ABRomics analyses platform

A *One Health* Antimicrobial Resistance Analysis Service

User Manual (UM)

2025-09-18

Version 1.2.0

Table of Content

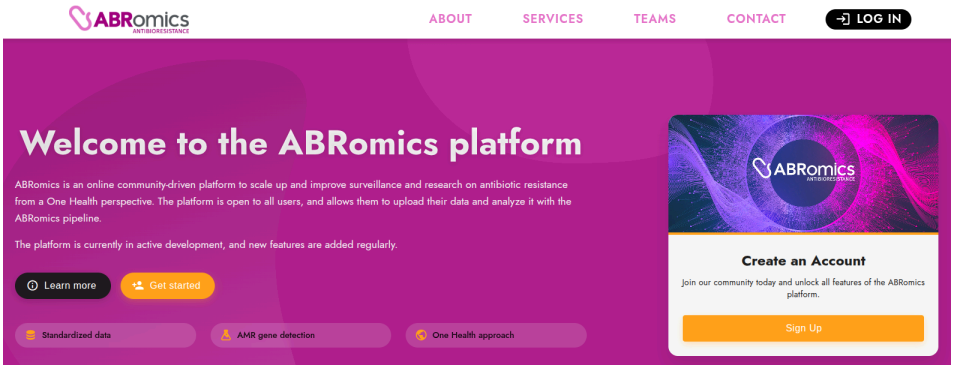
VERSION HISTORY

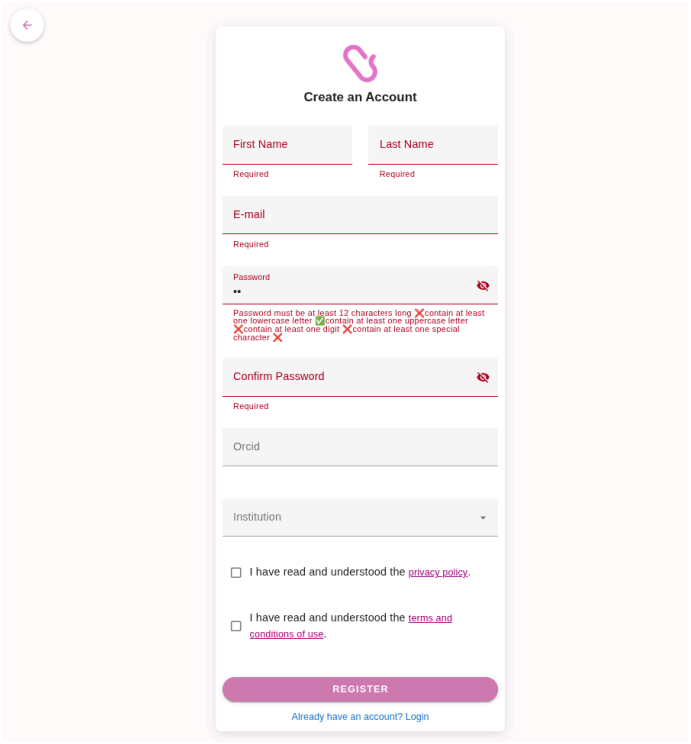
VERSION (of ABRomics analyses)	UPDATES	DATE
1.0.0	Document creation	2024-12-10
1.1.0	Added tutorial on how to use demo files (FASTQ), Removed publishing feature, Updated analysis report section	2025-01-17
1.1.7	Added new landing and home page information, Updated "EXPLORE RESULTS OF THE COMMUNITY USING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

REGISTRATION & ACCOUNT MANAGEMENT

Landing page, register and login

To use the platform, 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.





When all required fields are completed, you should read the "ABRomics user charter" (the first page highlights the main points of this charter) and the "terms and conditions of use" before accepting them by checking the two checkboxes. Then, you will be able to click on the "Register" button.

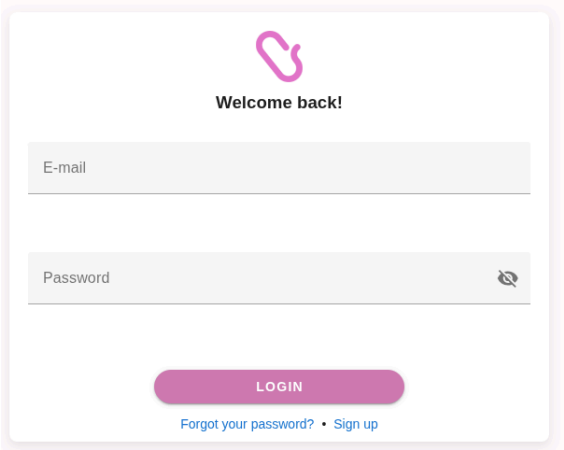
An account confirmation email will be sent to you: follow the link in the email to activate your account.

Warning:

- *The email address has to be institutional and part of ABRomics' whitelist.*
- *The password should 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 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:

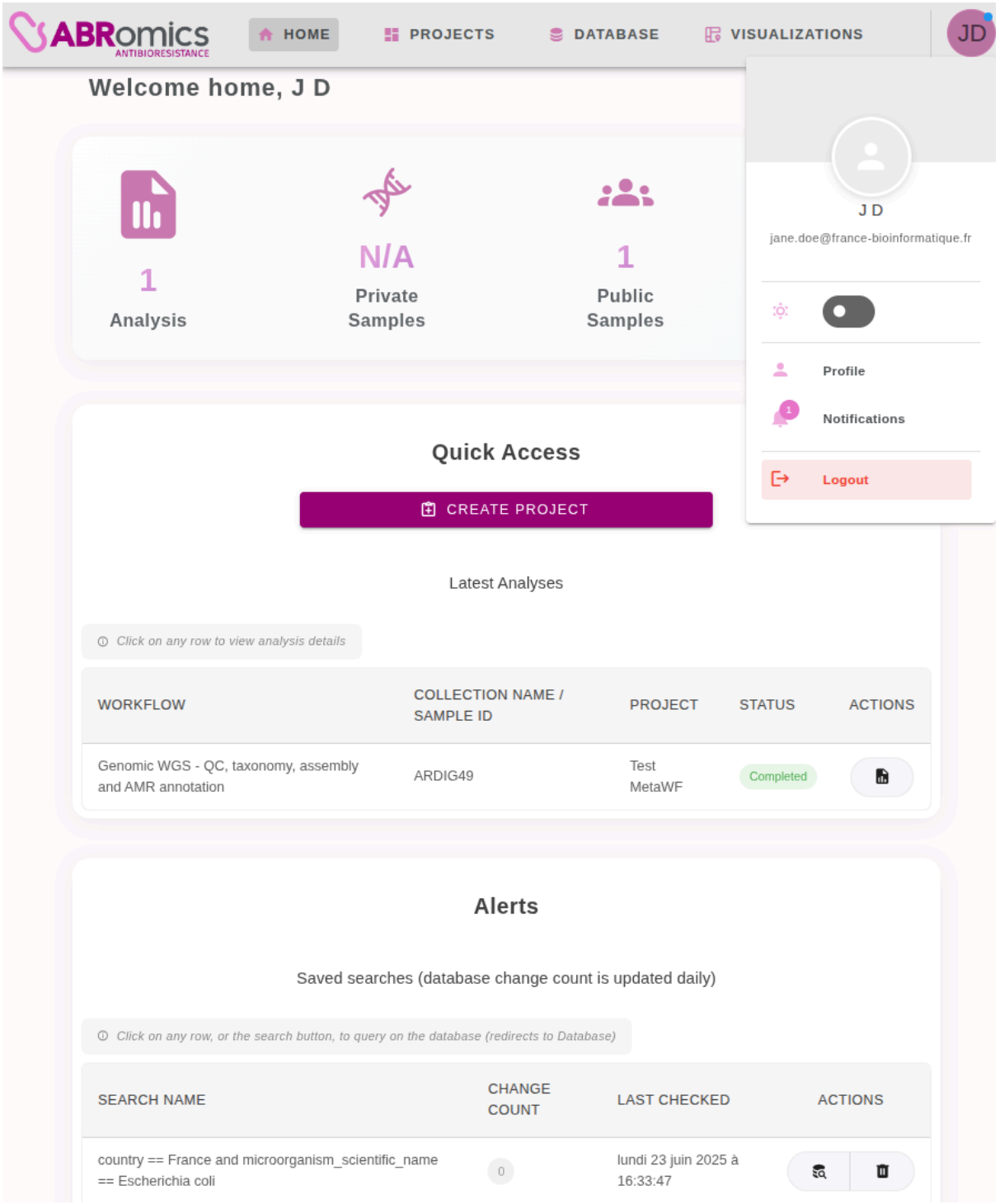
- Learn more about the ABRomics project ("Learn more" in the "Welcome to the ABRomics platform" section)
- Access and download the demo files ("Get demo files" in the "Upload" card)
- Learn more about the workflows used for our analyses ("Learn more" in the "Analysis" card)
- Learn more about our *One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

You can find a tutorial on how to use the demo files in the **Appendix 1**.

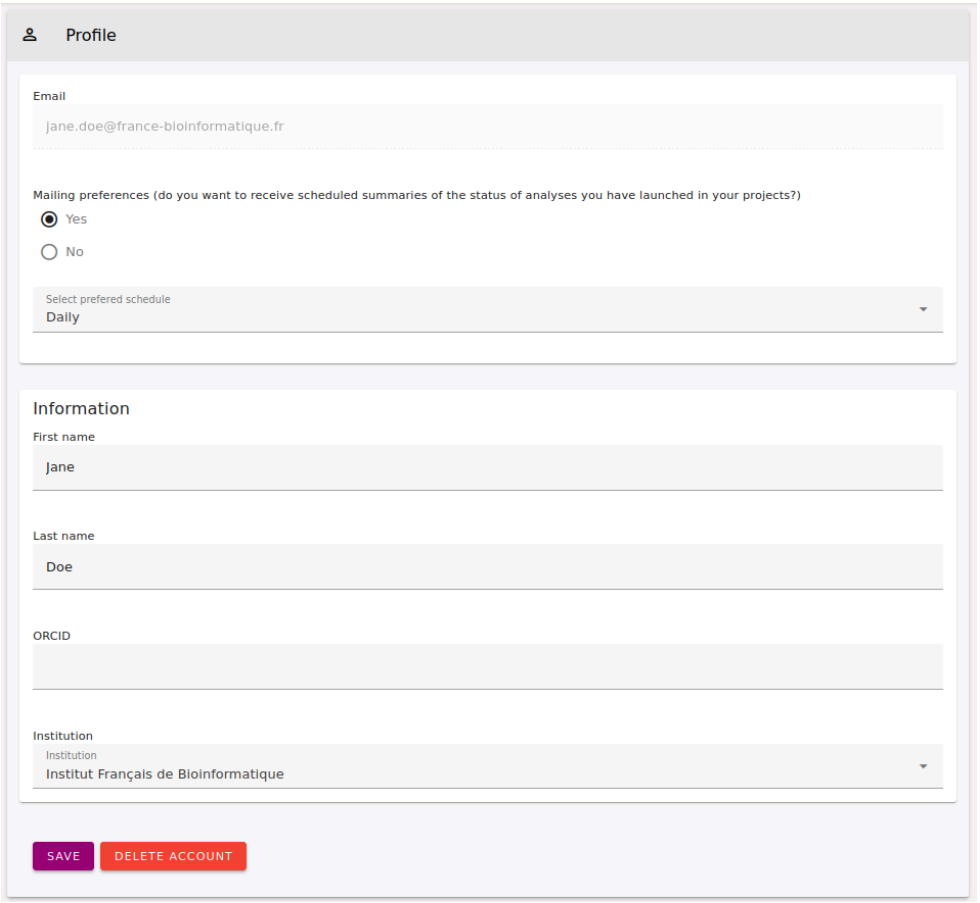
User profile

When connected, you arrive on your personal homepage on which you can see metrics of projects you own or are participating in. Information about the 10 last analyses you have launched is available. Finally, you can manage the different alerts saved during your research on the ABRomics community Database.

If it is your first time on ABRomics, an optional interactive tour will start, showcasing all features on the platform.



The User menu enables you to log out, view your notifications, or access your profile. It is accessible by clicking on the thumbnail in the upper right corner of the page. The "Profile" menu is used to edit the personal information provided in the registering form (with the exception of your email address) and to choose your mailing preferences (whether you want, or not, to receive scheduled summaries of the status of analyses you have launched, and if yes, at which frequency - Daily, Weekly, or Monthly).

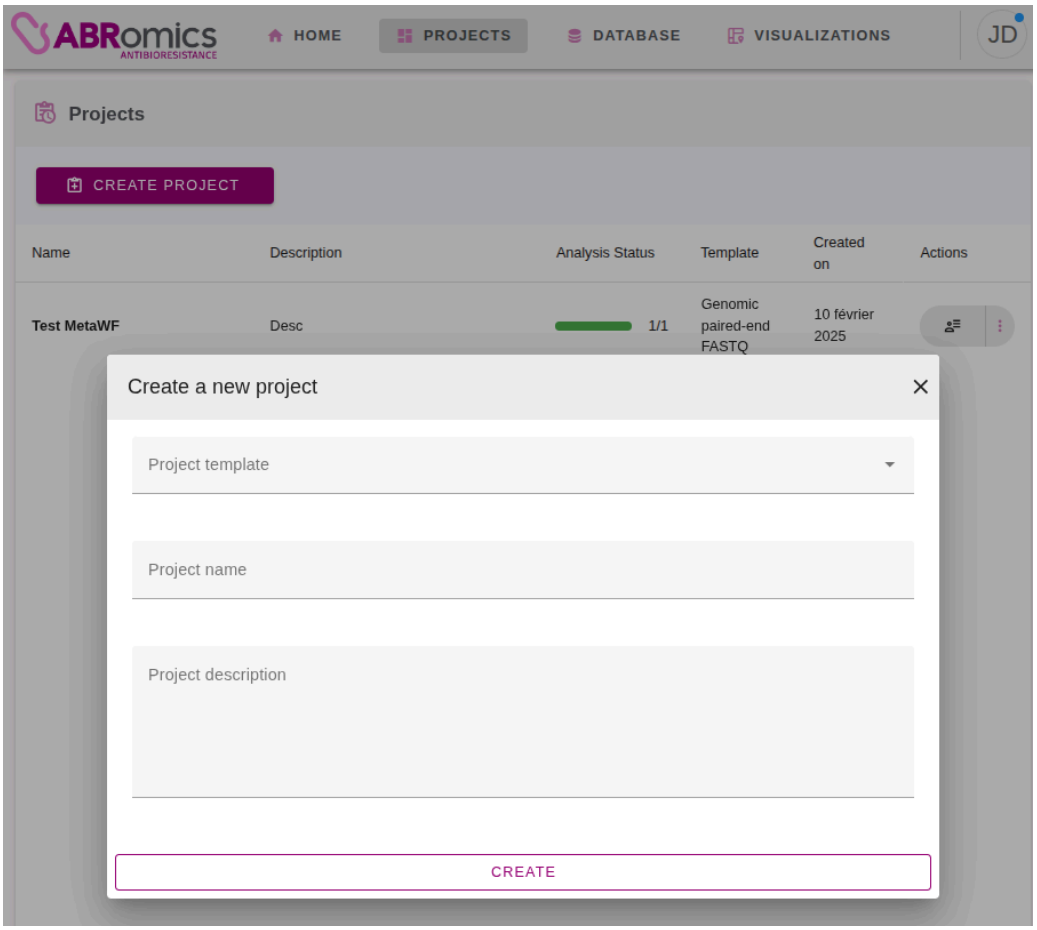


You can also decide to delete your account. A pop-up will appear and you must confirm your choice since this action will permanently delete all the projects you are supervising.

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

PROJECTS & PROJECT MANAGEMENT

The first main page of the ABRomics homepage is "PROJECTS". You can create new projects or access your projects by clicking on the "PROJECTS" menu. A list of projects you have either created or were added to is then listed on the page with the following information (Name of the project, Description, Template, Created on). You can also create a project by clicking on the "Create Project" pink button. A quick access "Create Project" button is also available on your Home page.



To create a project, you must choose a file format template, and enter a project name and a short description of the project.

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.

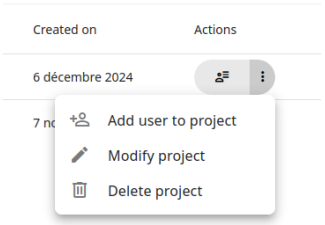
In essence, a template determines the type of results collection table associated with a project, influencing both the inputs (metadata, file type) and outputs (analysis results). It establishes the framework for managing input data and the range of analytical processes available in the project.

ABRomics V1.2.0 enables the analysis of sequencing (FastQ) and assembly (FastA) data.

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 are now the supervisor of the project and you may add other users[1] to the project (the supervisor must know the email address of the collaborators' ABRomics account), change the project name or description, or delete the project. Deleting a project will delete all private samples and analyses performed on the sequences of the samples in 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, running, or failed.

[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 – ***Five pink action buttons***: Directly below the template name of the project (here "Genomic paired-end FASTQ"), these 5 action buttons can be used to manage batches of samples in the project : IMPORT SAMPLES; CREATE ANALYSIS; DOWNLOAD xlsx; PUBLISH SAMPLE(S); DELETE SAMPLE(S)

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. Precise information on these metadata are given in the appendix "Table of "Templates & metadata"

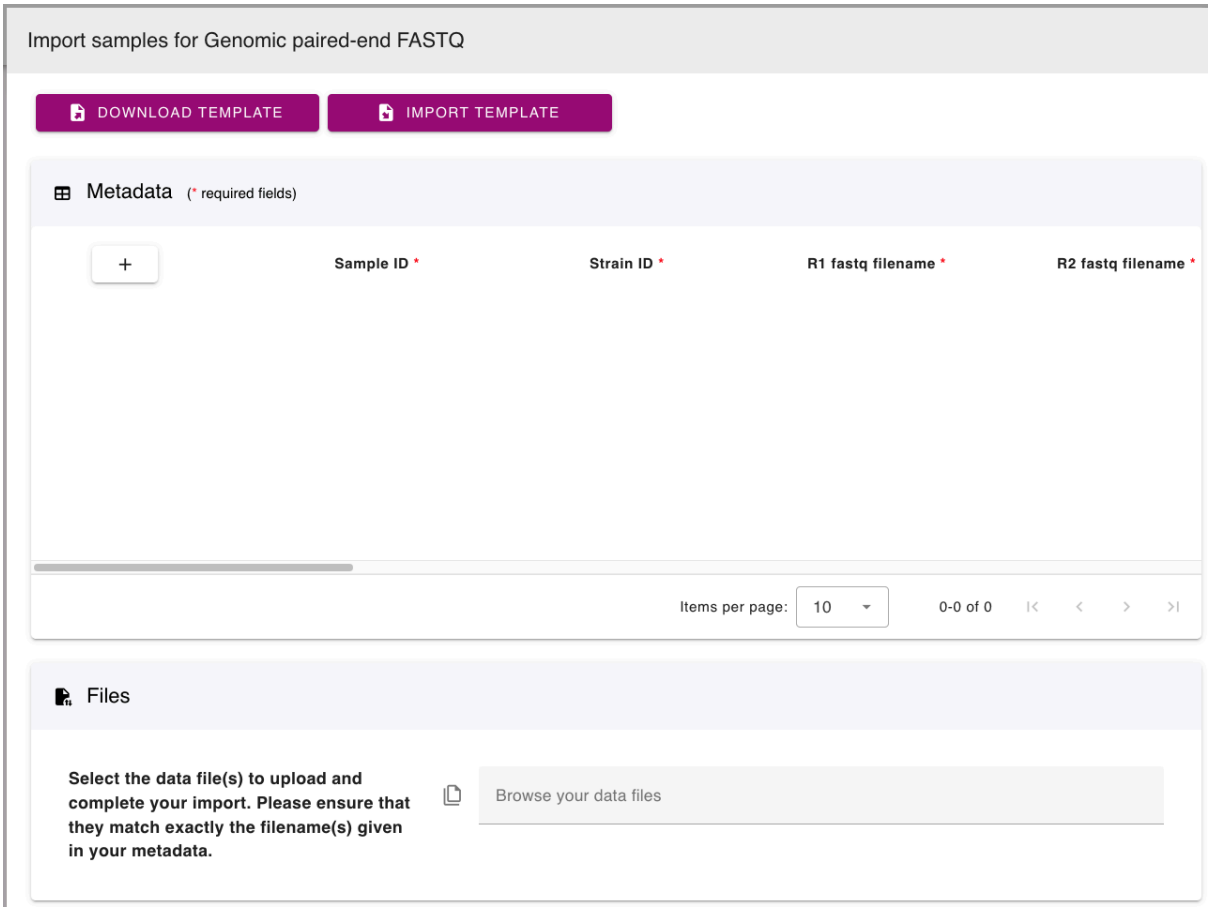
Specific actions for a given sample can be done with the "Actions" button at the right end of the row (see below for more description of these Actions).

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

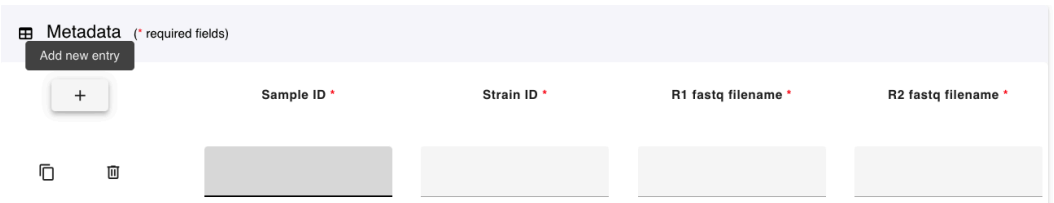
Upload a sample & metadata validation

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



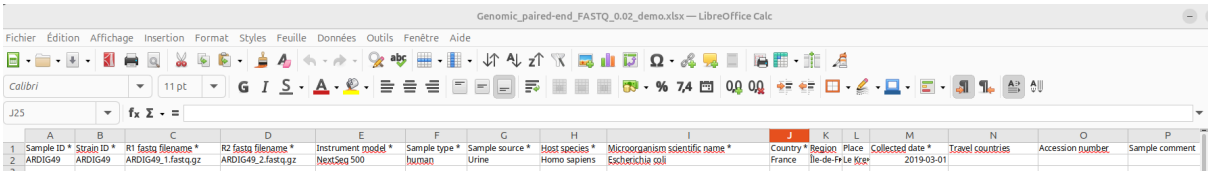
All mandatory metadata files are indicated with an asterisk *. The information can be completed:

- **Manually** : click on the "+" rectangle to add a new entry (i.e. a new sample in the project); a line containing empty rectangles under each metadata field will appeared:



This option should be used only if you have few samples to add in your project.

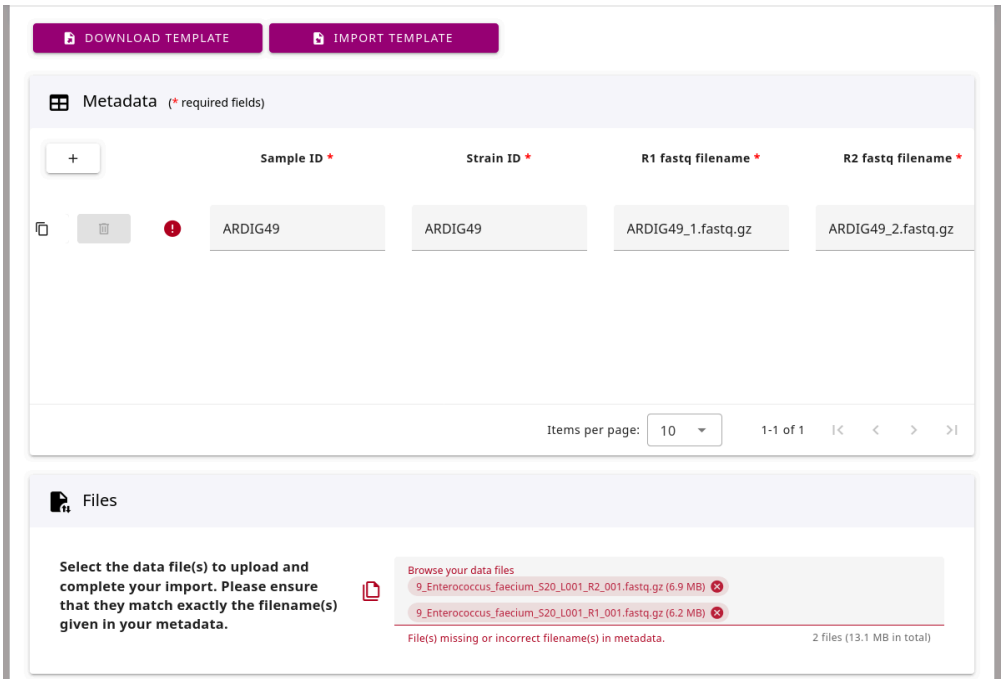
- Or by **downloading** an excel file **template** (pink button "DOWNLOAD TEMPLATE") which contains the 15 metadata columns to field for each sample. Like the interface, the .xlsx template gives clues on how to complete the information through selectable lists and tooltips. The demo file "Genomic_paired-end_FASTQ_0.02_demo.xlsx" contains only one line :



After completing all mandatory data for the genomic samples to be analysed, you should click on "IMPORT TEMPLATE" to select the .xlsx file and upload the data into the ABRomics interface.

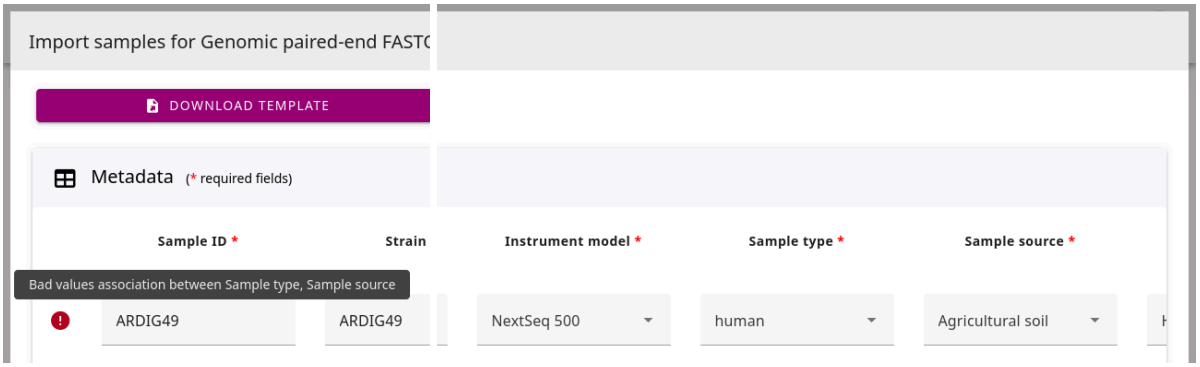
Warning: *the .xlsx file sheet name must match the current version of the template used in ABRomics, for example here "Genomic WGS 0.02". An error will be displayed if the file is an older / different version than the current one accepted on the platform. See* ***"Tables of Templates and Metadata"***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

The next step is to upload the sequence files (R1 and R2) associated with each sample. It is important to note that **the file names indicated in the "R1 fastq filename" and "R2 fastq filename" fields of the metadata must be in accordance with the uploaded file names**.

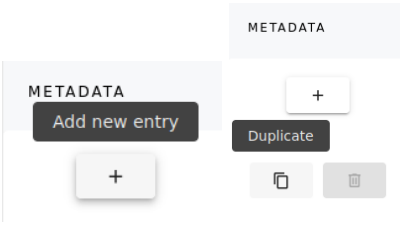


In the previous example, the names of the two uploaded files are not equal to "ARDIG49_1.fastq.gz" and "ARDIG49_2.fastq.gz" leading to the following error message "incorrect filename(s) in metadata".

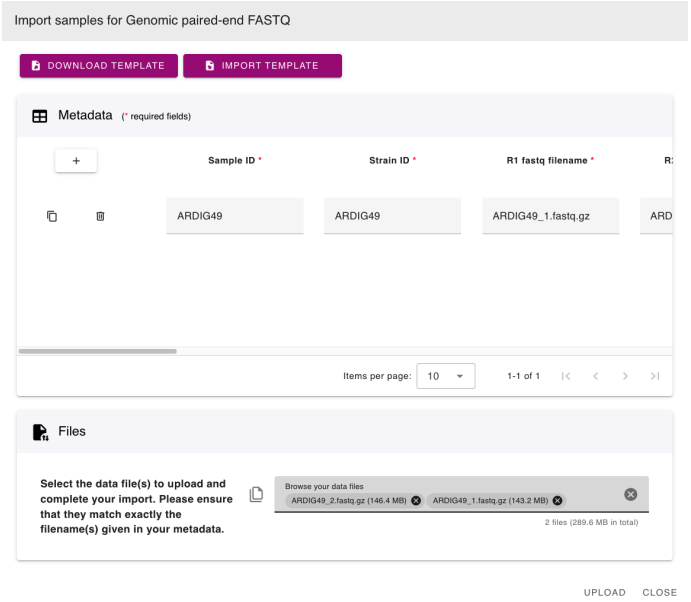
If an error was made during the completion of metadata, information will be given to help you correct it. In the example below, there is a wrong value association between the sample type "human" and the sample source "Agricultural soil".



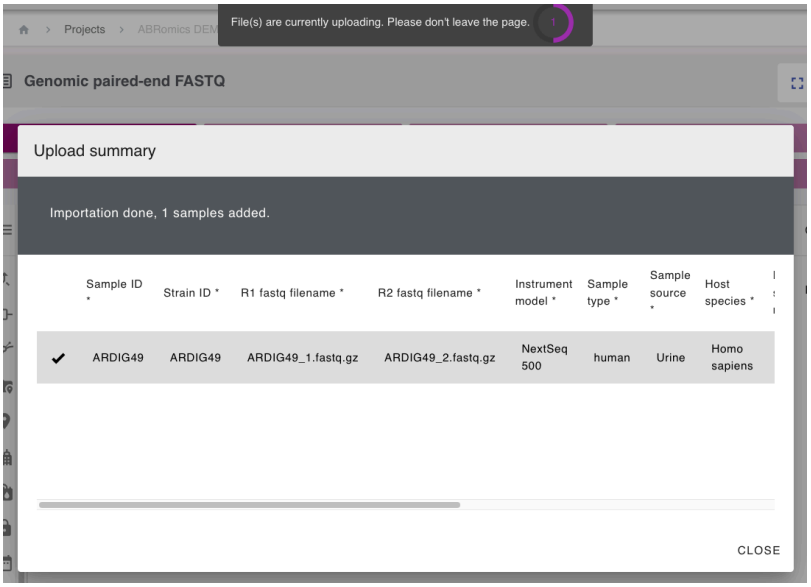
You can duplicate sample rows or add new ones in the interface with the following buttons:



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

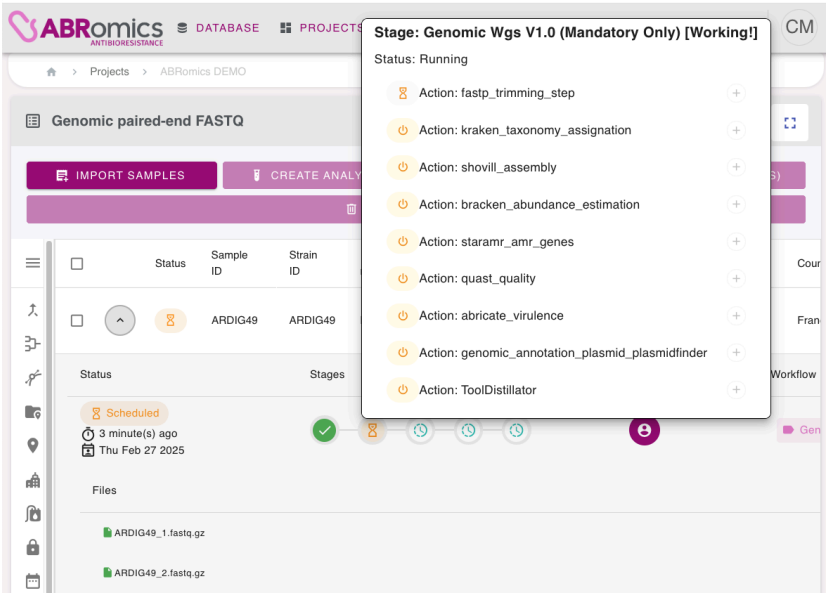


If every row is completed correctly, a summarizing pop-up will show up as well as an alert informing you to stay on the current page and wait until the server processes the input files. After adding a sample, the supervisor can edit it or delete it at any time by using the action buttons under the right-end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



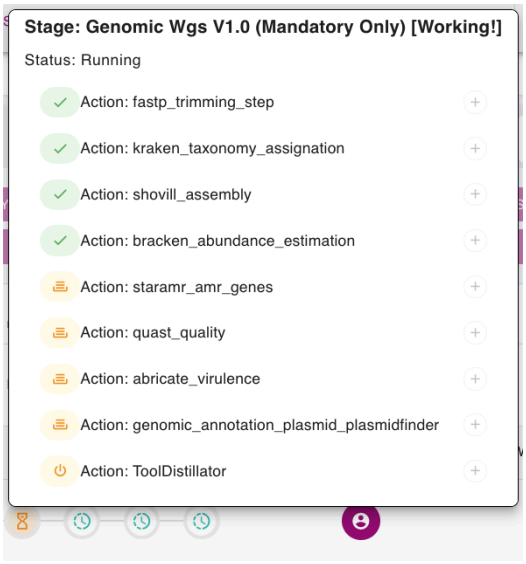
Run an analysis

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

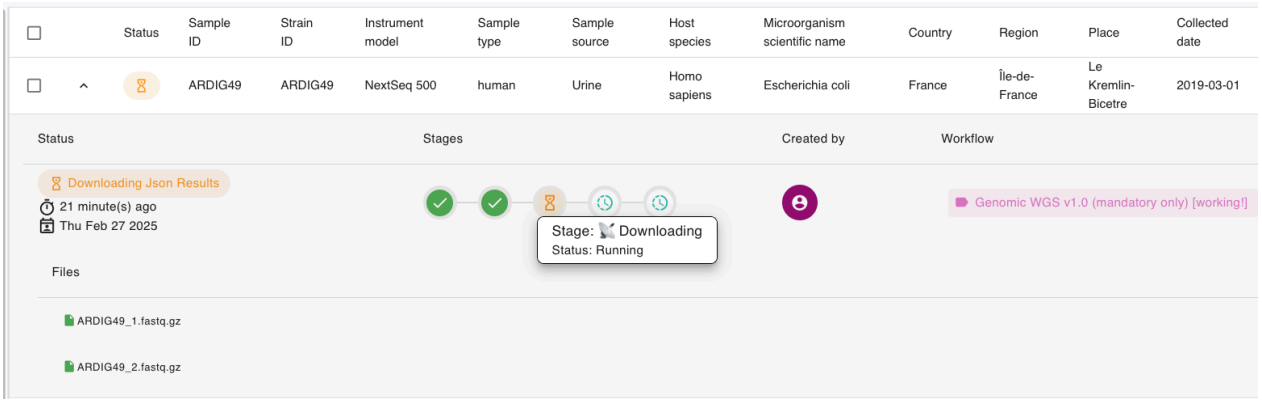


This screenshot shows that the DNA sequence (R1 and R2 in green) has been successfully uploaded and the genomic pipeline is currently running with the various steps listed on the pop-up window. Explanations on these steps can be found on the ABRomics portal: https://www.abromics.fr/home/abromics-platform/workflows-and-analyses/.

Once a step is completed, a green tick is shown next to the completed analysis

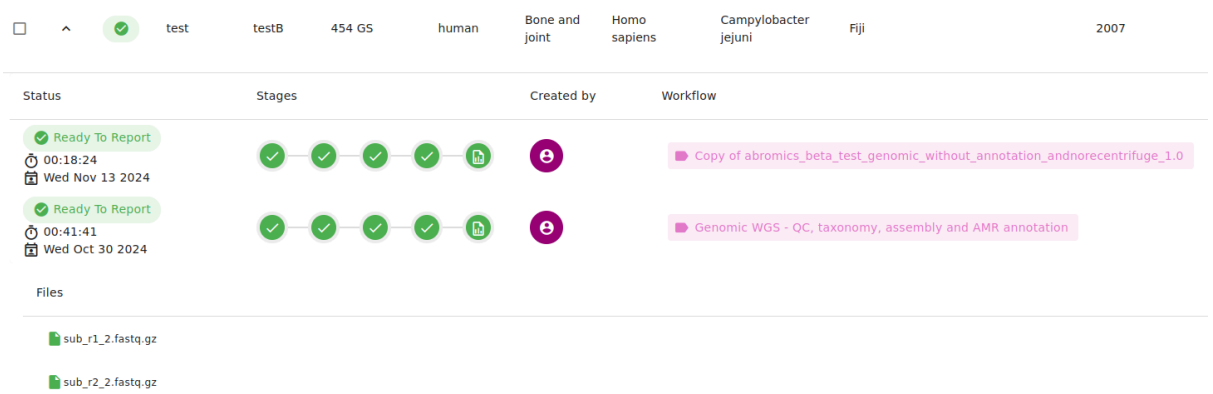


From 30 minutes to 1 hour after the demo sequence and metadata upload, the workflow is at the stage "Downloading":

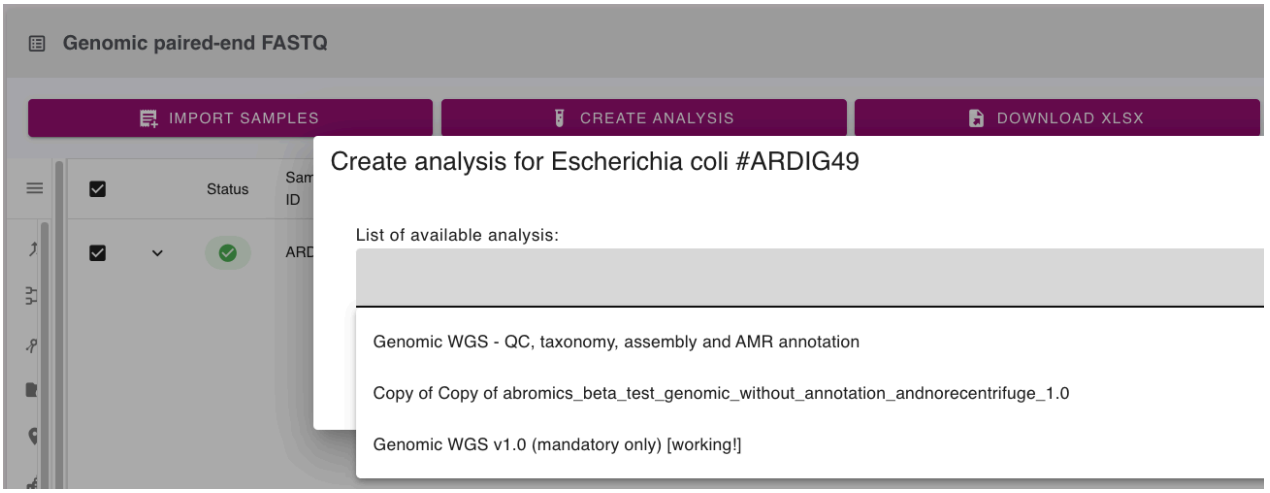


And 3 minutes later the workflow is done.

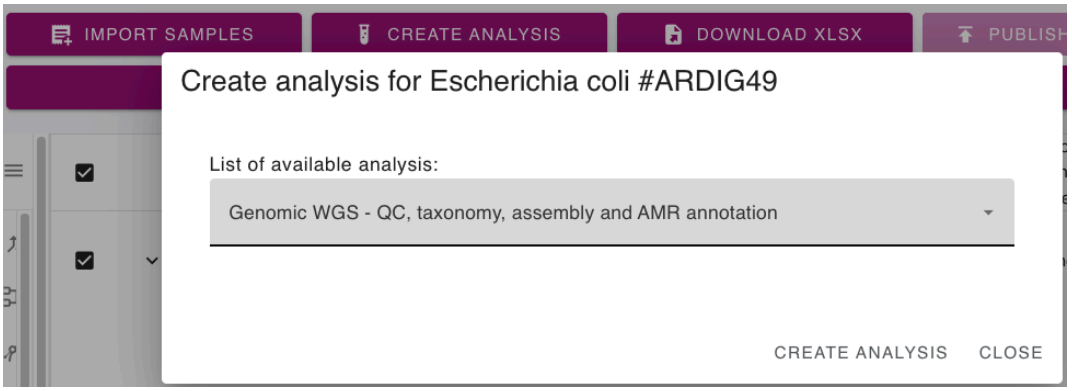
Different analyses workflows can be run on a sample. However, duplicate analyses of the same type are not allowed on the platform. If the user wishes to re-run a specific analysis, the old analysis must be deleted.



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.



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**, **Quality Control** 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.

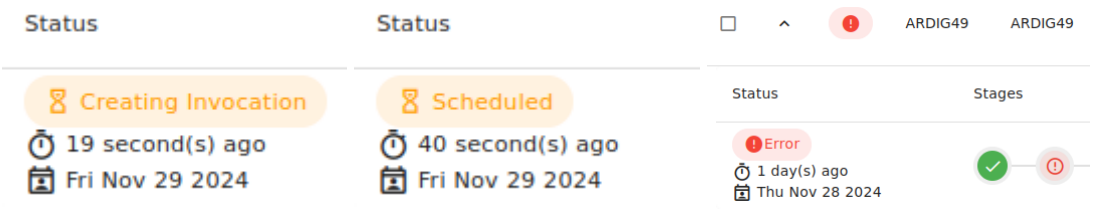
- ***Elapsed time***: The elapsed time since the analysis was created can be found directly below the status of the analysis.
- ***Created date***: The creation date of the analysis can be found below the elapsed time.

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).

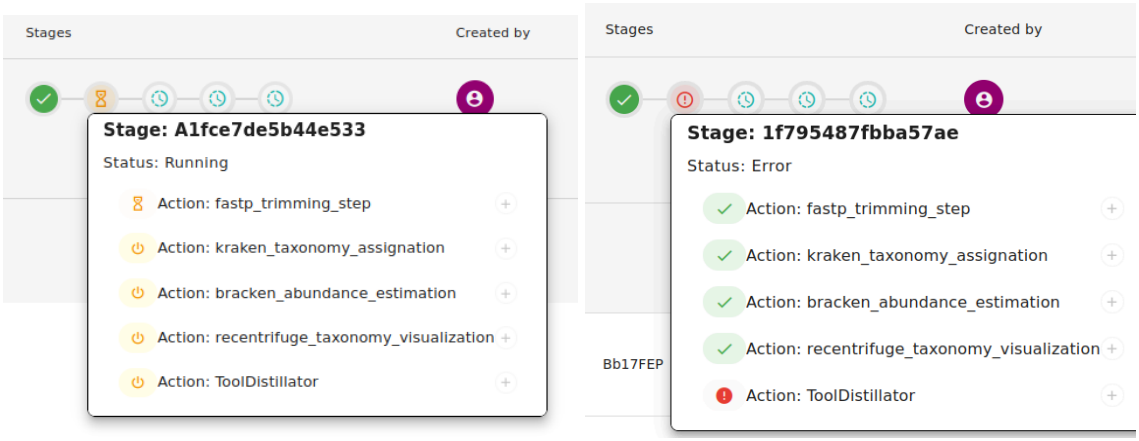
Here is a table of analysis stages and statuses:

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 - 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)

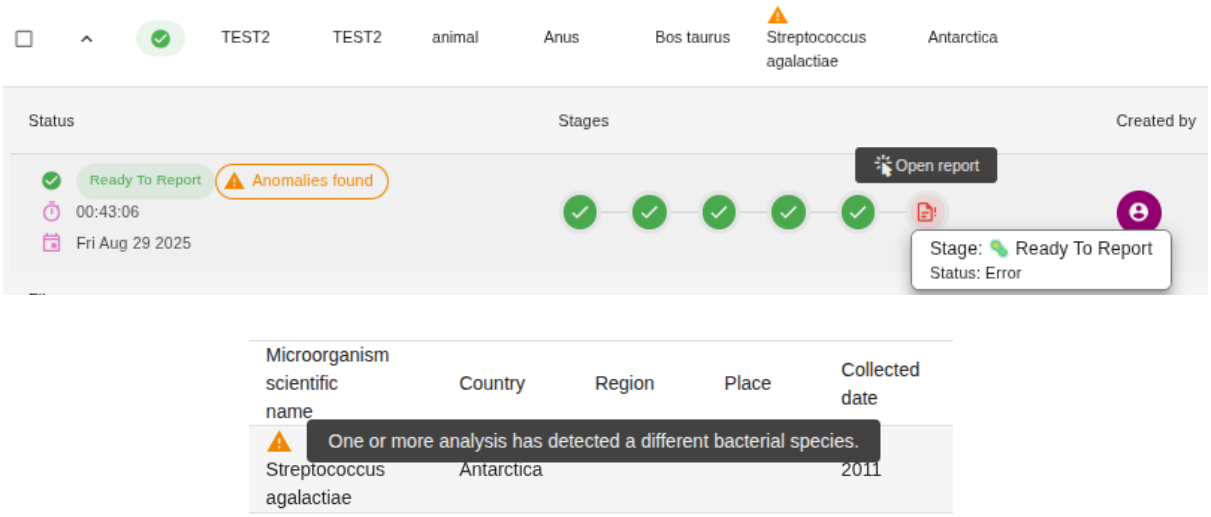
Here are some examples of stages and statuses displayed:



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



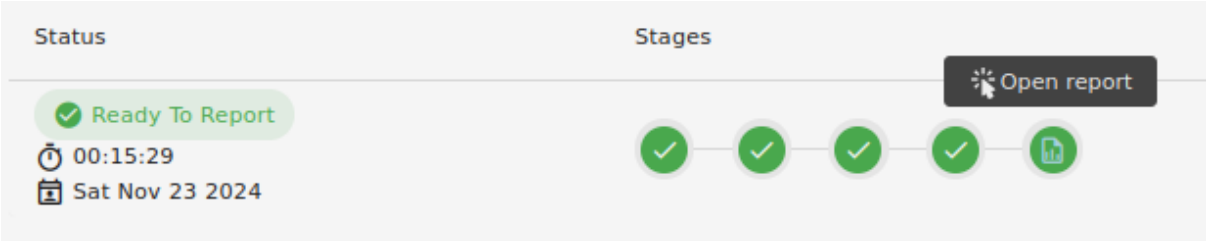
When an analysis fails during the "Scheduled" phase, an automatic retry of the analysis will be done. This will be done only once; however, if the analysis fails again, a project member can retry it manually or delete it.



If anomalies were found during the quality control of the results, warnings will be displayed for the user. In this case (see figures above), the workflow detected a different bacterial species and the user is advised to change the metadata to the detected value.

*Warning: Changing the taxonomy metadata will **not** relaunch the analysis with the new species.*

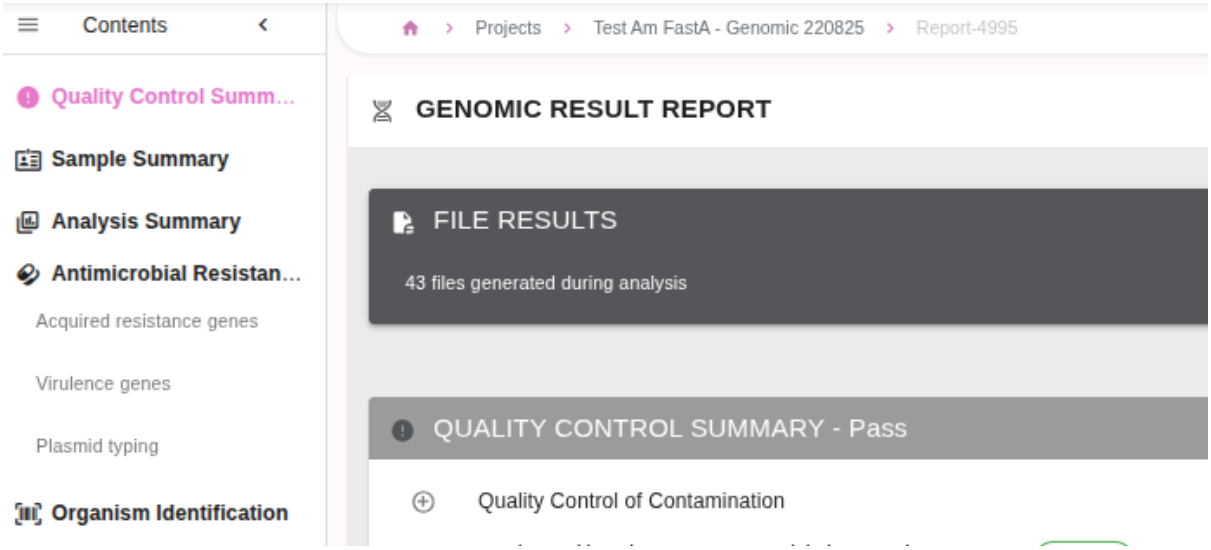
When an analysis is successful, project members can open the report which is automatically generated or delete the analysis.



If at least one analysis of a sample is successful, the project supervisor can publish the sample and its analyses, thus making the results public and accessible to every ABRomics user. Users cannot publish samples with analyses on which quality control has found anomalies (warnings or failures) or with analyses lacking any quality control. If the quality control only raised warnings (and no failures), the analysis will still be shown on the community database.

View a report

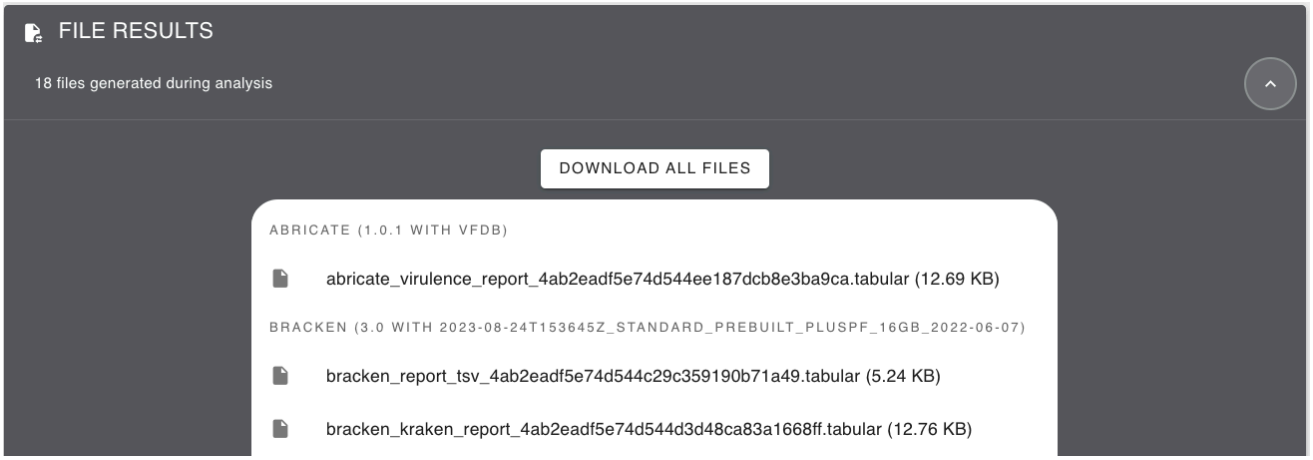
After clicking on the "Open report" button, you are redirected to the analysis report pages.
On the left side of this page a *Table of Content* is available to access easily the section you want without scrolling the overall report:



Every analysis report in the ABRomics 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 (for example "*Short paired-end read analysis to provide, assembly, typing, genome annotation and AMR gene detection* »)

Then the report will have the following sections:

- **FILE RESULTS**: Result files of tools used in the analysis. These files can be downloaded one by one or all together in an archive.



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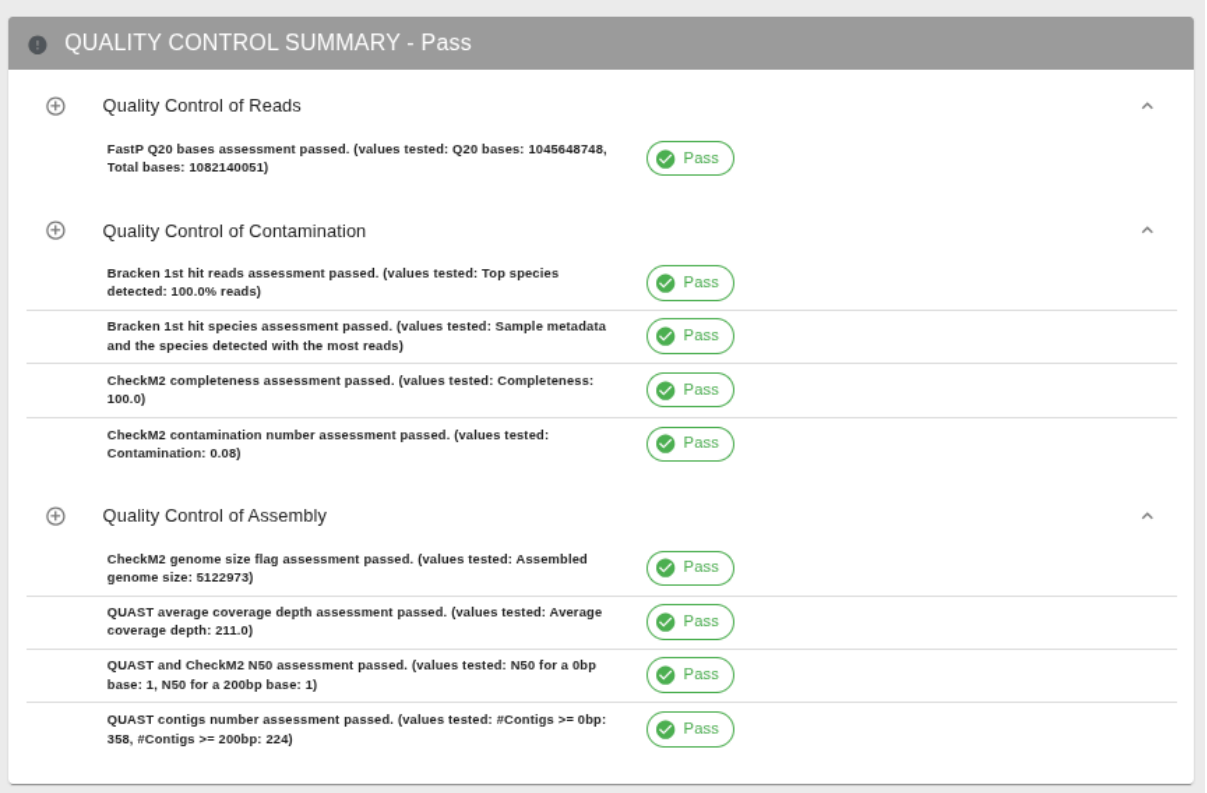
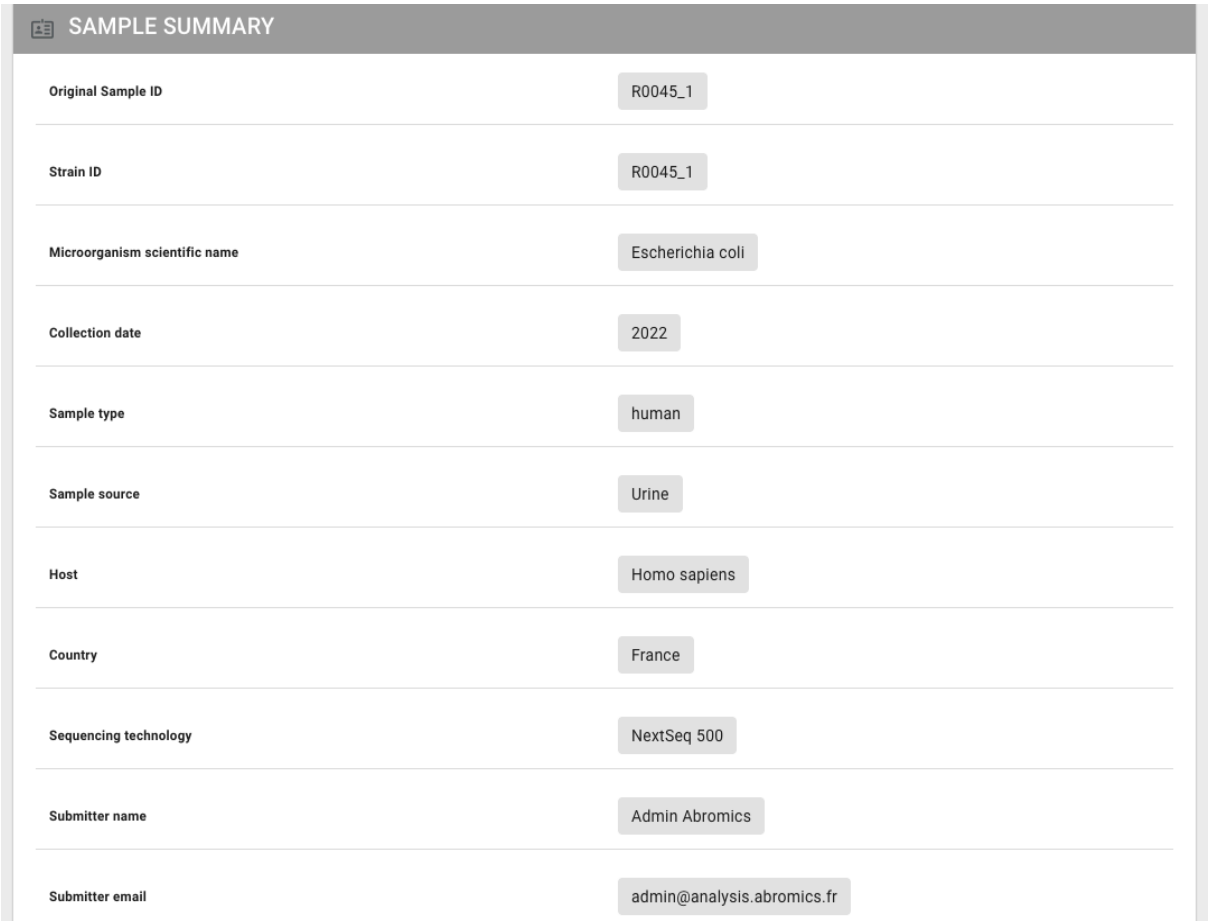
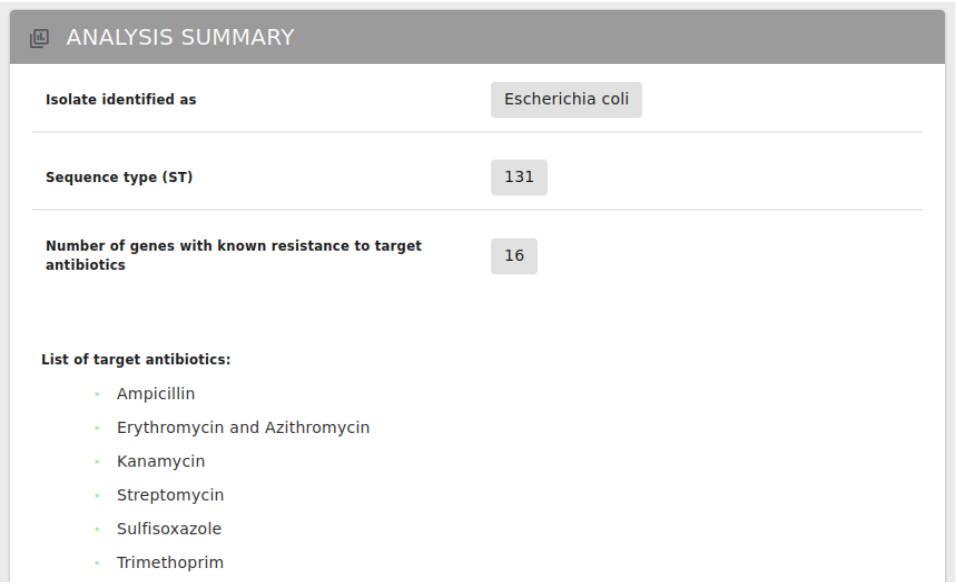
- **QUALITY CONTROL SUMMARY**: this section, splitted in subsections ("Quality Control of Reads" - only for Genomic FastQ, "Quality Control of Contamination" and "Quality Control of Assembly"), displays flags informing the user of any issues found within the workflow's results.



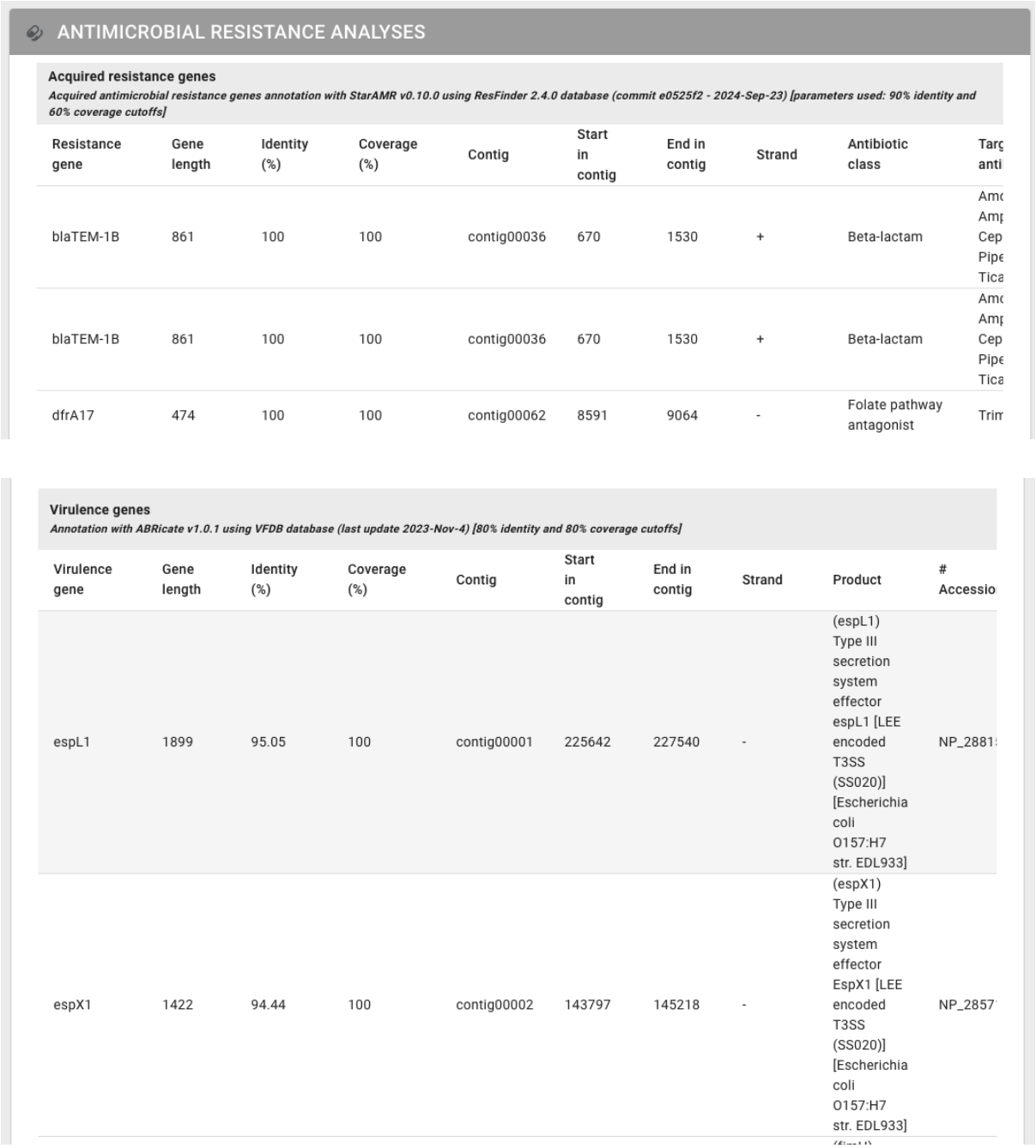
- **SAMPLE SUMMARY**: this section gives an overview of the sample metadata (given by the owner of the analyzed sample).



- **ANALYSIS SUMMARY**: this section gives a summary of key results of the analysis. This includes: the isolate identified, the number of genes with known resistance to target antibiotics, and the list of these target antibiotics.



- **ANTIMICROBIAL RESISTANCE ANALYSES**: this section has 3 sub-sections: acquired resistance genes, virulence genes and plasmid typing. 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

Items per page: 10 1-4 of 4

- **ORGANISM IDENTIFICATION:** this section is only available with the genomic WGS paired-end FASTQ template. It shows the results of taxonomic assignment with Kraken2, the detected Sequence Type and its associated MLST scheme and MLST species found.

ORGANISM IDENTIFICATION

Tool description missing.

Species name	NCBI ID	Fraction of reads
Escherichia coli	562	0.94254

MORE...

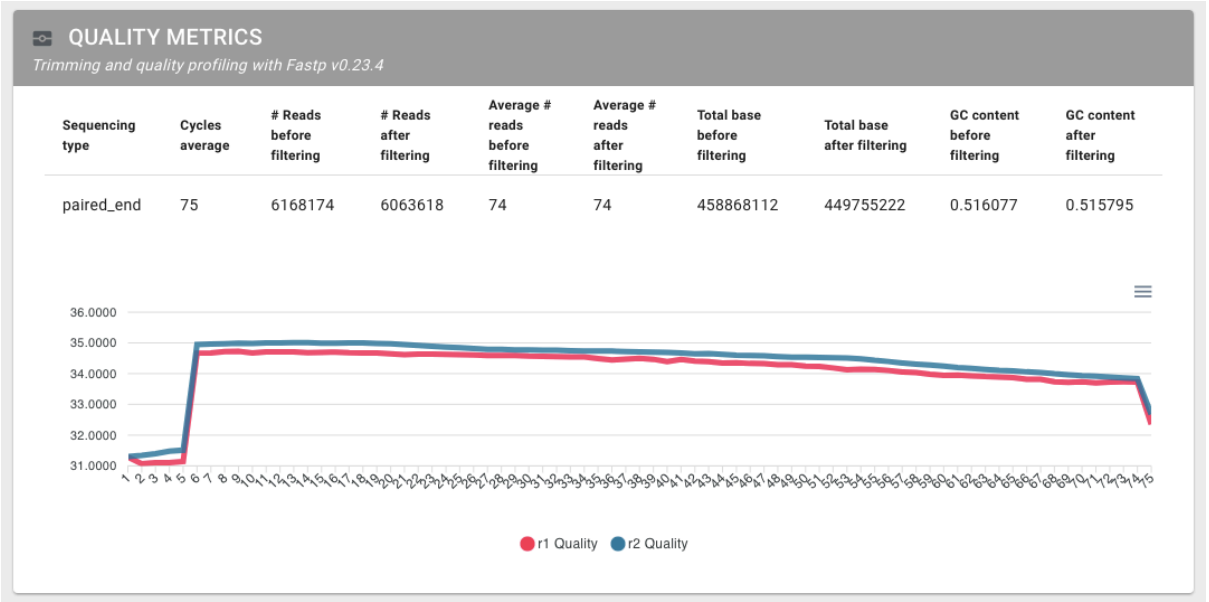
Strain typing: mlst v2.23.0

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

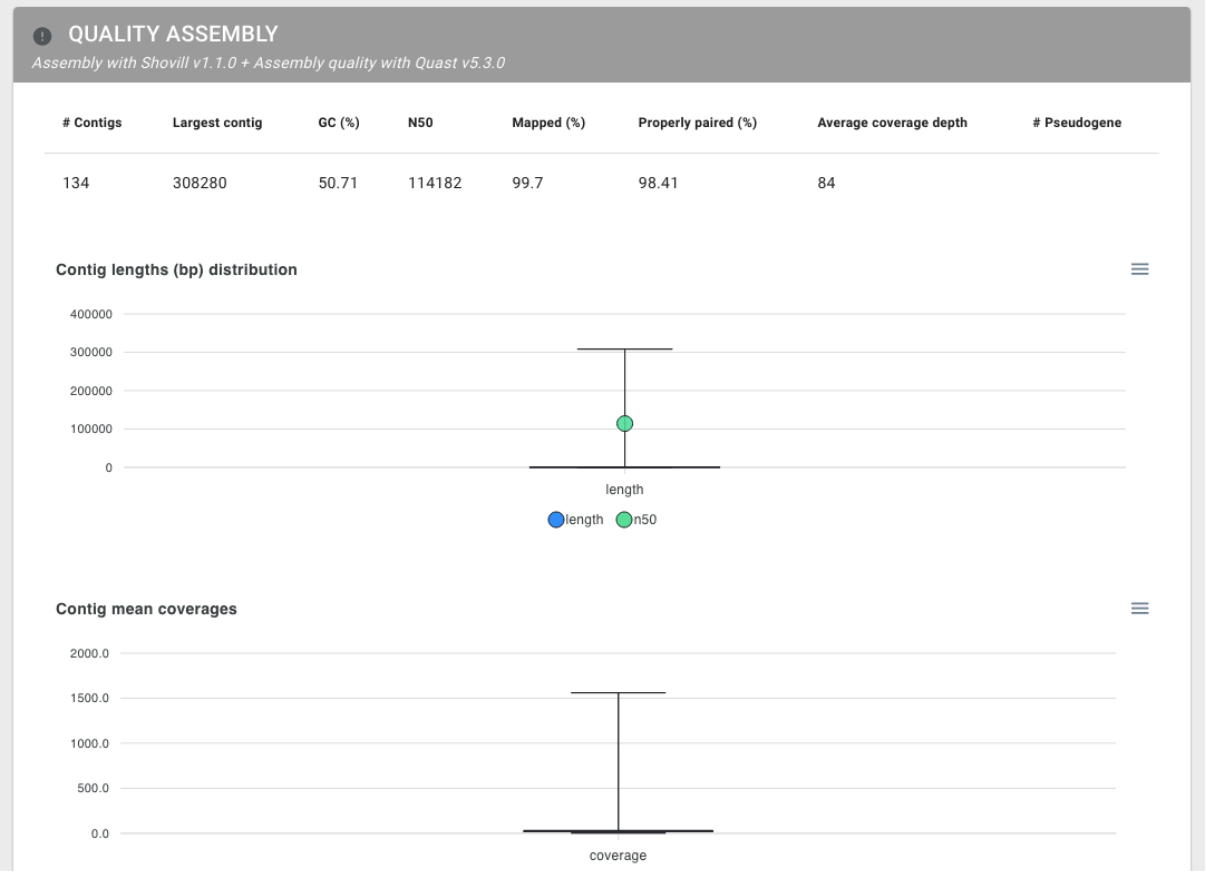
Scheme

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

- **QUALITY METRICS**: 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 as follow:



- **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.

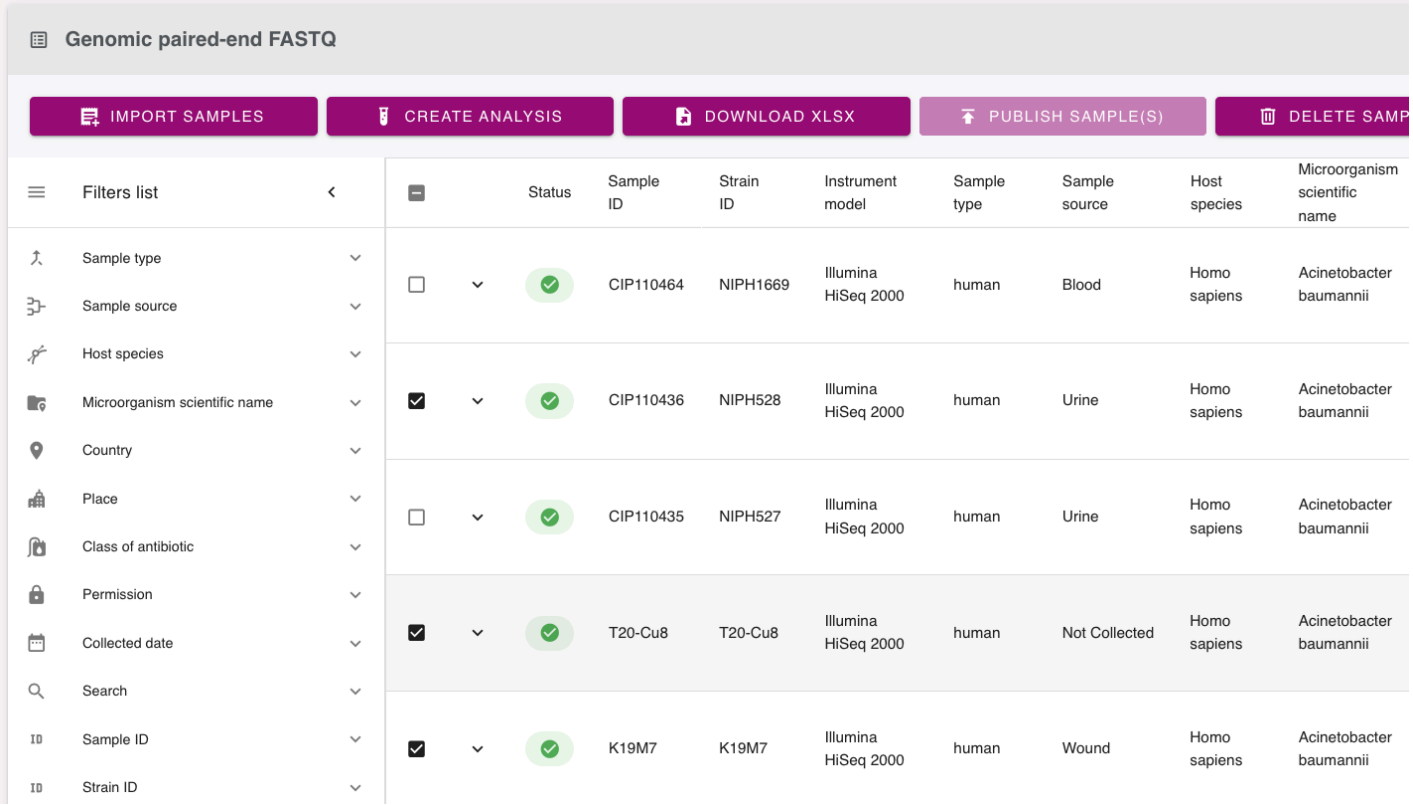


EXPLORE RESULTS IN A PROJECT

Filter, download 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 .xlsx file of the results of selected samples. As of ABRomics v1.2, the .xlsx contains 7 sheets with, respectively, information about the sheets themselves in **Sheet info**, the sample **Metadata**, **MLST** results, **Resfinder** results, **Virulence** results, **Plasmidfinder** results, **Functional Annotation** results, **Taxonomies Detected** and quality control (**Read QC**, **Assembly QC**, and general **Quality Control Flags**).
- Only the project supervisor can publish or delete samples.

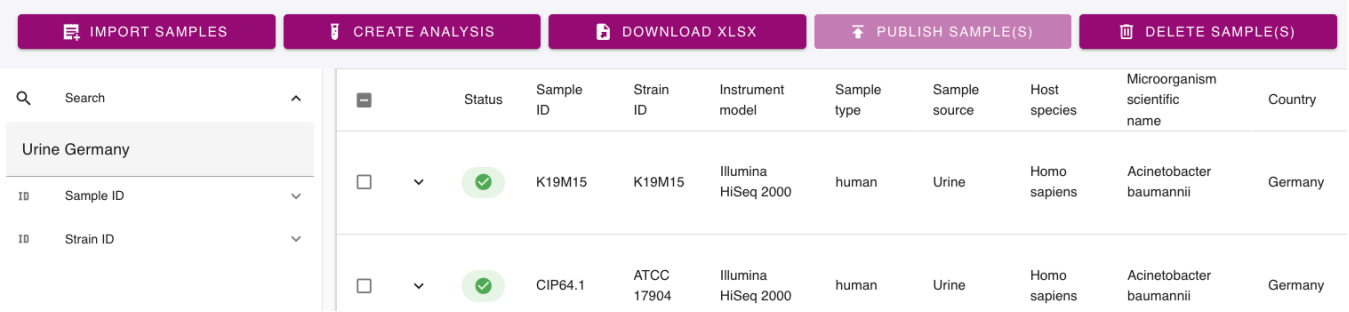


You can select samples either one by one by clicking on the checkbox at the beginning of a row in the sample collection table or by choosing all samples shown on the page by clicking on the checkbox at the left of the column titles.

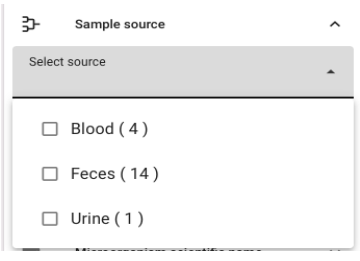
You can filter out samples in the sample collection table by using the filter menu ("Filter list" on the left).

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".
- or by using the free input "Search" bar which will search the entered keyword(s) 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". In the example below 2 *A. baumannii* genomes of Sample source=Urine AND Country=Germany have been found using Search "Urine Germany".



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.



[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.

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 »

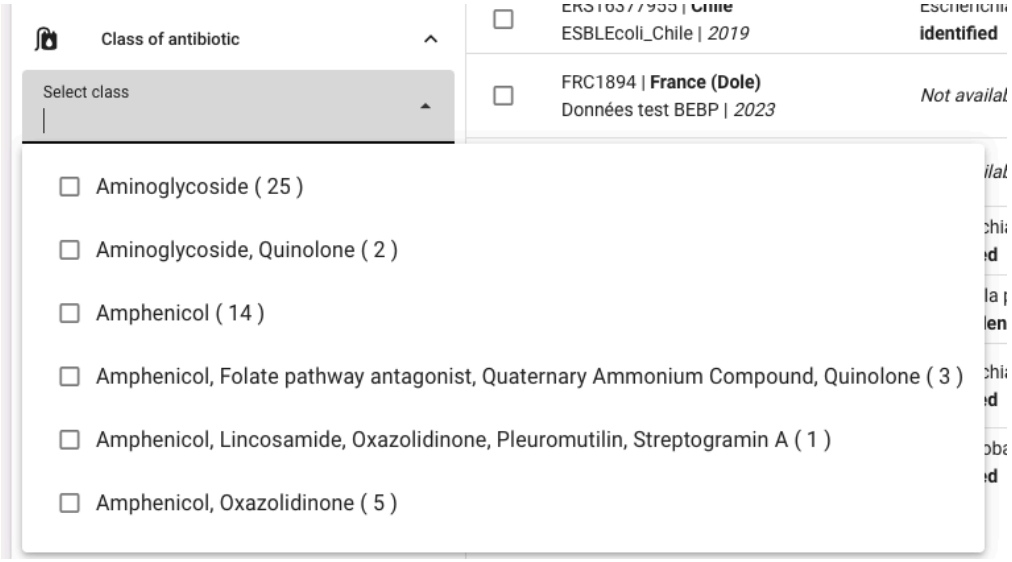
If you filter by selecting the 2 values independently (check box behind « Aminoglycoside » and check box behind « Quinolone »), this will return these results:

« *Resistance genes known to target Aminoglycoside class antibiotics only* »

and

« *Resistance genes known to target Quinolone class antibiotics only* »

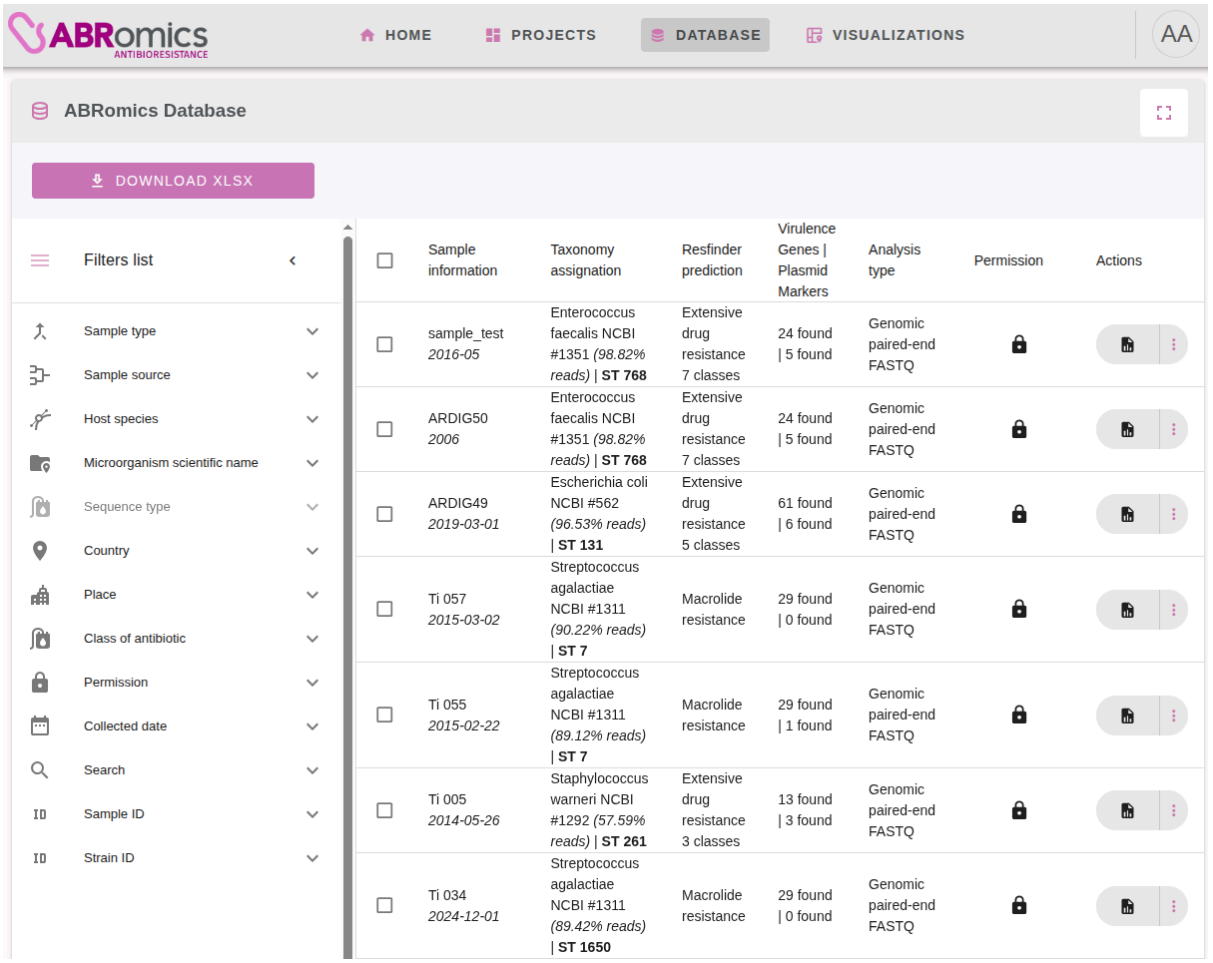
To illustrate this, the following example shows that 2 results match the filter criterion « Aminoglycoside, Quinolone». These 2 results are not part of the 25 results matching the « Aminoglycoside » filter criterion. In total, the database contains 27 results with at least one resistance gene known to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



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.

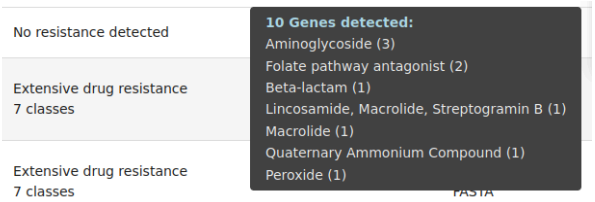


There are currently 2 different ways of seeing results on ABRomics, either a "List" view on the current "DATABASE" page or a "Map" view accessible on the "VISUALIZATIONS" page. The extend button "[ ]" at the very far right enables you to maximize and minimize the results table.

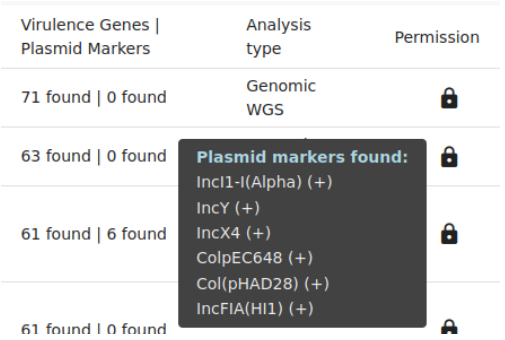
Here, each result (row in the table) is described with 6 columns:

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

- **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;



- **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;

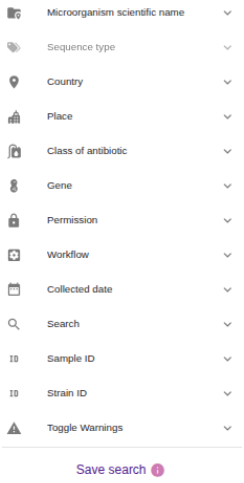


- **Analysis type**: indicates the type of template associated with the project from which the sample was uploaded;

- **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:

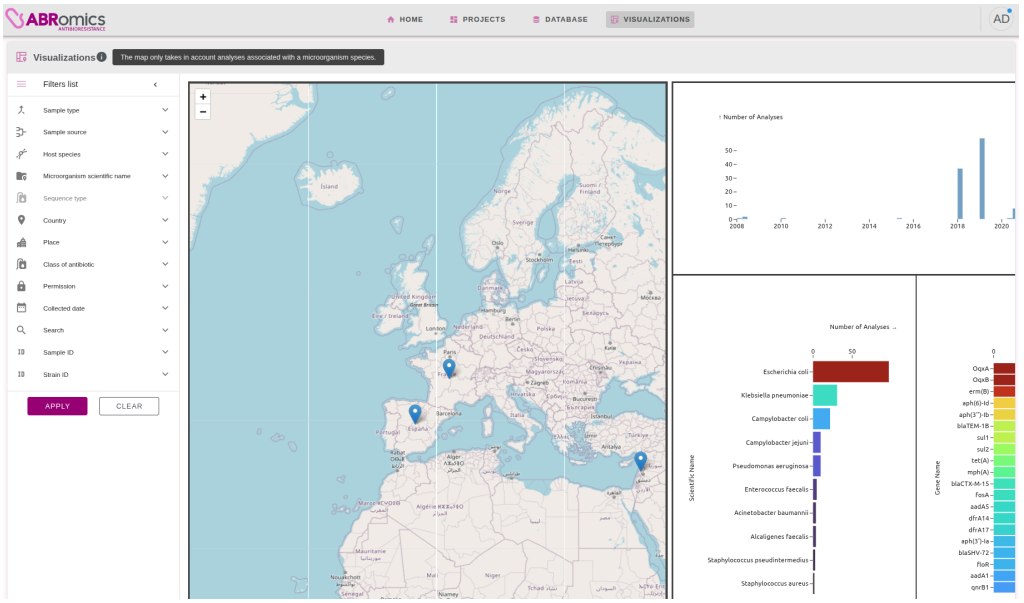


- You can filter out according to sample metadata: "Sample type", "Sample source", "Host species", "Country", "Place", "Collected date", "Sample ID", "Strain ID";

- 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".

- 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".

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 on new analyses added to the community database.

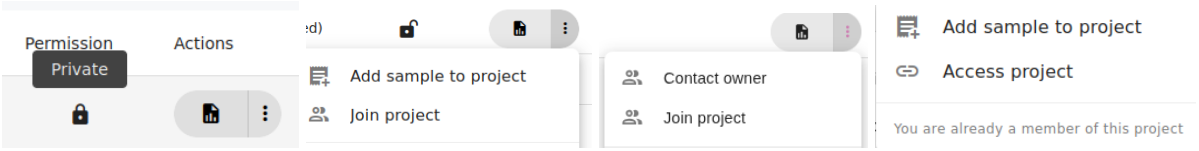


[4] The filter "Microorganism scientific name", in this case, corresponds to the name of the taxonomy chosen by the user who completed metadata information and uploaded the sample.

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

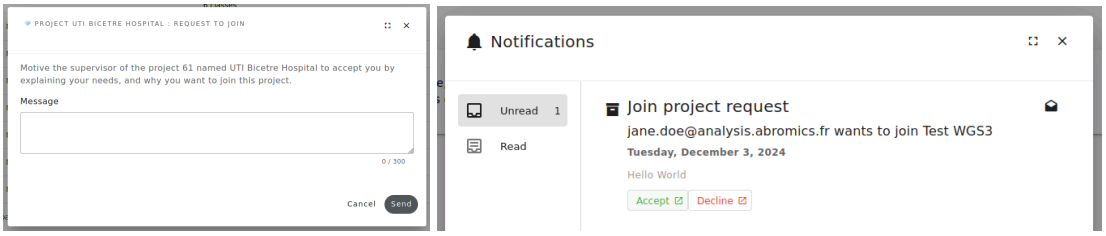
The "map" view in "VISUALIZATIONS", the third main page of ABRomics, shows the locations of samples according to their "country" metadata. Hovering over a country will highlight the corresponding number of samples and the three most represented antibiotic classes in the detected AMR genes of these samples 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, join a project, add a public sample to a project



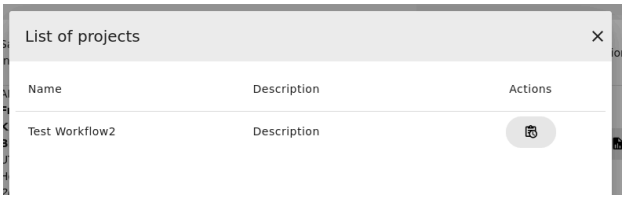
Any logged-in user can access a "light" version of an analysis report (for privacy, these light reports do not show any information about the provider of the sample). If a sample was made public by the supervisor of the project the sample was imported in, then other users can access the "full" report 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 already sent a request, you will not be able to spam messages.



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.



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.

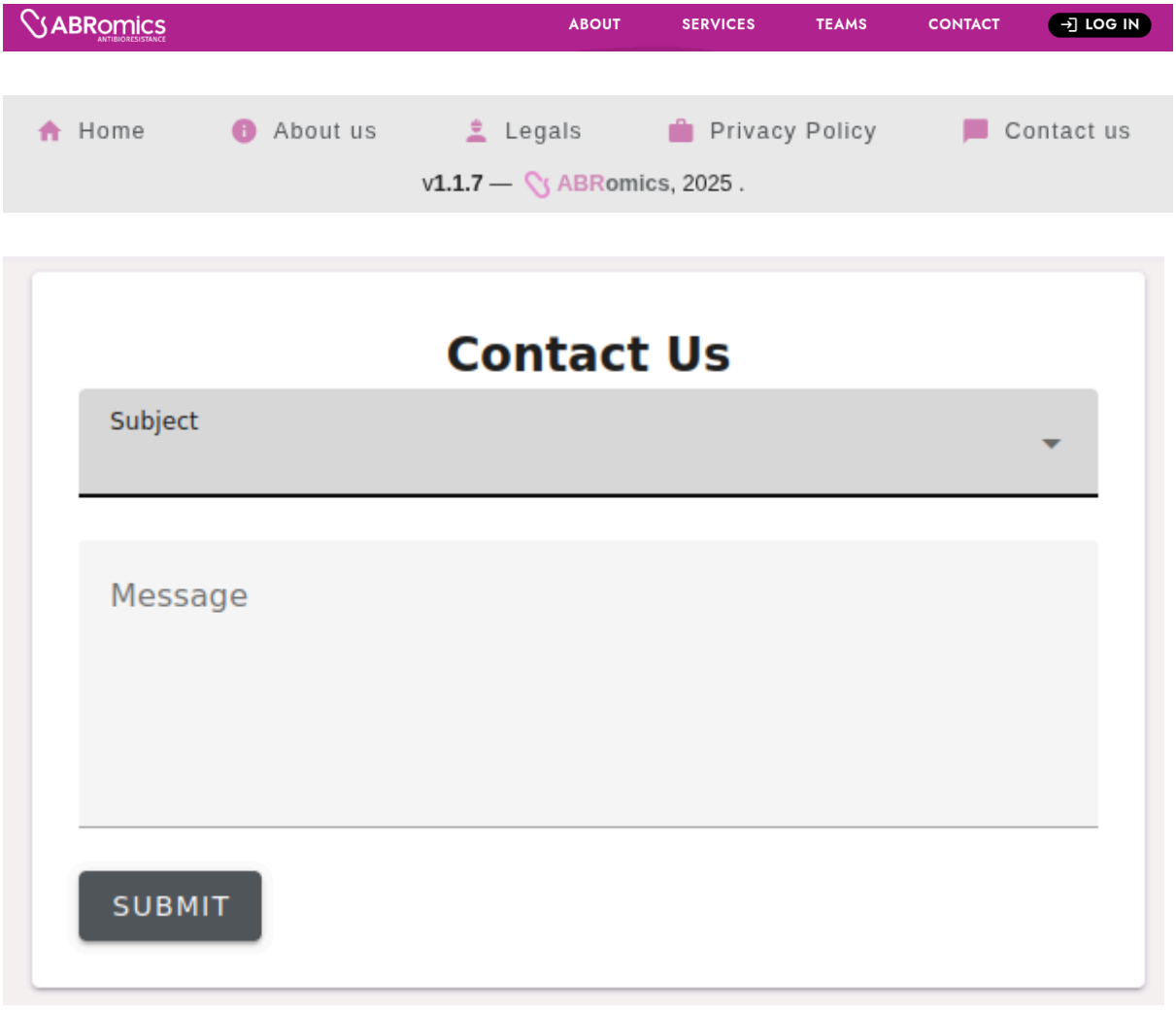
CONTACT US

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 accessible on the footer. The footer appears on every page of ABRomics analyses.

If logged out, you can access the contact page with the "CONTACT" button on the navigation menu.

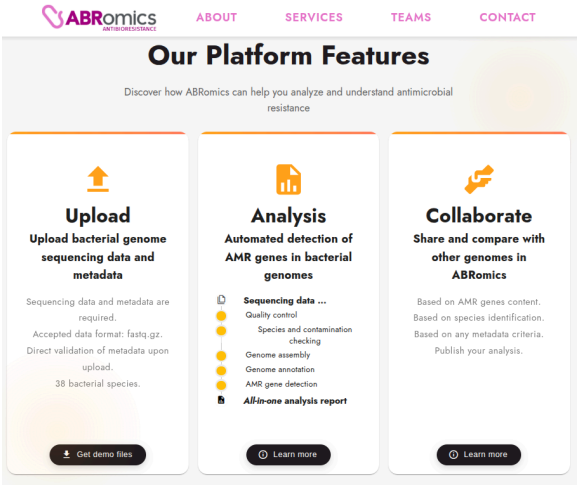
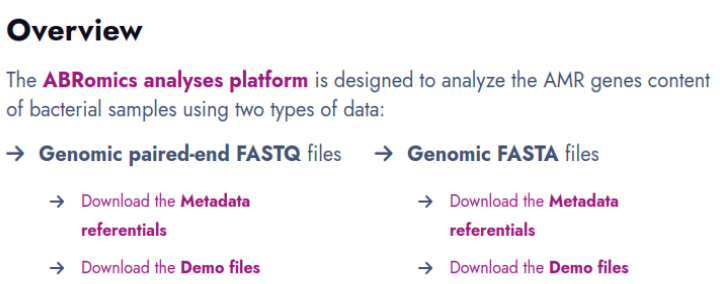
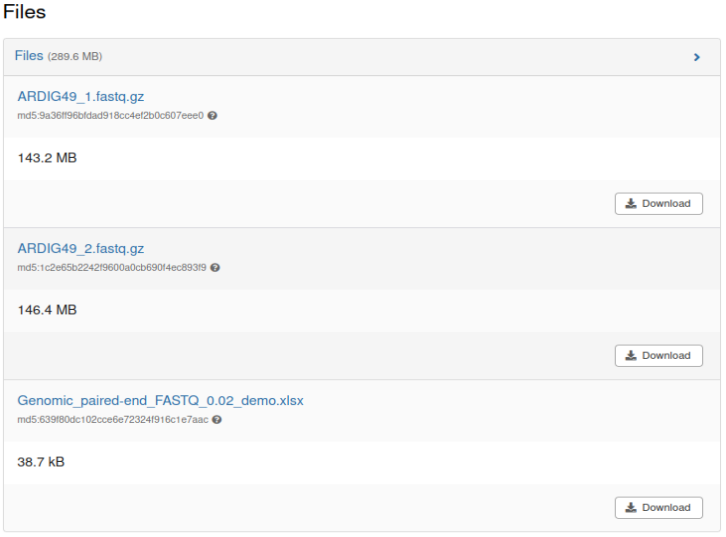


You can select a subject between 4 choices: "Bug", "Feature" (any feature you would like to see on ABRomics), "Account creation" (if you have any issues when creating your account) and "Other".

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**.	
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)	
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**.	

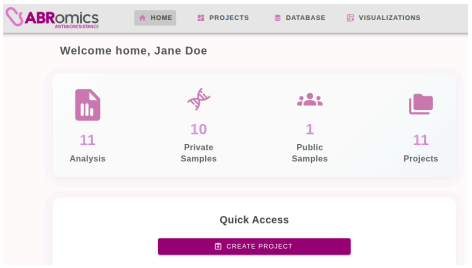
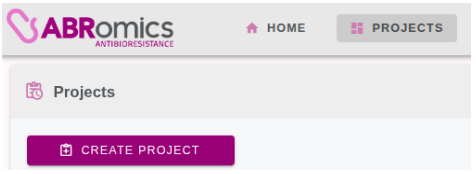
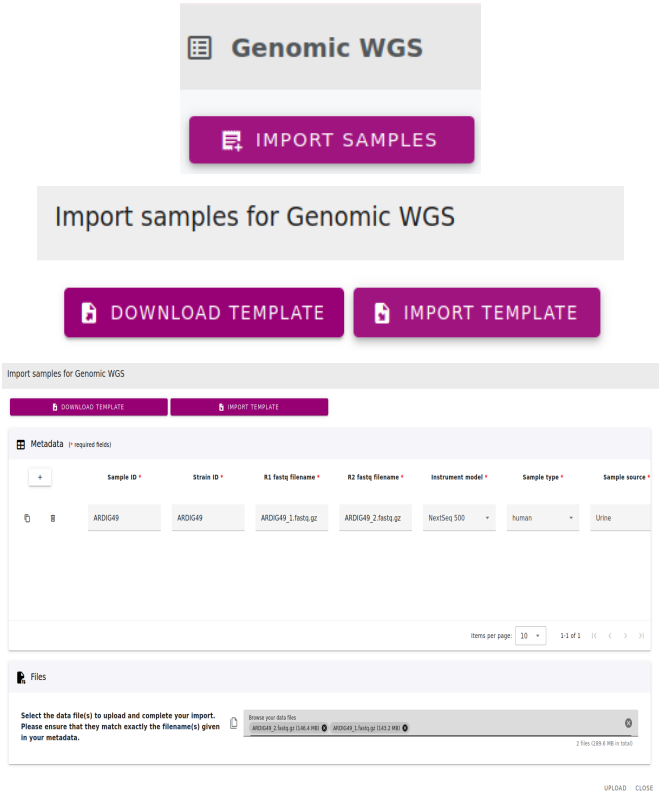
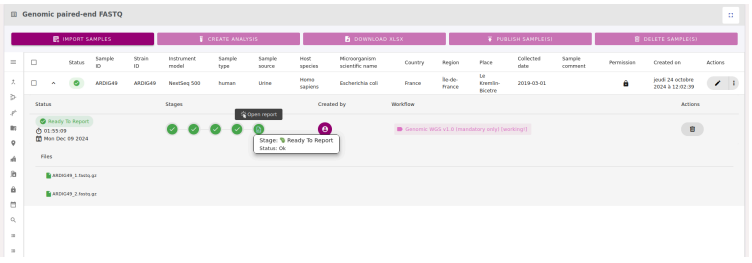
Follow the steps described in section **"PROJECTS & PROJECT MANAGEMENT"** to create your demo project* **Select a template associated with the type of demo files (ex: a WGS template for fastq.gz demo files).*	1  OR 2 
Follow the steps described in section **"Upload a sample & metadata validation"** and 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.	 *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 🎉	

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/