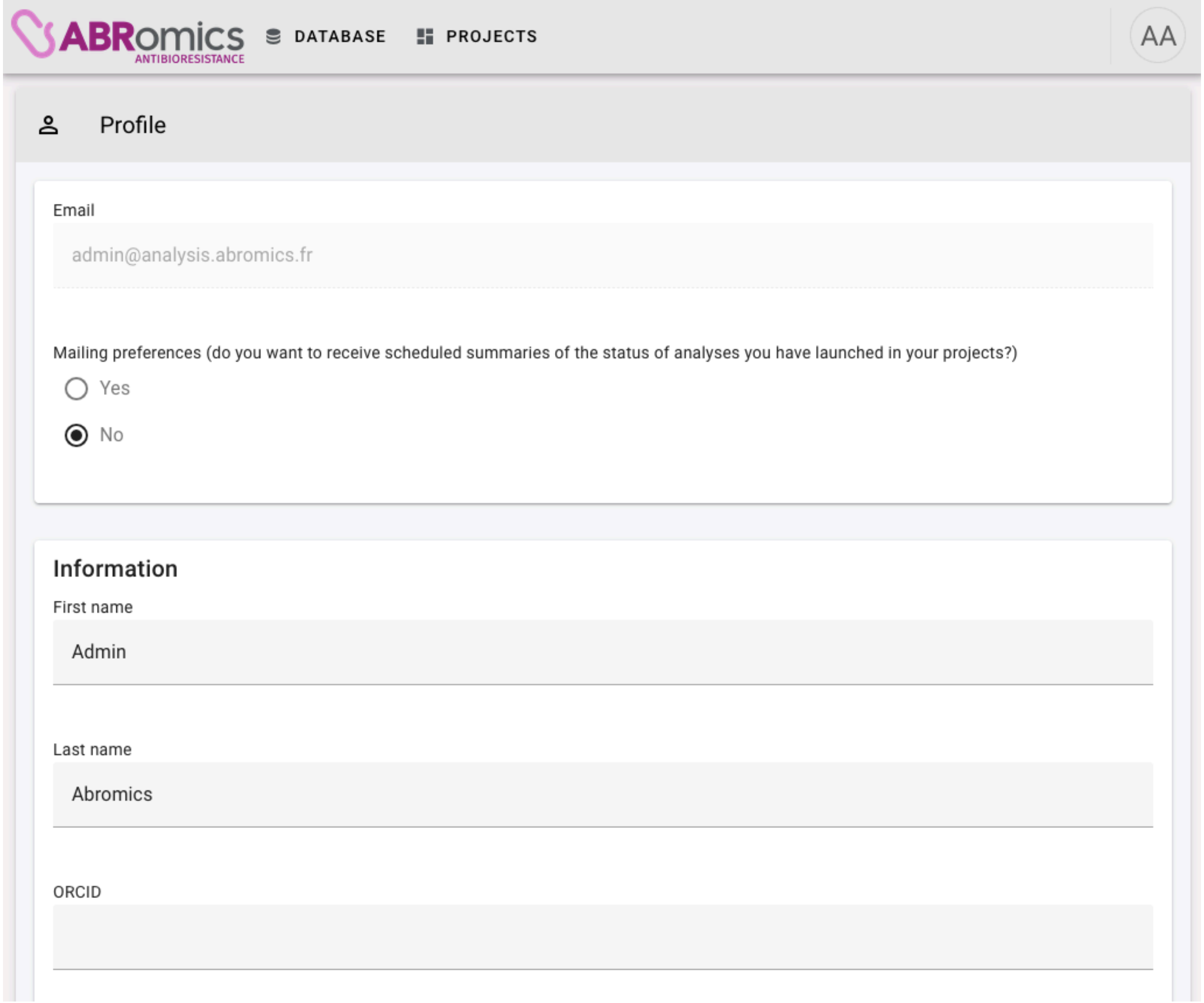
Know more about the ABRomics project on the ABRomics portal

New to ABRomics? Please read our **User Manual**

When connected, you can log out, view your notifications, or access your profile by clicking on the thumbnail in the upper right corner of the page.

In the “Profile”, you can edit the personal information you gave on the registering form (except for your email address) and choose your mailing preferences (whether you want to receive scheduled summaries of the status of analyses you have launched in your projects, or not, and at which frequency - Daily, Weekly, or Monthly).

You can also choose to delete your account. A pop-up will appear and you must confirm your choice since this action will permanently delete all the projects you are supervising.



Email

admin@analysis.abromics.fr

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

○ Yes

● No

Information

First name

Admin

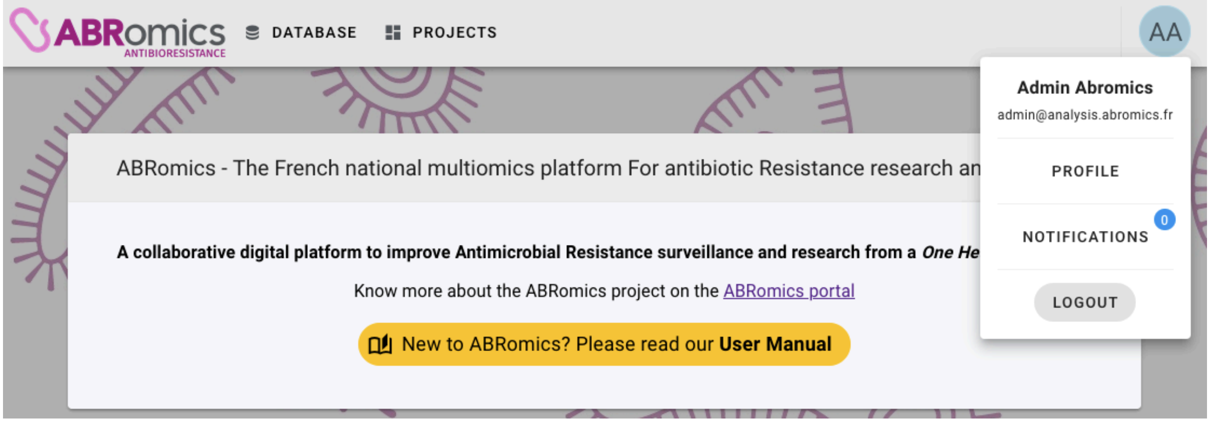
Last name

Abromics

ORCID

PROJECTS & PROJECT MANAGEMENT

The first main page on ABRomics is "Projects". You can access your projects by clicking on the "Projects" button on the navigation menu. On the "Projects" page, you can create a project ("Create Project" button) and see a list of projects you have either created or were added to.



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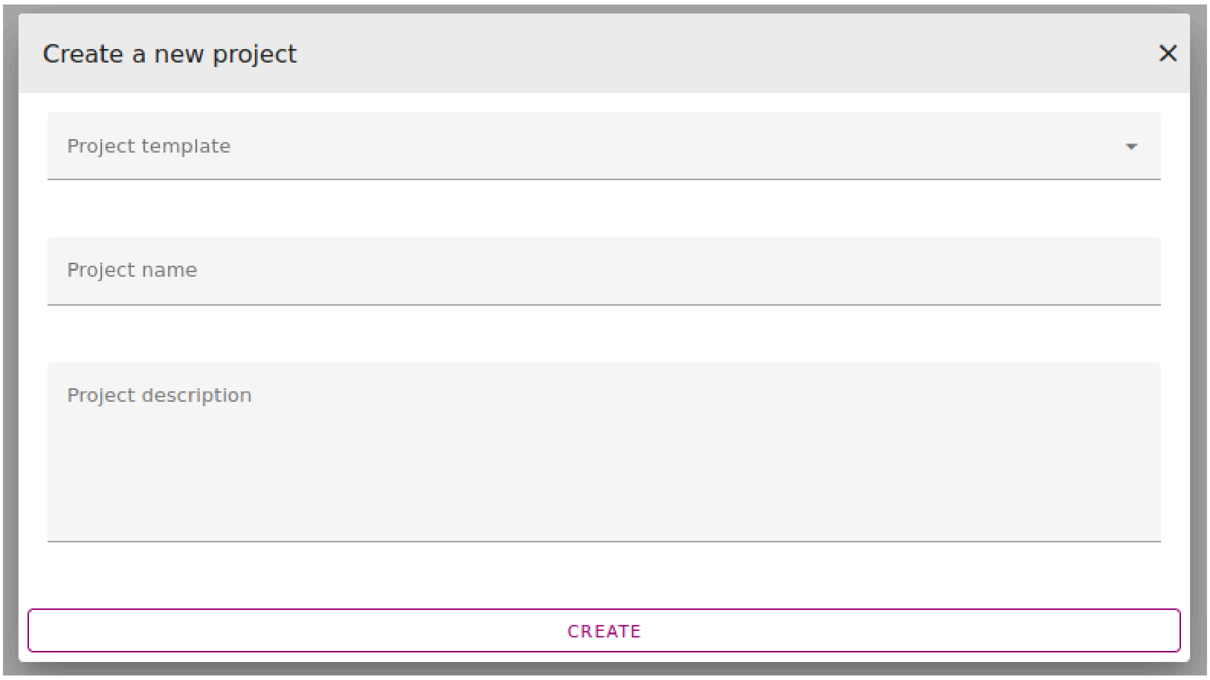


To create a project, you must choose between a selection of templates, choose a project name, and add a short description to it.

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

1. The type of metadata that will be attached to input files, thus shaping the data structure and organization.

2. The type of analysis workflows that can be performed, along with the corresponding results generated.

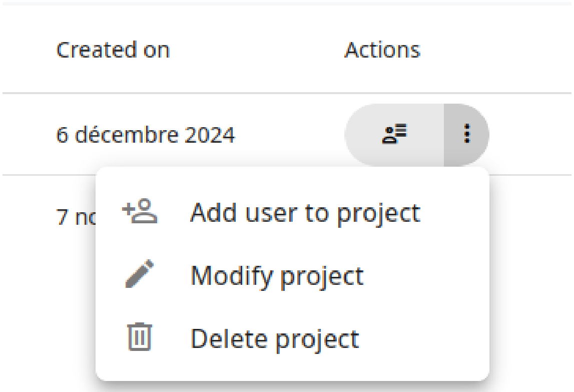
In essence, a template determines the type of results collection table associated with a project, influencing both the inputs (metadata, file type) and outputs (analysis results). It establishes the framework for managing input data and the range of analytical processes available in the project.

ABRomics V1.0 enables the analysis of two types of genomic data:

- Sequencing data
- Assembly data

The expected inputs and which template to choose to enable the analysis are described in this table

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



After creating a project, you are now the supervisor of the project and you may add other users* to the project (the supervisor needs to know the coworkers' ABRomics account email), modify the name, or the description of the project, or delete** the project. Deleting a project will delete all private samples and analyses run in the sample collection of the project.

*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.

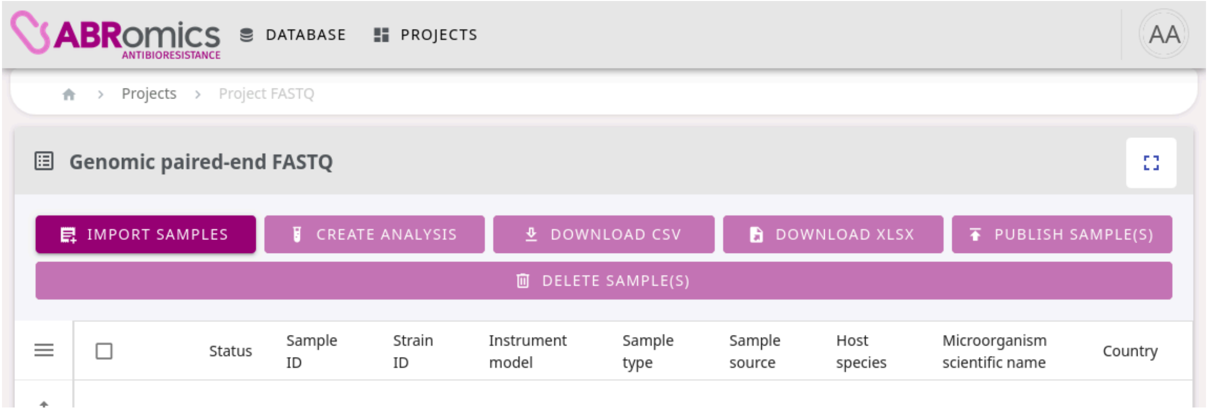
You can see the details of a project by clicking on the new entry that was added on the “Projects” page and you can start uploading samples in your project.

An important notice for v1.0 is that the supervisor of the project cannot delete a project that contains public samples/analyses. However, these public samples can still be deleted if the supervisor chooses to delete their account. In a future version of the platform the samples and analyses made public will stay on the platform. The concept of permission will be further explained in **“Run an analysis” and **“Access reports, join a project, add a public sample to a project”**.

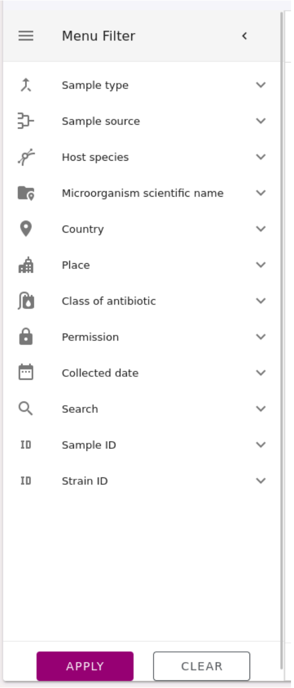
GENOMIC WORKFLOWS ANALYSES

Upload a sample & metadata validation

You can manage the data and results of a given project. For this, the page is split into three sections:



1 - ***Project actions buttons***: Directly below the template name of the project, these 6 action buttons can be used to manage batches of samples in the project.

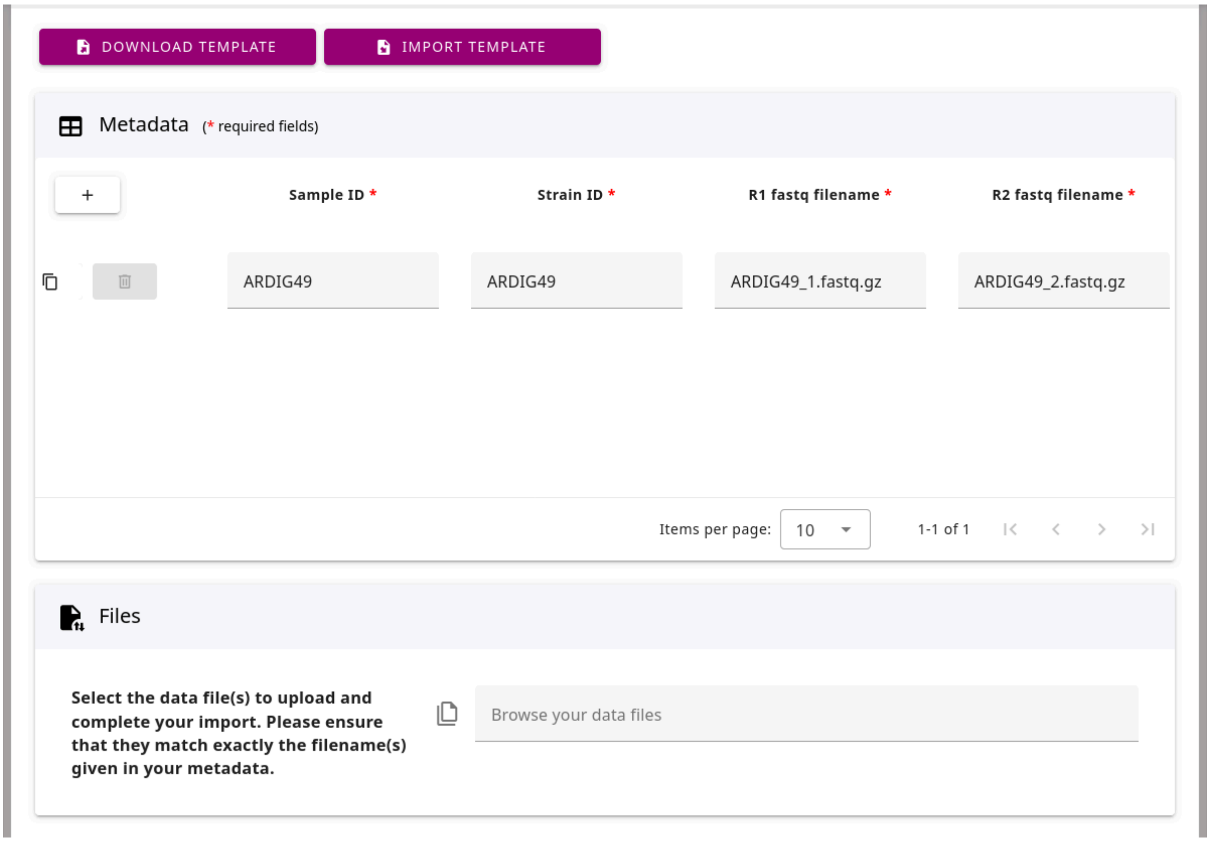


2 - ***Collection of samples table***: Then, below the action buttons, the list of all samples in the project can be found. Each sample (row in the table) is described with 15 metadata columns (“Status”, “Sample ID”, “Strain ID”, “Instrument model”, “Sample type”, “Sample source”, “Host species”, “Microorganism scientific name”, “Country”, “Region”, “Place”, “Collected date”, “Sample comment”, “Permission”, “Created on”).

This list can vary with the type of template linked to the project. Specific actions for a given sample can be done with 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.

To add a sample to a project, you must be the project's supervisor (i.e., creator) and click on the “Import Samples” button to display a pop-up.



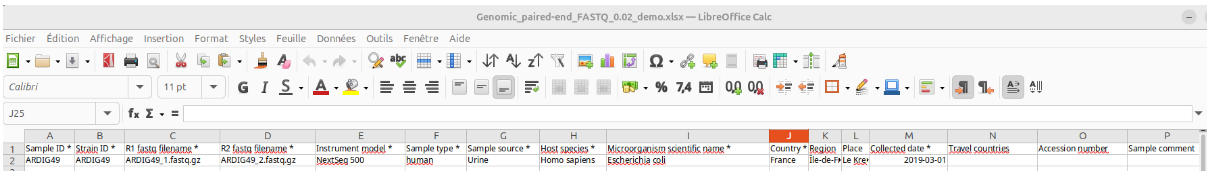
Metadata (* required fields)

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.

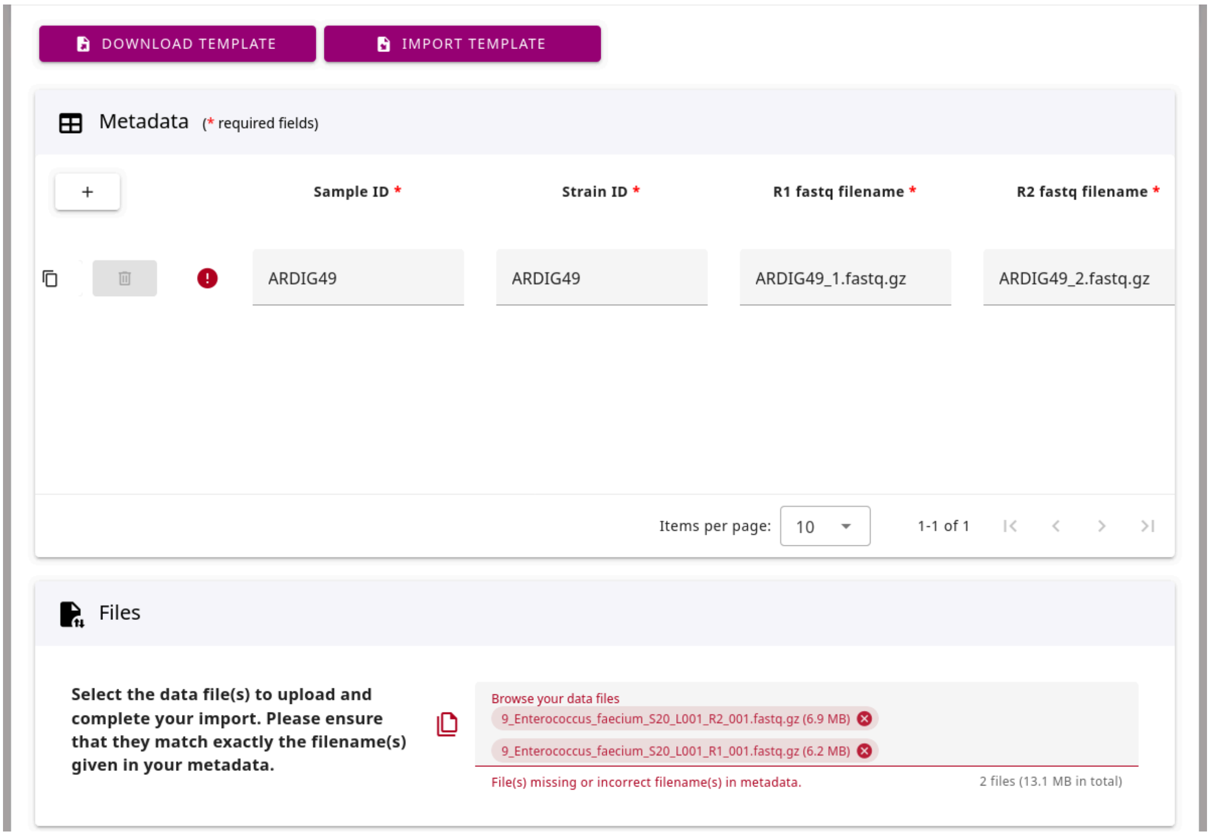
Browse your data files



	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			

You then need to complete all mandatory metadata (they are indicated with an asterisk *). You can either complete the information manually through the ABRomics interface or by **downloading** a .xlsx **template** and **importing** the completed .xlsx file. The downloaded .xlsx template, like the interface, gives clues on how to complete the information through selectable lists and tooltips. After completing all mandatory data and uploading the input file(s) you must click on the "Upload" button to proceed.

Warning: *the .xlsx file sheet name must match the current version of the template used in ABRomics, for example here "Genomic WGS 0.02". An error will be displayed if the file is an older / different version than the current one accepted on the platform. See* ***"Tables of Templates and Metadata"*** *for more details.*

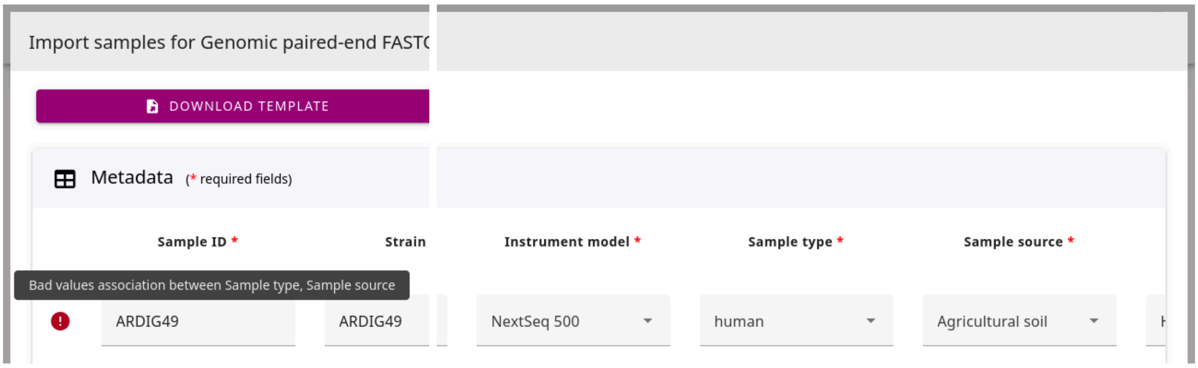


Sample ID *	Strain ID *	R1 fastq filename *	R2 fastq filename *
ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz

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_R2_001.fastq.gz (6.9 MB)
9_Enterococcus_faecium_S20_L001_R1_001.fastq.gz (6.2 MB)
File(s) missing or incorrect filename(s) in metadata.
2 files (13.1 MB in total)

It is important to note that the file names must be in accordance with the uploaded file names.

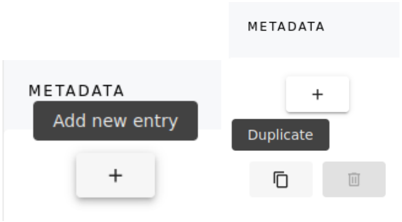


Bad values association between Sample type, Sample source

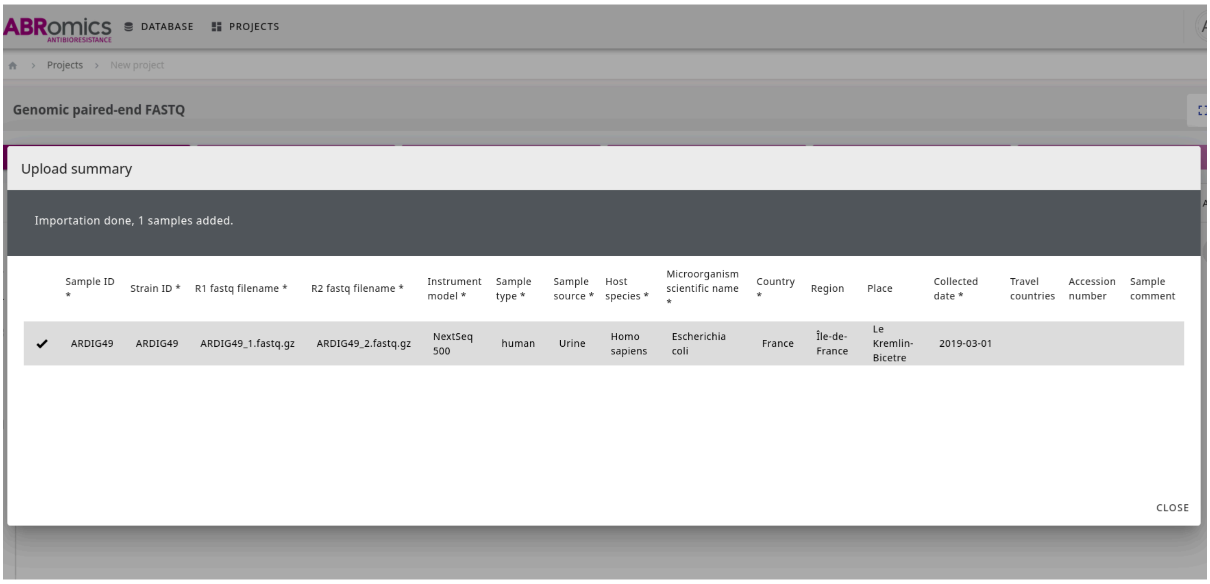
Sample ID *	Strain	Instrument model *	Sample type *	Sample source *
ARDIG49	ARDIG49	NextSeq 500	human	Agricultural soil

If an error was made during the completion of metadata, information will be given to you to help correct it. In this example, there is a wrong value association between the sample type “human” and the sample source “Agricultural soil”.

You can duplicate sample rows or add new ones in the interface with the following buttons:



You can also complete multiple rows on the .xlsx sheet before import.



Upload summary

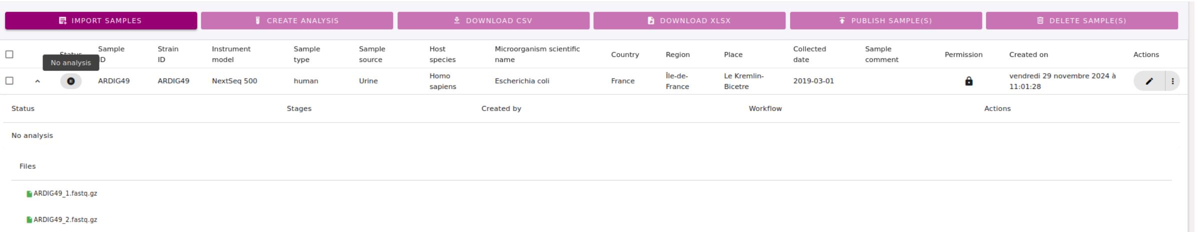
Importation done, 1 samples added.

	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
✓	ARDIG49	ARDIG49	ARDIG49_1.fastq.gz	ARDIG49_2.fastq.gz	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-France	Le Kremlin-Bicetre	2019-03-01			

If every row is completed correctly, a summarizing pop-up will show up as well as an alert informing you to stay on the current page and wait until the server processes the input files. After adding a sample, the supervisor can edit it or delete it at any time by using the action buttons under the right-end column “Actions”.

Run an analysis

After uploading the sample, the default analysis will start automatically. This step can take a few seconds to start.



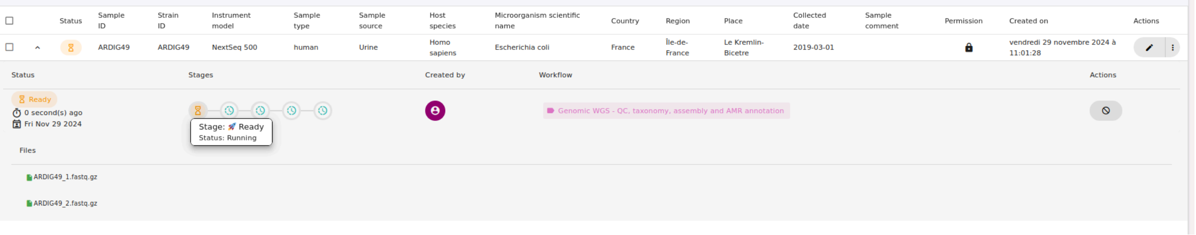
☐		Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country	Region	Place	Collected date	Sample comment	Permission	Created on	Actions
☐	^		ARDIG49	ARDIG49	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-France	Le Kremlin-Bicetre	2019-03-01			vendredi 29 novembre 2024 à 11:01:28	

Status	Stages	Created by	Workflow	Actions
No analysis				

Files

ARDIG49_1.fastq.gz

ARDIG49_2.fastq.gz



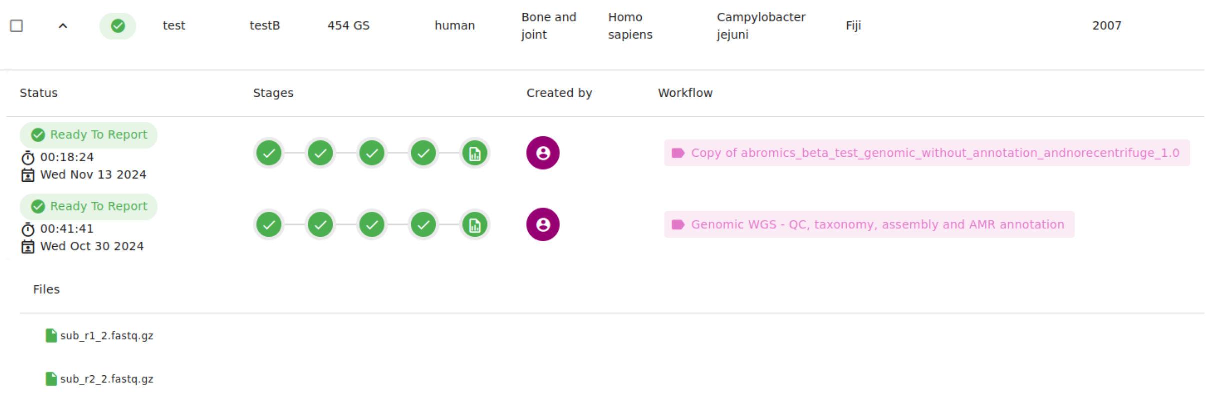
☐		Status	Sample ID	Strain ID	Instrument model	Sample type	Sample source	Host species	Microorganism scientific name	Country	Region	Place	Collected date	Sample comment	Permission	Created on	Actions
☐	^		ARDIG49	ARDIG49	NextSeq 500	human	Urine	Homo sapiens	Escherichia coli	France	Île-de-France	Le Kremlin-Bicetre	2019-03-01			vendredi 29 novembre 2024 à 11:01:28	

Status	Stages	Created by	Workflow	Actions
Ready 0 second(s) ago Fri Nov 29 2024			Genomic WGS - QC, taxonomy, assembly and AMR annotation	

Files

ARDIG49_1.fastq.gz

ARDIG49_2.fastq.gz



☐	^	✓	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

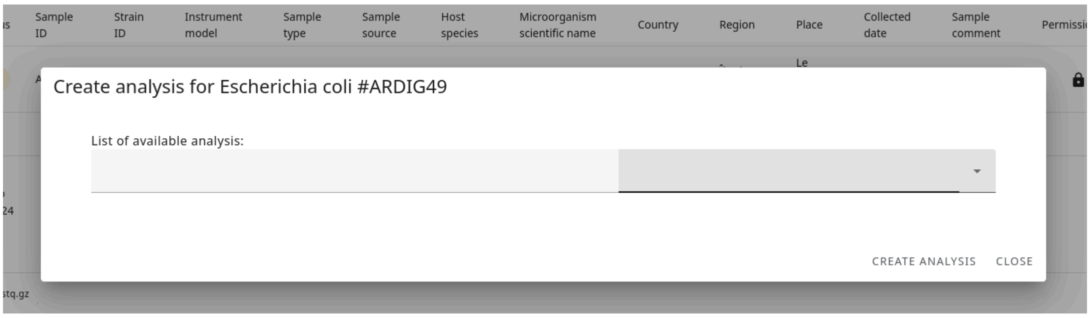
sub_r1_2.fastq.gz

sub_r2_2.fastq.gz

Multiple analyses can be run on a sample. However, duplicate analyses are not allowed on the platform. If the user wishes to re-run a specific analysis, the old results will be deleted.

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

To do so, you must select one (or multiple) sample(s) by clicking on the checkbox(es) and then click on the “Create Analysis” action button. Then choose one type of analysis given in the selection field and finally click on “Create Analysis” in the pop-up.


Create analysis for Escherichia coli #ARDIG49

List of available analysis:

Project members can follow the progress of an analysis. Information is displayed for each analysis:

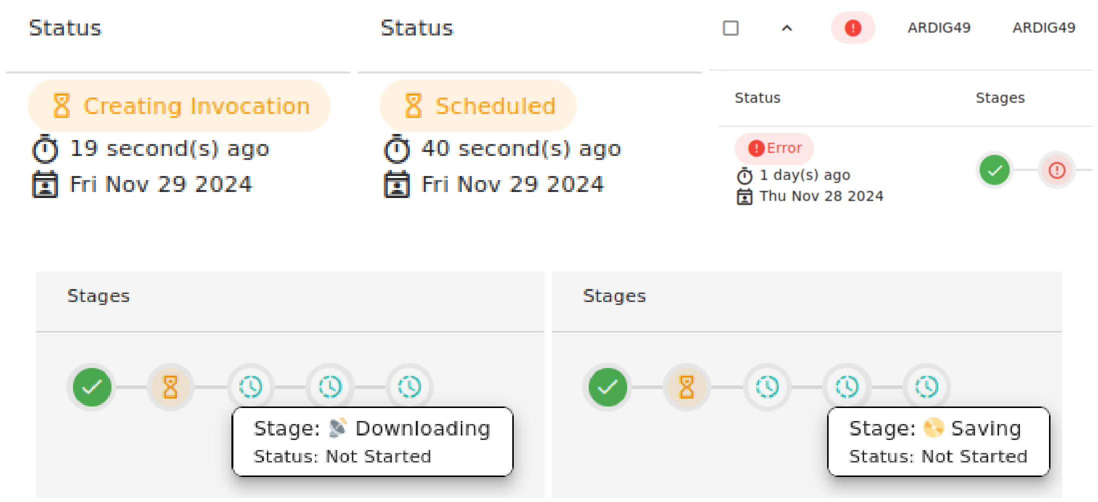
- ***Stages***: The global state of the analysis. A successful analysis will go through these 5 stages in the following order: **Ready**, **Scheduled**, **Downloading**, **Saving**, and **Ready to report**. If the analysis fails the displayed stage will be **Error.**
- ***Status***: The precise state of the analysis in the current stage. The list of statuses for each stage is described in the table below.
- ***Created by***: The project member who created the analysis.
- ***Workflow***: The type of analysis launched.
- ***Elapsed time***: The elapsed time since the analysis was created can be found directly below the status of the analysis.
- ***Created date***: The creation date of the analysis can be found below the elapsed time.

Any project member may choose to cancel the progress of an analysis as long as it did not reach a final stage (“Ready to report” for a successful analysis or “Error” for a failed analysis).

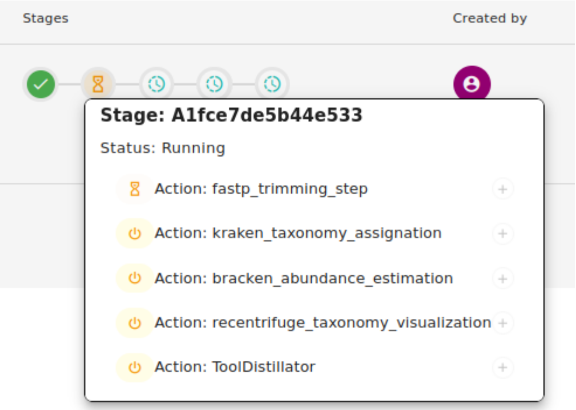
Here is a table of analysis stages and statuses:

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 - Ready to report	Ready to report (report was generated and is accessible on ABRomics)
Error	Error (analysis failed)

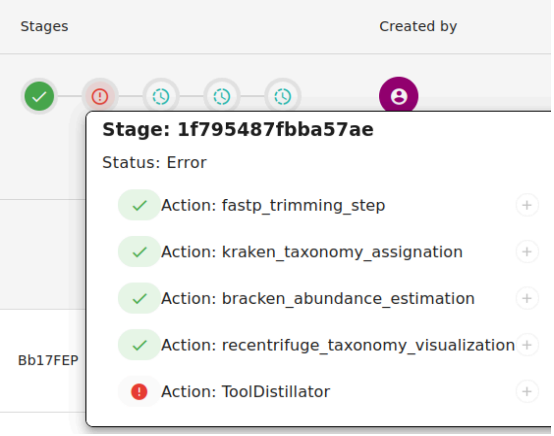
Here are some examples of stages and statuses displayed:



The scheduled stage includes more details on the current jobs running and the tools used for the analysis in progress.

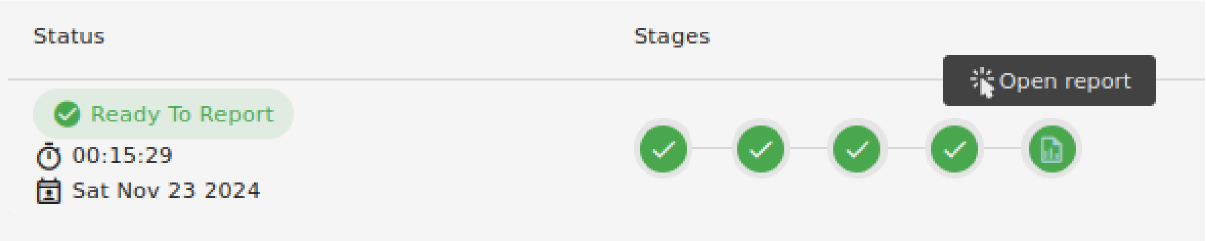


Stage: A1fce7de5b44e533
Status: Running
- Action: fastp_trimming_step
- Action: kraken_taxonomy_assignation
- Action: bracken_abundance_estimation
- Action: recentrifuge_taxonomy_visualization
- Action: ToolDistillator



Stage: 1f795487fbba57ae
Status: Error
- ✓ Action: fastp_trimming_step
- ✓ Action: kraken_taxonomy_assignation
- ✓ Action: bracken_abundance_estimation
- ✓ Action: recentrifuge_taxonomy_visualization
- Action: ToolDistillator

When an analysis fails during the “Scheduled” phase, an automatic retry of the analysis will be done. The automatic retry will only be done once, however, if the analysis fails again, a project member can retry it manually or delete it.



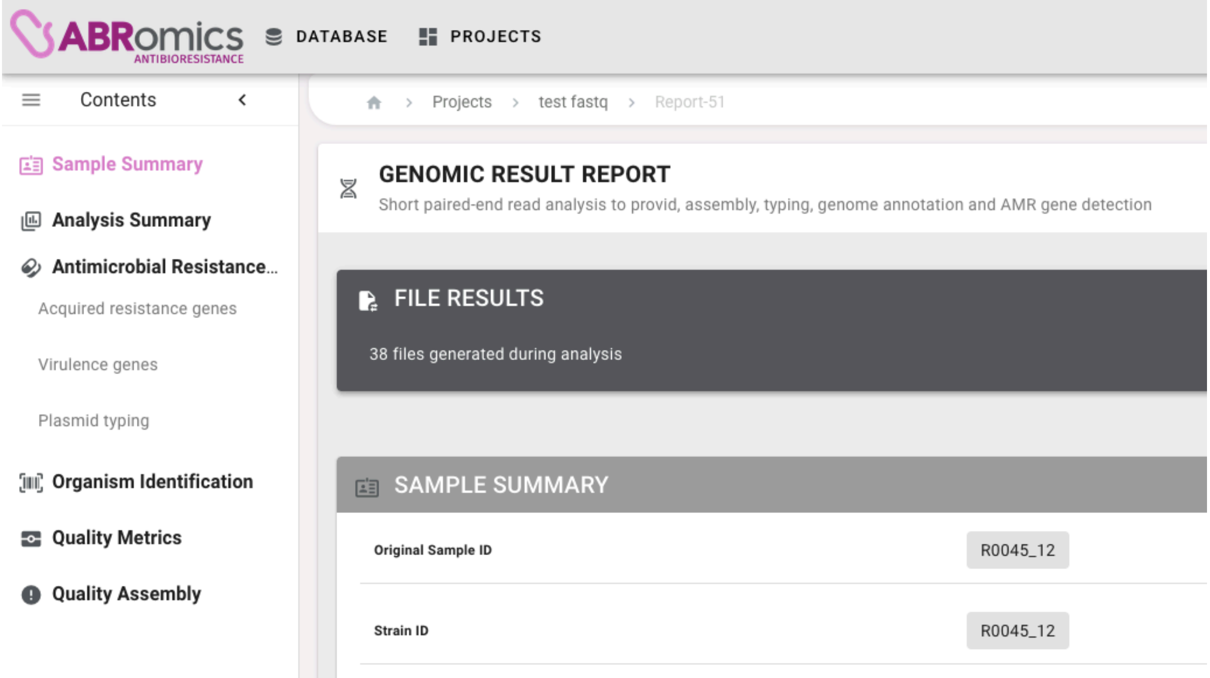
Ready To Report
00:15:29
Sat Nov 23 2024

When an analysis is successful, project members can access or delete the report automatically generated.

If every analysis of a sample is successful, the project supervisor can publish the sample, thus making the results public and accessible to every ABRomics user.

View a report

After clicking on the “Open report” button, you are redirected to the analysis report pages.
On this page on the left side you will find a *Table of Content* to access easily the section you want without scrolling the page:



GENOMIC RESULT REPORT

Short paired-end read analysis to provid, assembly, typing, genome annotation and AMR gene detection

FILE RESULTS

38 files generated during analysis

SAMPLE SUMMARY

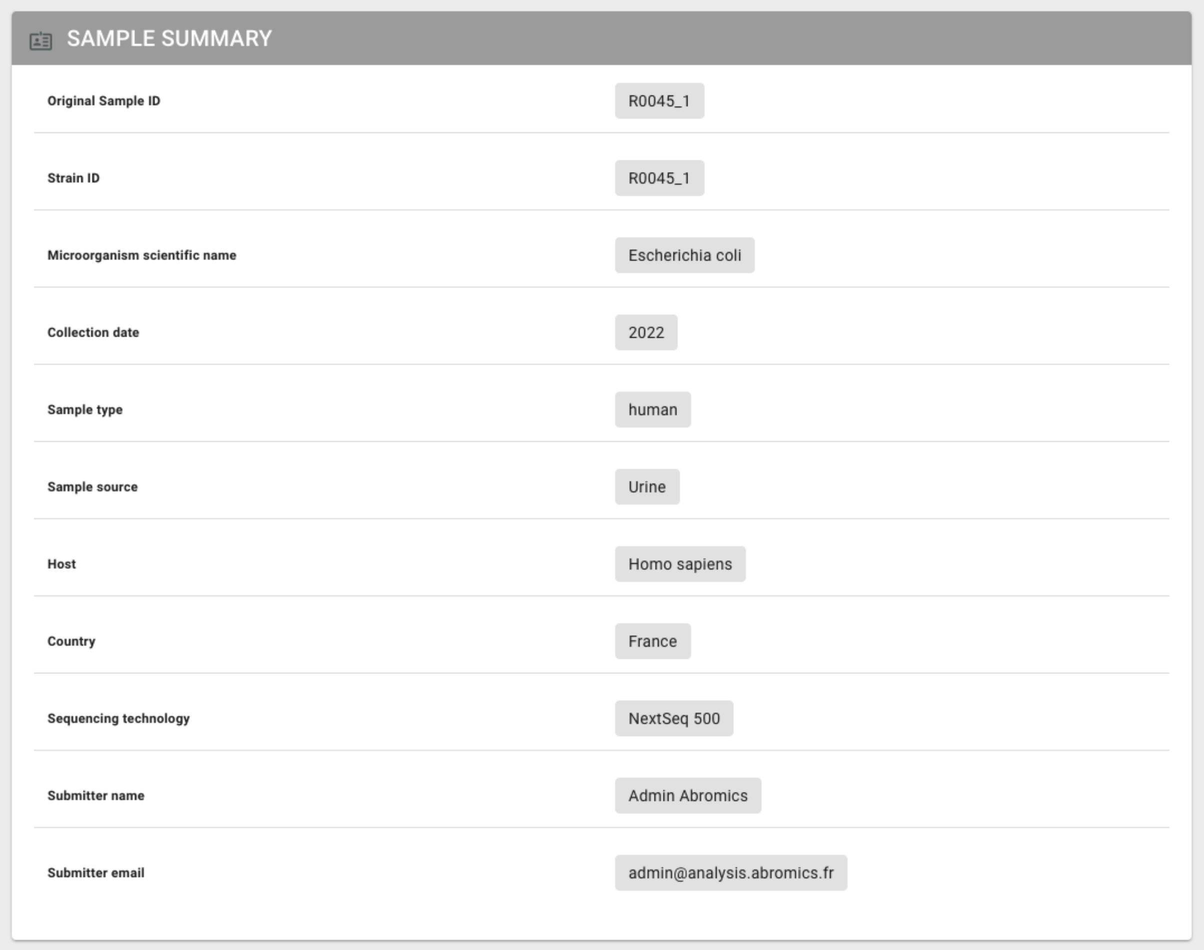
Original Sample ID	R0045_12
Strain ID	R0045_12

Every analysis report in the ABRomics analyses platform is called « Genomic result report ». A brief description of the analyses done to generate the report can be found directly below the report title.

Then the report will have the following sections:

- **File results**: Result files of tools used in the analysis. It can be downloaded one by one or all as an archive.

- **Sample summary**: An overview of the sample metadata (given by the owner of the sample

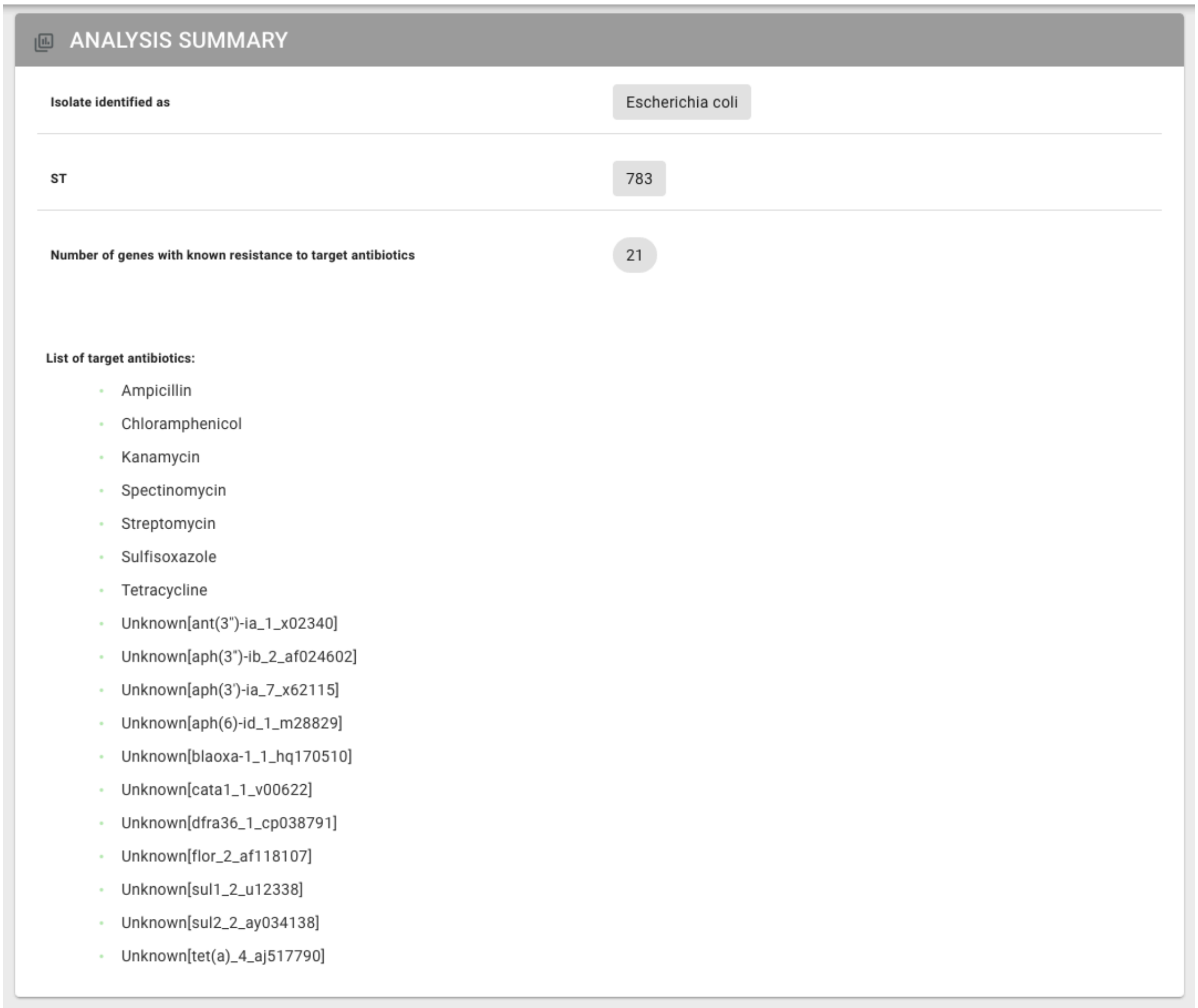


SAMPLE SUMMARY

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**: A summary of key results of the analysis. With the Genomic paired-end FASTQ template, the isolate identified, the number of genes with known resistance to target antibiotics, and the list of these target antibiotics will be shown. With the Genomic FASTA template, the isolated identified will not be shown.



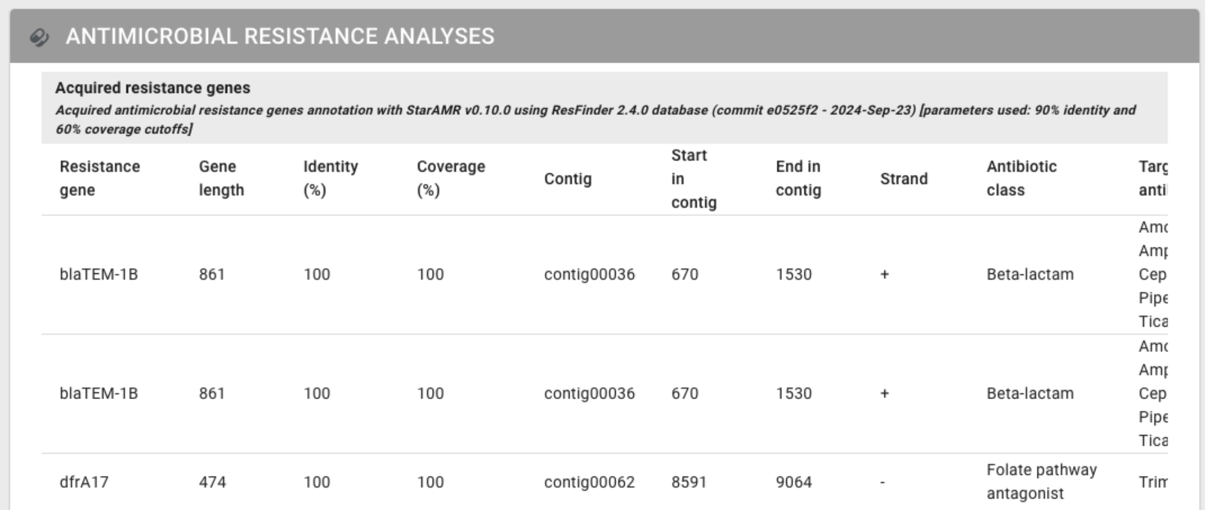
ANALYSIS SUMMARY

Isolate identified as	Escherichia coli
ST	783
Number of genes with known resistance to target antibiotics	21

List of target antibiotics:

- Ampicillin
- Chloramphenicol
- Kanamycin
- Spectinomycin
- Streptomycin
- Sulfisoxazole
- Tetracycline
- Unknown[ant(3")-ia_1_x02340]
- Unknown[aph(3")-ib_2_af024602]
- Unknown[aph(3')-ia_7_x62115]
- Unknown[aph(6)-id_1_m28829]
- Unknown[blaoxa-1_1_hq170510]
- Unknown[cata1_1_v00622]
- Unknown[dfra36_1_cp038791]
- Unknown[flor_2_af118107]
- Unknown[sul1_2_u12338]
- Unknown[sul2_2_ay034138]
- Unknown[tet(a)_4_aj517790]

- **Antimicrobial resistance analyses**: This section has 3 sub-sections: acquired resistance genes, virulences genes and plasmid typing. The following information was found using respectively the Resfinder database of 2022/05/24, the VFDB database updated on 2023/11/04 and the Plasmidfinder database version 2.1.6. Information about the tools used and their versions are given in the report.

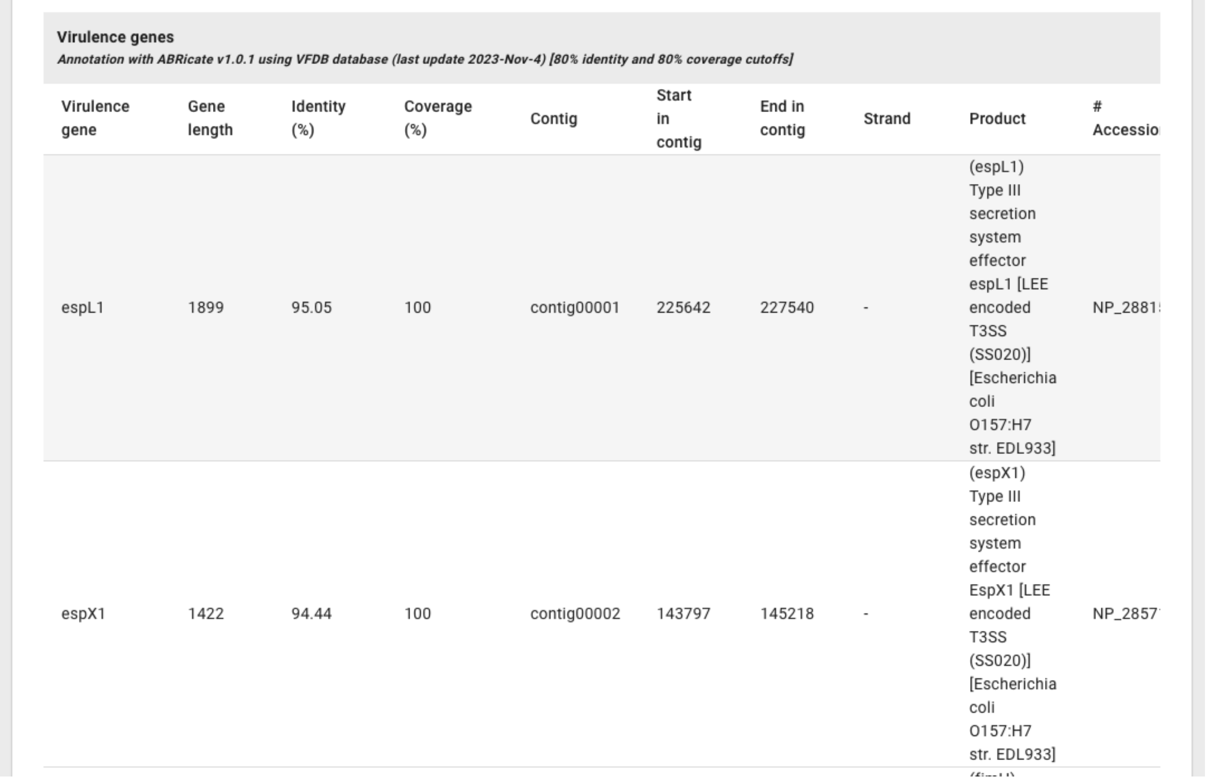


ANTIMICROBIAL RESISTANCE ANALYSES

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]

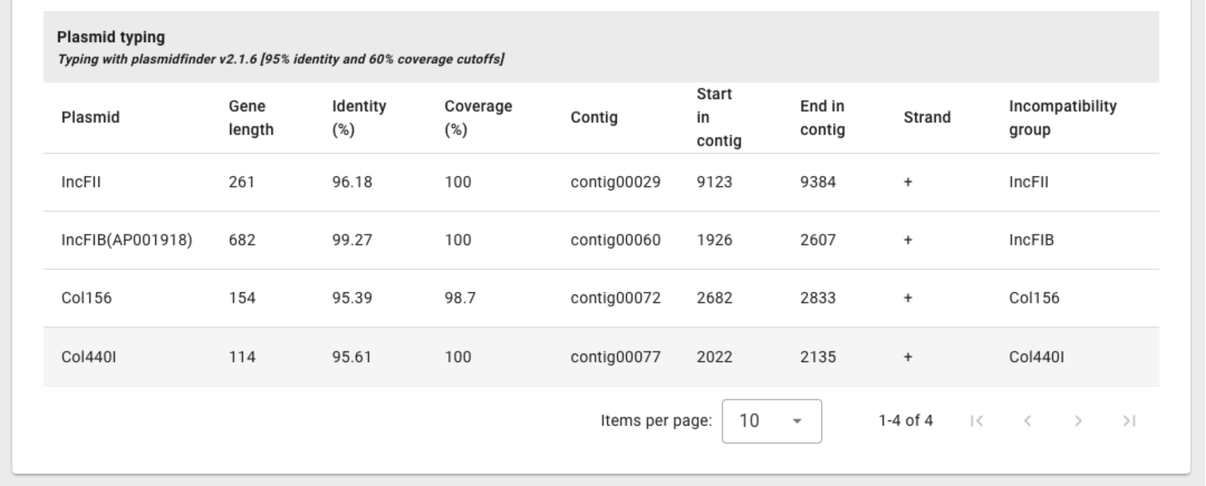
Resistance gene	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Antibiotic class	Targ anti
blaTEM-1B	861	100	100	contig00036	670	1530	+	Beta-lactam	Amo Amp Cep Pipe Tica
blaTEM-1B	861	100	100	contig00036	670	1530	+	Beta-lactam	Amo Amp Cep Pipe Tica
dfrA17	474	100	100	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]

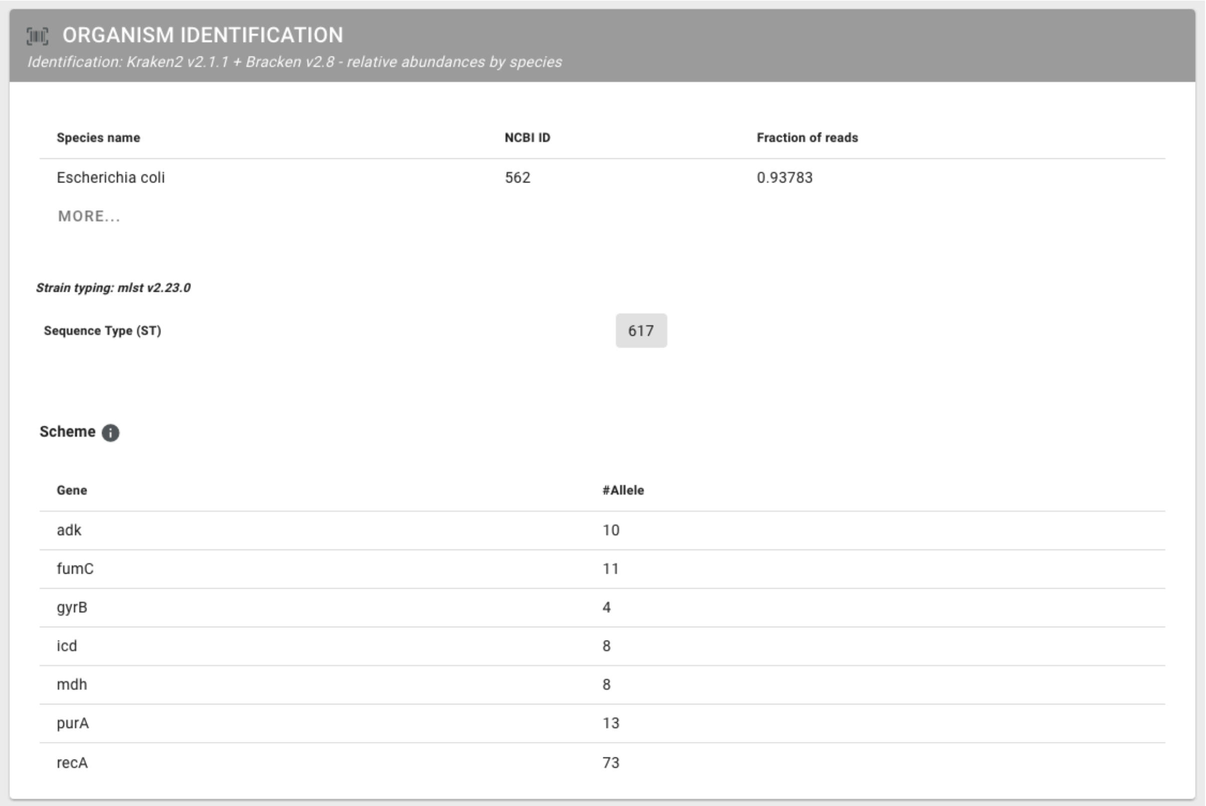
Virulence gene	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Product	# Accessio
espL1	1899	95.05	100	contig00001	225642	227540	-	(espL1) Type III secretion system effector espL1 [LEE encoded T3SS (SS020)] [Escherichia coli O157:H7 str. EDL933]	NP_2881
espX1	1422	94.44	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:** This section is only available with the genomic WGS paired-end FASTQ template. It shows the results of taxonomic assignation with Kraken2 and the detected Sequence Type.



ORGANISM IDENTIFICATION
Identification: Kraken2 v2.1.1 + Bracken v2.8 - relative abundances by species

Species name	NCBI ID	Fraction of reads
Escherichia coli	562	0.93783

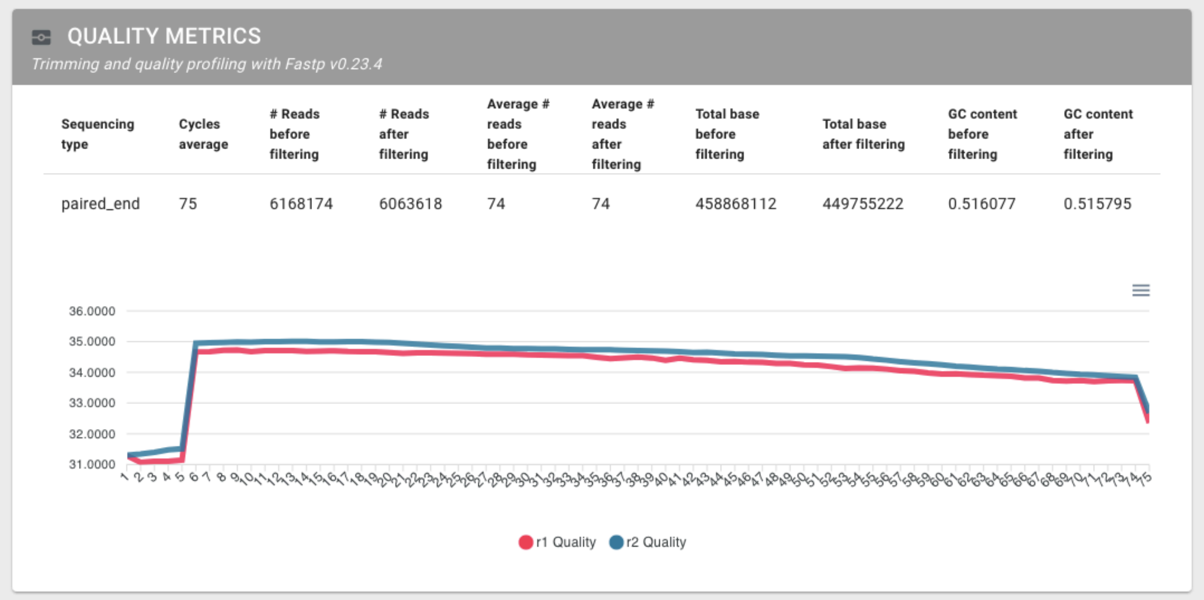
Strain typing: mlst v2.23.0

Sequence Type (ST): 617

Scheme

Gene	#Allele
adk	10
fumC	11
gyrB	4
icd	8
mdh	8
purA	13
recA	73

- **Quality metrics**: This section is only available for genomic paired-end FASTQ template as it shows the results of quality control of FASTQ data with Fastp. The quality before and after trimming for R1 and R2 files is shown.



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**: This section is only available for genomic WGS paired-end FASTQ template as it shows the results of quality control of the assembled sequences with Shovill.

QUALITY ASSEMBLY

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

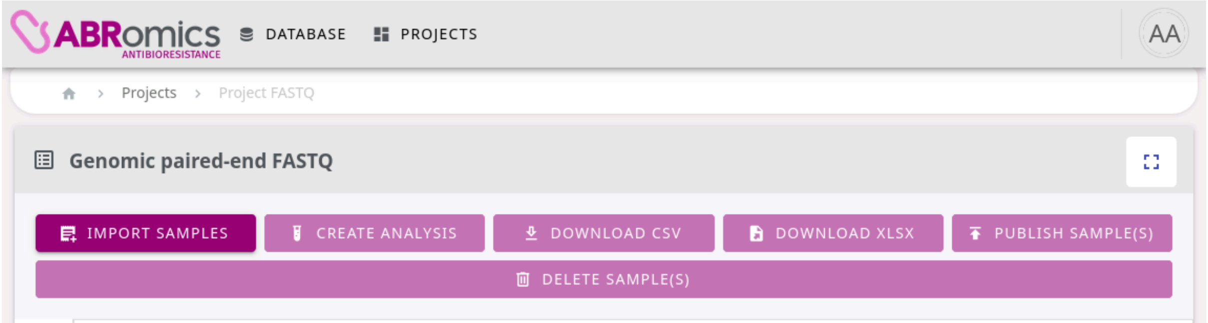
# Contigs	Largest contig	GC (%)	N50	Mapped (%)	Properly paired (%)	Average coverage depth	# Pseudogene
134	308280	50.71	114182	99.7	98.41	84	

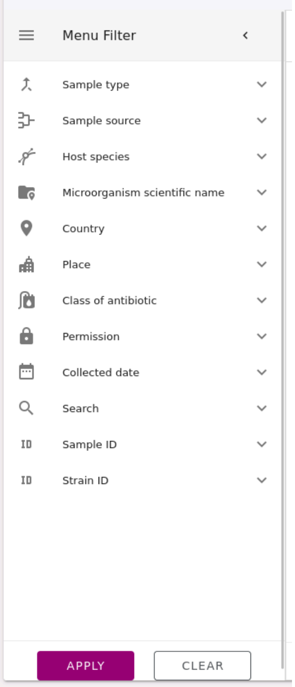
Contig lengths (bp) distribution

Contig mean coverages

EXPLORE RESULTS IN A PROJECT

Filter, download, publish, or delete data





Other actions that can be done in a project are the following:

- Any project member can create analyses in a batch;
- Any project member can download a .csv file of the results of selected samples. First, you must select the results you want on your .csv (for example: AssemblyQC, MLST, Resfinder results…). Each row of the .csv corresponds to an analysis made on the selected samples and has information on both the sample and the results of the analysis.
- Any project member can download a .xlsx file of the results of selected samples. As of ABRomics v1.0, the .xlsx contains 4 sheets with, respectively, information about the sample **Metadata**, **Resfinder** results, **Virulence** results, **Plasmidfinder** results, and **MLST** results.
- Only the project supervisor can delete samples in a batch.

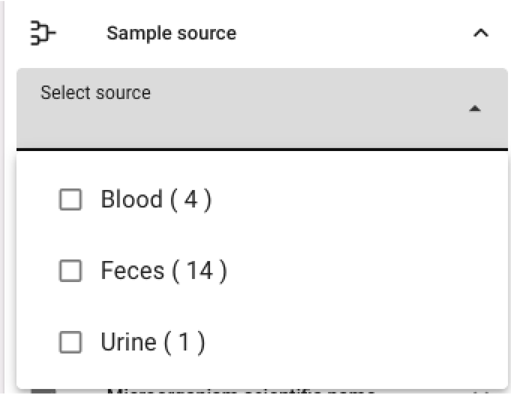
You can select samples either one by one by clicking on the checkbox at the beginning of a row in the sample collection table or by choosing every sample shown on the page by clicking on the checkbox at the left of the column titles.

You can filter out samples in the sample collection table by using the filter menu:

- You can filter out according to sample metadata: “Sample type”, “Sample source”, “Host species”, “Microorganism scientific name”, “Country”, “Place”, “Permission”, “Collected date”, “Sample ID”, “Strain ID”;
- Or according to analyses results: “Class of antibiotic”.

- Or by using the free input "Search" bar which will search in "Sample type", "Sample source", "Host species", "Microorganism scientific name", "Country", "Sample ID", MLST result "Sequence type", project name, experiment "Creation time", "Collected date", "Accession number" and "Comments".

For each filter, the list of possible values is 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)

If you want to retrieve analyses with the following results:

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

You will need to filter only by this single value: « Aminoglycoside, Quinolone ».

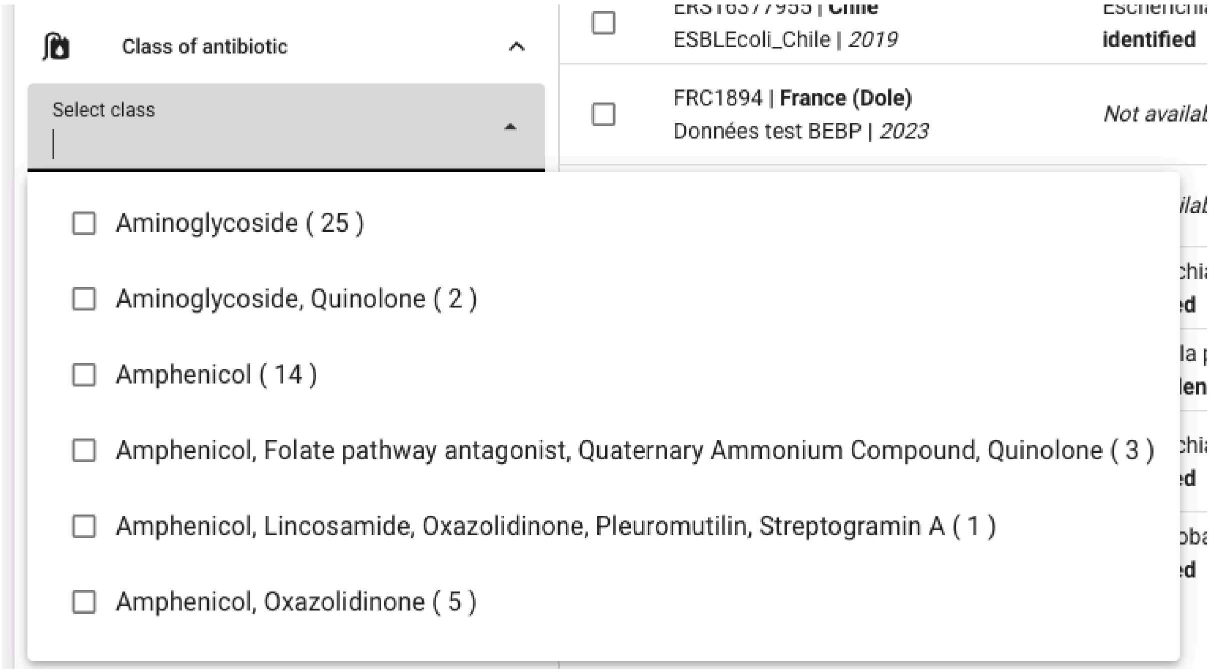
If you filter by 2 values (selection of « Aminoglycoside » and « Quinolone », this will return analyses following these results:

« 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 the value « Aminoglycoside, Quinolone» 2 analyses match the filter criterion. These 2 analyses are not part of the 25 analyses matching the « Aminoglycoside » filter criterion. In total, the database has 27 analyses with at least one resistance gene known to target Aminoglycoside class antibiotics.



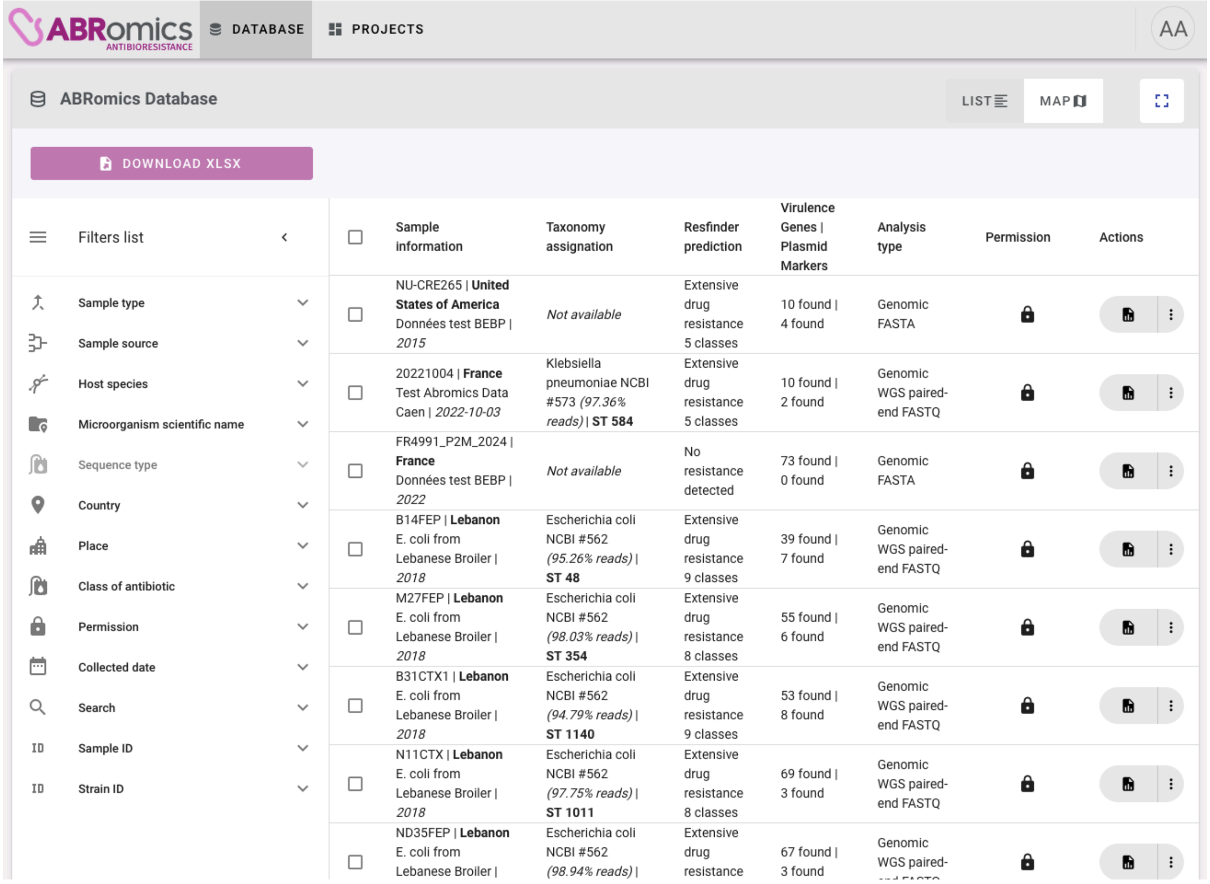
☐ Aminoglycoside (25)
☐ Aminoglycoside, Quinolone (2)
☐ Amphenicol (14)
☐ Amphenicol, Folate pathway antagonist, Quaternary Ammonium Compound, Quinolone (3)
☐ Amphenicol, Lincosamide, Oxazolidinone, Pleuromutilin, Streptogramin A (1)
☐ Amphenicol, Oxazolidinone (5)

☐ ESBLEcoli_Chile | *2019* **identified**

☐ FRC1894 | **France (Dole)**
Données test BEBP | *2023*

EXPLORE RESULTS OF THE COMMUNITY USING THE ABROMICS DATABASE

Filter, download, and visualize data



☐	Sample information	Taxonomy assignation	Resfinder prediction	Virulence Genes | Plasmid Markers	Analysis type	Permission	Actions
☐	NU-CRE265 | **United States of America** Données test BEBP | *2015*	*Not available*	Extensive drug resistance 5 classes	10 found | 4 found	Genomic FASTA	🔒	
☐	20221004 | **France** Test Abromics Data Caen | *2022-10-03*	Klebsiella pneumoniae NCBI #573 *(97.36% reads)* | **ST 584**	Extensive drug resistance 5 classes	10 found | 2 found	Genomic WGS paired-end FASTQ	🔒	
☐	FR4991_P2M_2024 | **France** Données test BEBP | *2022*	*Not available*	No resistance detected	73 found | 0 found	Genomic FASTA	🔒	
☐	B14FEP | **Lebanon** E. coli from Lebanese Broiler | *2018*	Escherichia coli NCBI #562 *(95.26% reads)* | **ST 48**	Extensive drug resistance 9 classes	39 found | 7 found	Genomic WGS paired-end FASTQ	🔒	
☐	M27FEP | **Lebanon** E. coli from Lebanese Broiler | *2018*	Escherichia coli NCBI #562 *(98.03% reads)* | **ST 354**	Extensive drug resistance 8 classes	55 found | 6 found	Genomic WGS paired-end FASTQ	🔒	
☐	B31CTX1 | **Lebanon** E. coli from Lebanese Broiler | *2018*	Escherichia coli NCBI #562 *(94.79% reads)* | **ST 1140**	Extensive drug resistance 9 classes	53 found | 8 found	Genomic WGS paired-end FASTQ	🔒	
☐	N11CTX | **Lebanon** E. coli from Lebanese Broiler | *2018*	Escherichia coli NCBI #562 *(97.75% reads)* | **ST 1011**	Extensive drug resistance 8 classes	69 found | 3 found	Genomic WGS paired-end FASTQ	🔒	
☐	ND35FEP | **Lebanon** E. coli from Lebanese Broiler |	Escherichia coli NCBI #562 *(98.94% reads)* |	Extensive drug resistance	67 found | 3 found	Genomic WGS paired-	🔒	

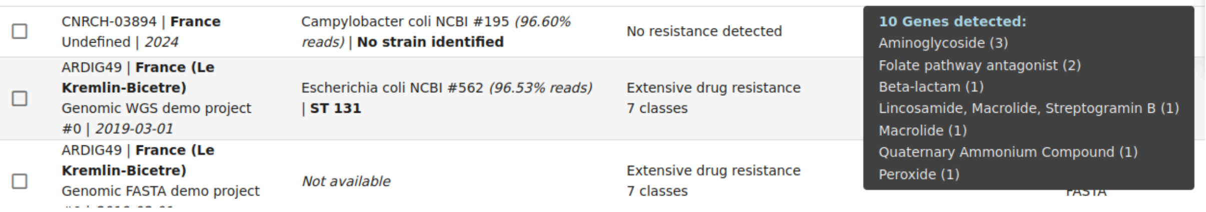
The second main page on ABRomics is "Database". Any connected ABRomics user can access this page and look up analysis results saved in the ABRomics database. There are currently 2 different ways of seeing results, either by a "List" view or by a "Map" view. You can navigate between both views by clicking on the "List" and "Map" buttons at the upper-right side of the page. The extend button "[ ]" at the very far right enables you to maximize and minimize the results table.

The "List" view is shown by default and each result (row in the table) is described with 6 columns:

- **Sample information**: information about the sample on which the analysis was made (Sample ID, Country (place) where the sample was sampled, name of the ABRomics project the sample was uploaded to, date of collection of the sample (YYYY, YYYY-MM, or YYYY-MM-DD));
- **Taxonomy assignation**: information about the taxonomy detected with the most reads (scientific name of the microorganism found after analyzing the

sample, corresponding NCBI ID, percentage of reads, MLST sequence type if identified);

- **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;



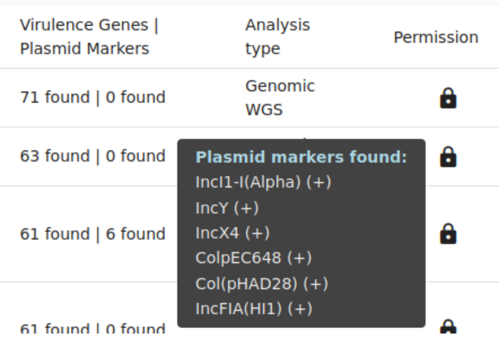
☐ CNRCH-03894 | **France** Undefined | *2024* — Campylobacter coli NCBI #195 *(96.60% reads)* | **No strain identified** — No resistance detected

☐ ARDIG49 | **France (Le Kremlin-Bicetre)** Genomic WGS demo project #0 | *2019-03-01* — Escherichia coli NCBI #562 *(96.53% reads)* | **ST 131** — Extensive drug resistance 7 classes

☐ ARDIG49 | **France (Le Kremlin-Bicetre)** Genomic FASTA demo project — *Not available* — 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**: 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;

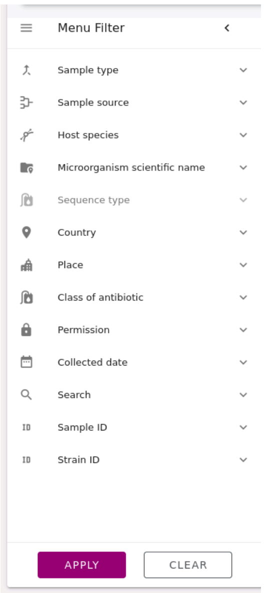


Virulence Genes | Plasmid Markers	Analysis type	Permission
71 found | 0 found	Genomic WGS	🔒
63 found | 0 found		🔒
61 found | 6 found		🔒

Plasmid markers found:
IncI1-I(Alpha) (+)
IncY (+)
IncX4 (+)
ColpEC648 (+)
Col(pHAD28) (+)
IncFIA(HI1) (+)

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

- **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".

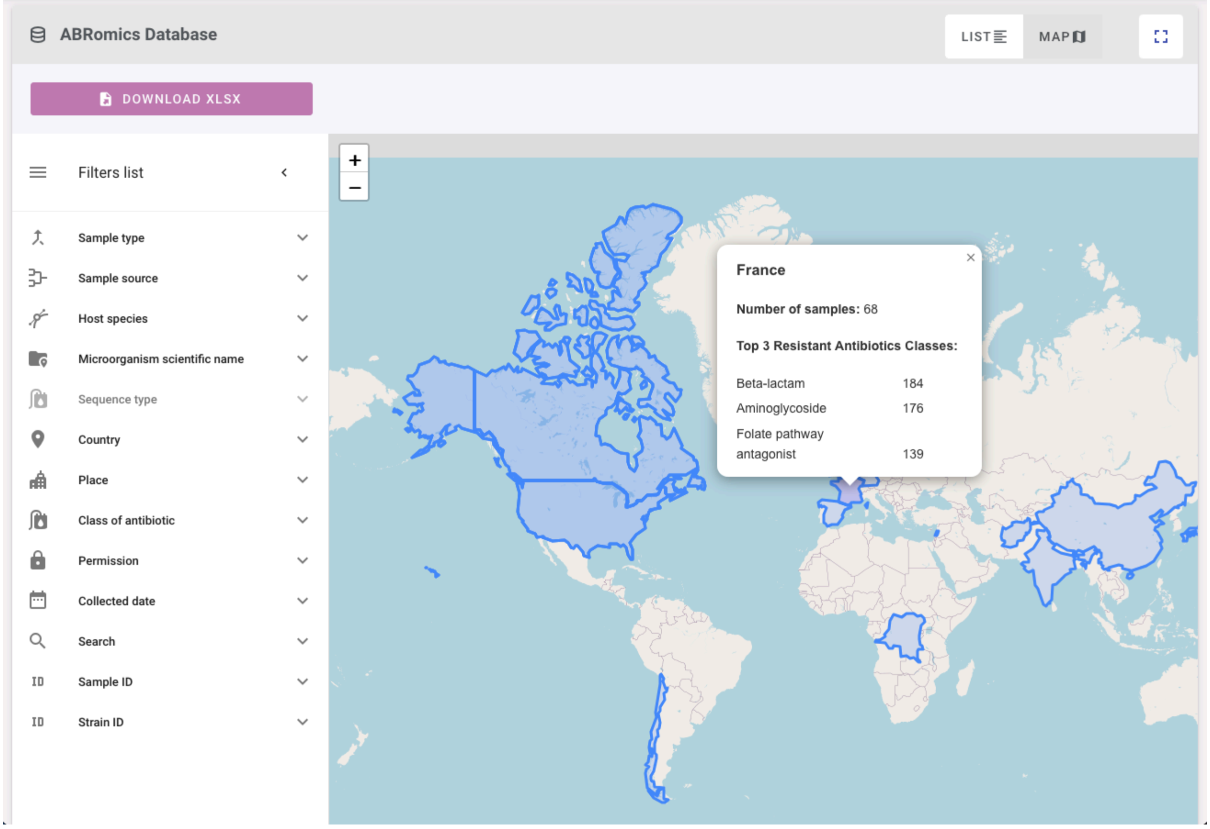
Similarly to the detailed project view, you can use a filter menu to filter according to the specific results you are searching for:

- 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"*, MLST result "Sequence type"**, "Class of antibiotic", "Permission".
- Or by using the free input "Search" bar which will search in "Sample type", "Sample source", "Host species", "Microorganism scientific name"***, "Country", "Sample ID", MLST result "Sequence type", project name, and "Collected date".

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

**The filter "Sequence type" can only be used if a "Microorganism scientific name" was selected.

***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.



France

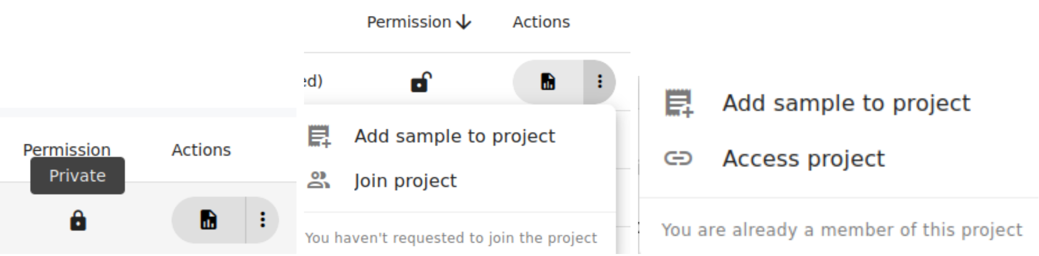
Number of samples: 68

Top 3 Resistant Antibiotics Classes:

Beta-lactam	184
Aminoglycoside	176
Folate pathway antagonist	139

The "map" view 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 run analyses on ABRomics.

Access reports, join a project, add a public sample to a project

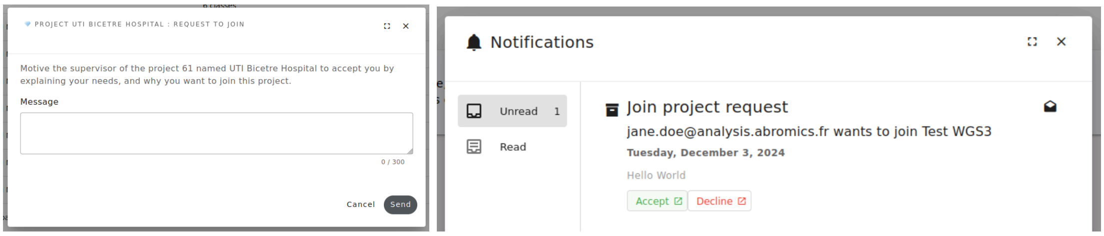


You haven't requested to join the project

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 demand 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 demand 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 already sent a request you will not be able to spam messages.

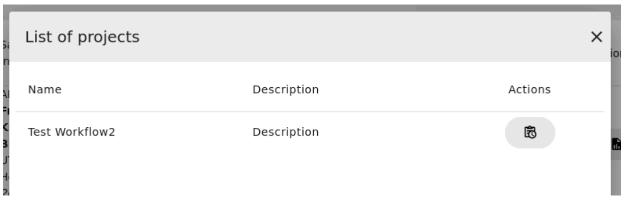


Motive the supervisor of the project 61 named UTI Bicetre Hospital to accept you by explaining your needs, and why you want to join this project.

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 add any sample made public into your own projects, providing that you have at least one project with a template compatible with the sample. You can do this by clicking on "Add sample to project" and on the icon button under the "Actions" column.



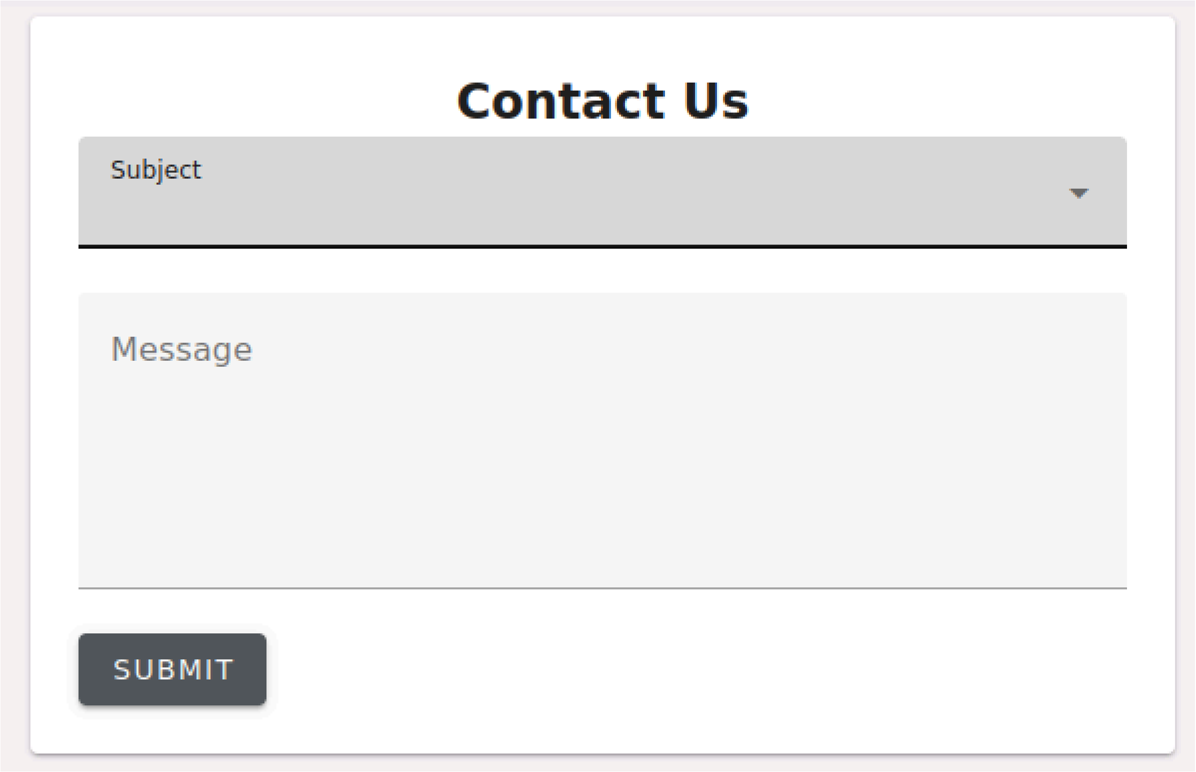
Name	Description	Actions
Test Workflow2	Description	

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@france-bioinformatique.fr.

You can also send a message directly on the platform through the "**Contact Us**" page accessible on the footer. The footer appears on every page of ABRomics analyses.



You can select a subject between 3 choices: "Bug", "Feature" (any feature you would like to see on ABRomics), and "Other".

APPENDIX

Table of "Roles in a project & permissions"

Appendix 1: 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 theirs)
Download input files	x	
View report	x	x
Download result files	x	x
Publish sample	x	

Table of “Templates & metadata”

Appendix 2: 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 3: 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
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/