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# **ABRomics analyses platform**

*A One Health Antimicrobial Resistance Analysis Service*

## **User Manual (UM)**

2025-09-18

Version 1.2.0

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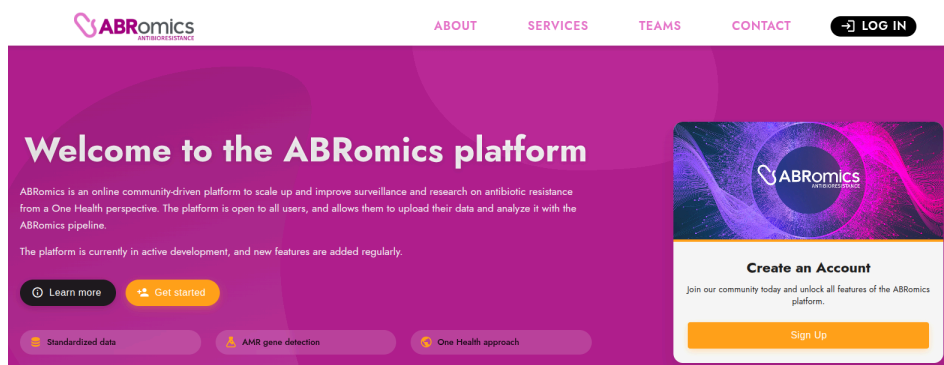
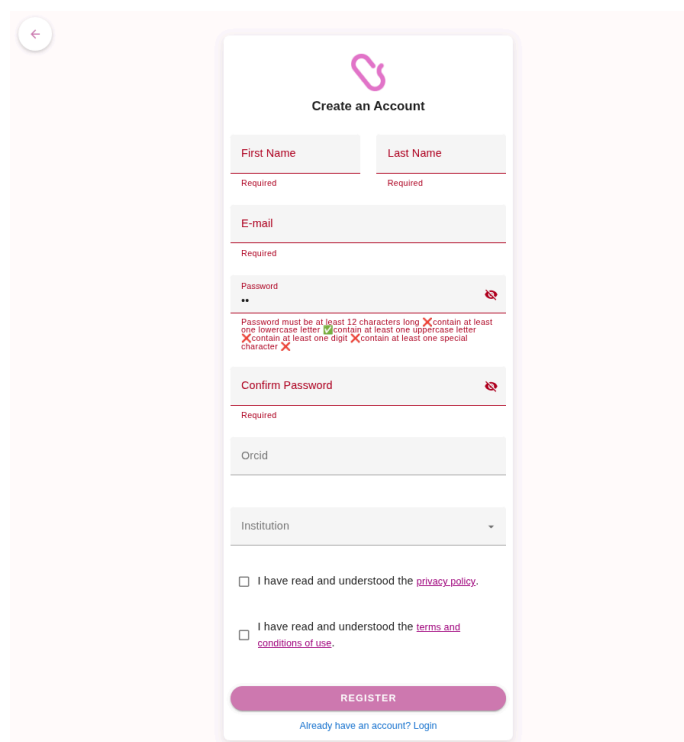
## VERSION HISTORY

| VERSION<br>(of ABRomics analyses) | UPDATES  | DATE       |
|-----------------------------------|--|------------|
| <b>1.0.0</b>                      | Document creation  | 2024-12-10 |
| <b>1.1.0</b>                      | Added tutorial on how to use demo files (FASTQ),<br>Removed publishing feature, Updated analysis report section                                | 2025-01-17 |
| <b>1.1.7</b>                      | Added new landing and home page information,<br>Updated "EXPLORE RESULTS OF THE COMMUNITY USING THE ABROMICS DATABASE" section and screenshots | 2025-06-20 |
| <b>1.2.0</b>                      | 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.

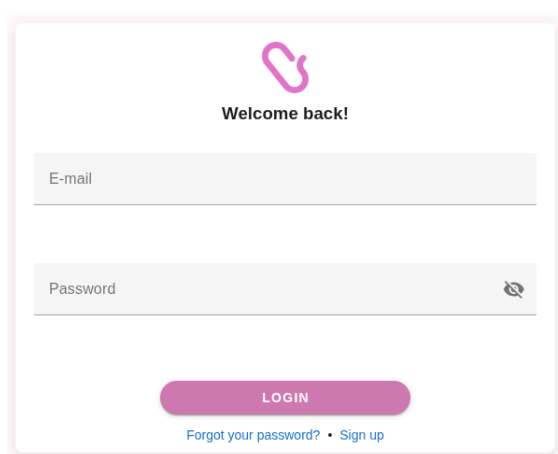
An account confirmation email will be sent to you: follow the link in the email to activate your account.

**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@groupe.france-bioinformatique.fr](mailto:abromics-support@groupe.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.

The screenshot shows the ABRomics login interface. At the top, there is a pink logo and the text "Welcome back!". Below this, there are two input fields: "E-mail" and "Password". The "Password" field has a small eye icon to its right. At the bottom, there is a pink "LOGIN" button. Below the button, there are two links: "Forgot your password?" and "Sign up".

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 screenshot displays the ABRomics user interface. At the top, there is a navigation bar with tabs for HOME, PROJECTS, DATABASE, and VISUALIZATIONS. A user profile dropdown menu is open on the right, showing the user's name 'J D', email 'jane.doe@france-bioinformatique.fr', a toggle for settings, and links for Profile, Notifications, and Logout.


The main content area starts with a 'Welcome home, J D' message. Below this are three summary cards: '1 Analysis', 'N/A Private Samples', and '1 Public Samples'. A 'Quick Access' section features a prominent 'CREATE PROJECT' button. The 'Latest Analyses' section includes a table with the following data:

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

The 'Alerts' section, titled 'Saved searches (database change count is updated daily)', contains another table:

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

The User menu 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).


**Profile**

**Email**

**Mailing preferences** (do you want to receive scheduled summaries of the status of analyses you have launched in your projects?)  
☒ Yes  
☐ No  
  
 Select preferred schedule

**Information**  
**First name**  
  
  
**Last name**  
  
  
**ORCID**  
  
  
**Institution**

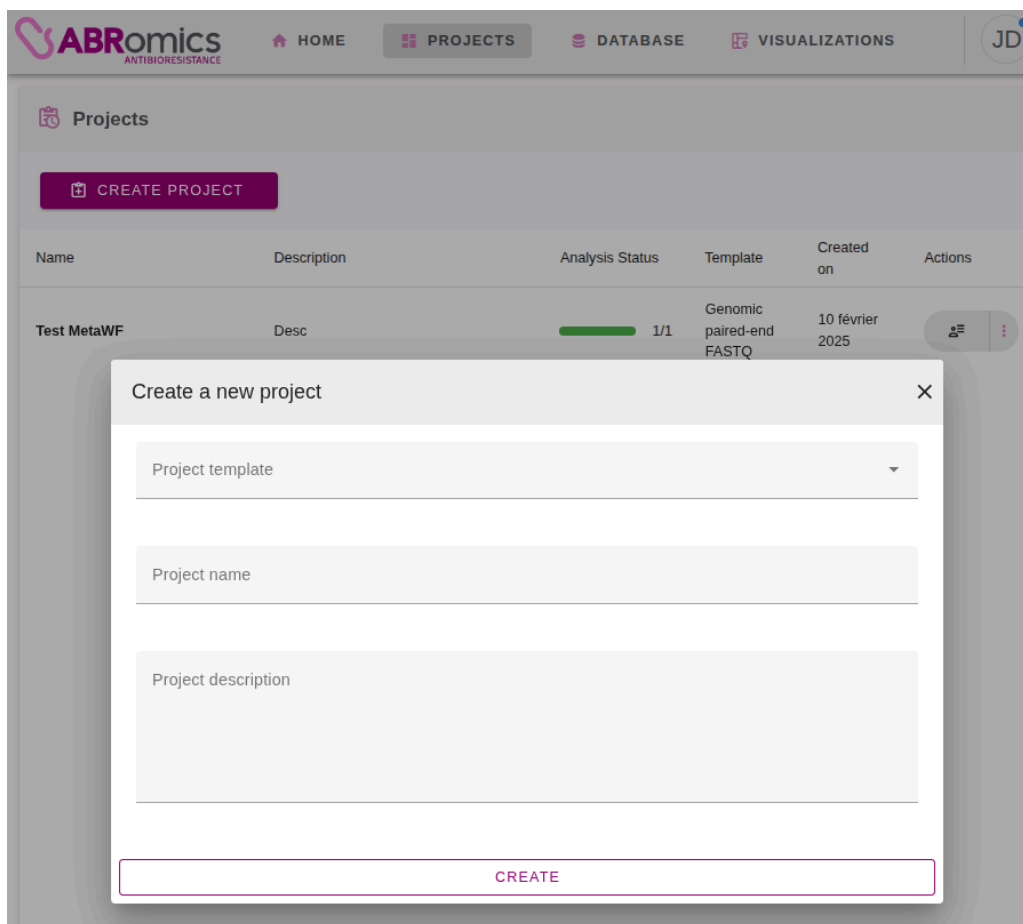
You can also decide to delete your account. A pop-up will appear and you must confirm your choice since this action will permanently delete all the projects you are supervising.

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.

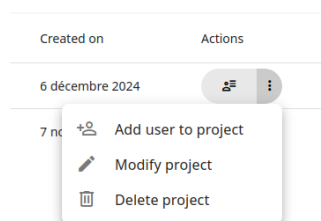
In essence, a template determines the type of results collection table associated with a project, influencing both the inputs (metadata, file type) and outputs (analysis results). It establishes the framework for managing input data and the range of analytical processes available in the project.

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 | <ul style="list-style-type: none"> <li>R1 fastq file (.fastq.gz, .fq.gz, fastqsanger.gz)</li> <li>R2 fastq file (.fastq.gz, .fq.gz, fastqsanger.gz)</li> </ul> | Genomic paired-end FASTQ |
| Assembly data   | <ul style="list-style-type: none"> <li>.fasta files</li> </ul>   | Genomic FASTA            |

After creating a project, you are now the supervisor of the project and you may add other users<sup>1</sup> 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.

<sup>1</sup>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 | <div style="width: 100%;"></div> 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)

Genomic paired-end FASTQ

IMPORT SAMPLES

CREATE ANALYSIS

DOWNLOAD XLSX

PUBLISH SAMPLE(S)

DELETE SAMPLE(S)

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

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”

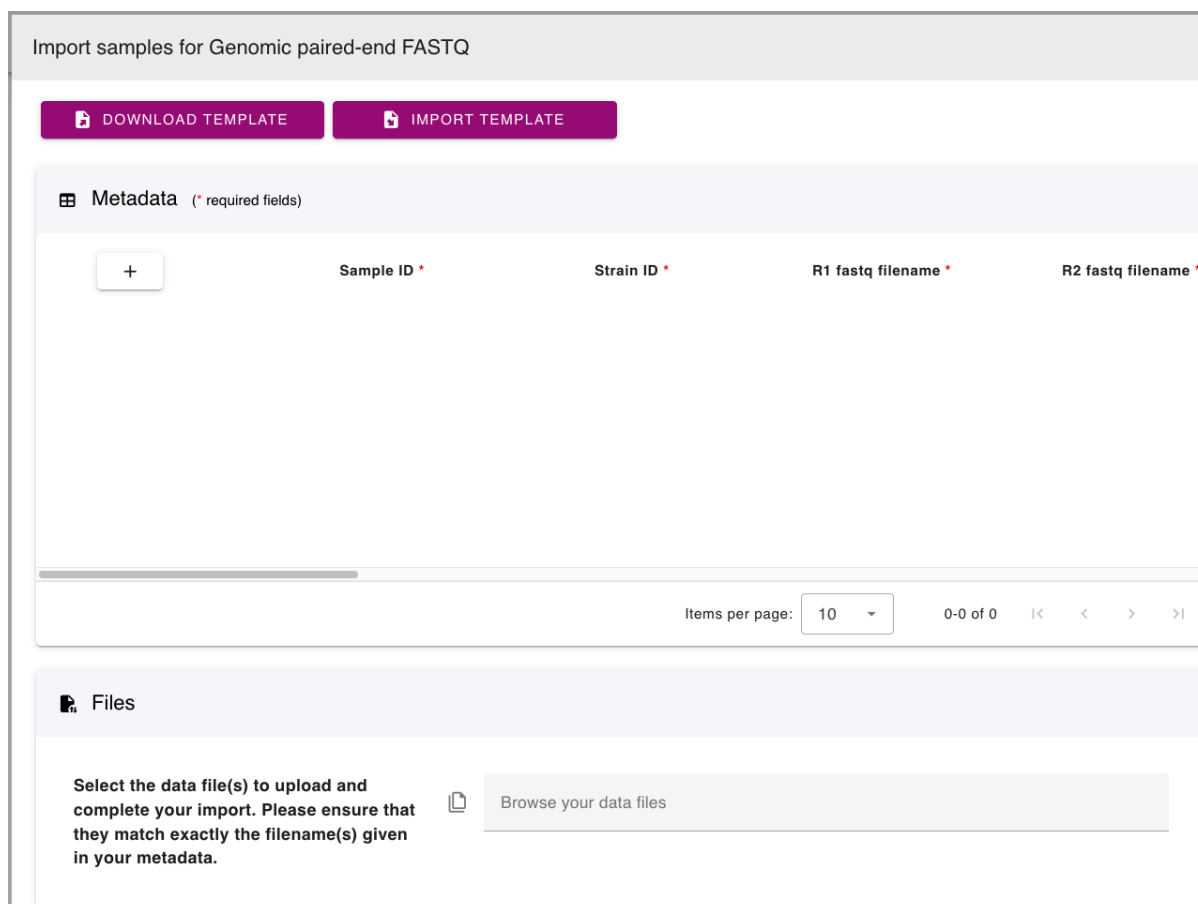
Specific actions for a given sample can be done with the “Actions” button at the right end of the row (see below for more description of these Actions).

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:



Import samples for Genomic paired-end FASTQ

[DOWNLOAD TEMPLATE](#) [IMPORT TEMPLATE](#)

**Metadata** (\* required fields)

|   | Sample ID * | Strain ID * | R1 fastq filename * | R2 fastq filename * |
|---|-------------|-------------|---------------------|---------------------|
| + |             |             |                     |                     |

Items per page: 10 0-0 of 0 |< < > >|

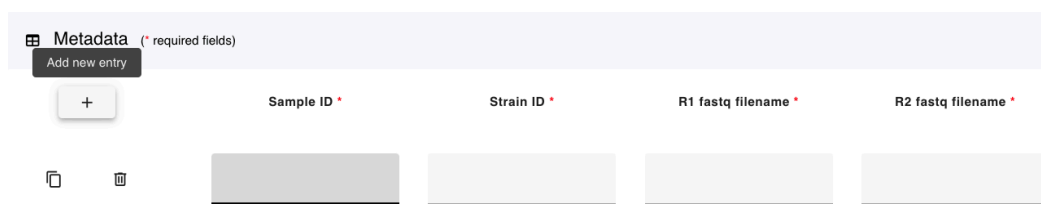
**Files**

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](#)

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:



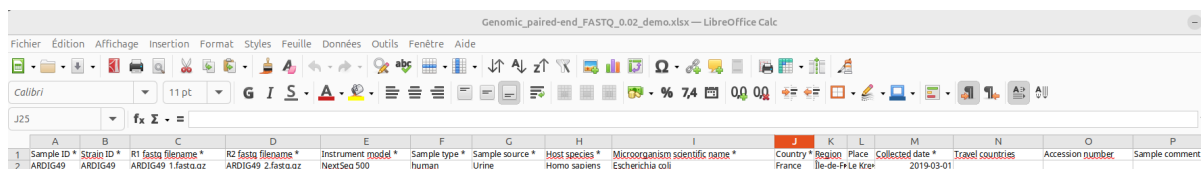
**Metadata** (\* required fields)

Add new entry

|   | Sample ID * | Strain ID * | R1 fastq filename * | R2 fastq filename * |
|---|-------------|-------------|---------------------|---------------------|
| + |             |             |                     |                     |

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 :

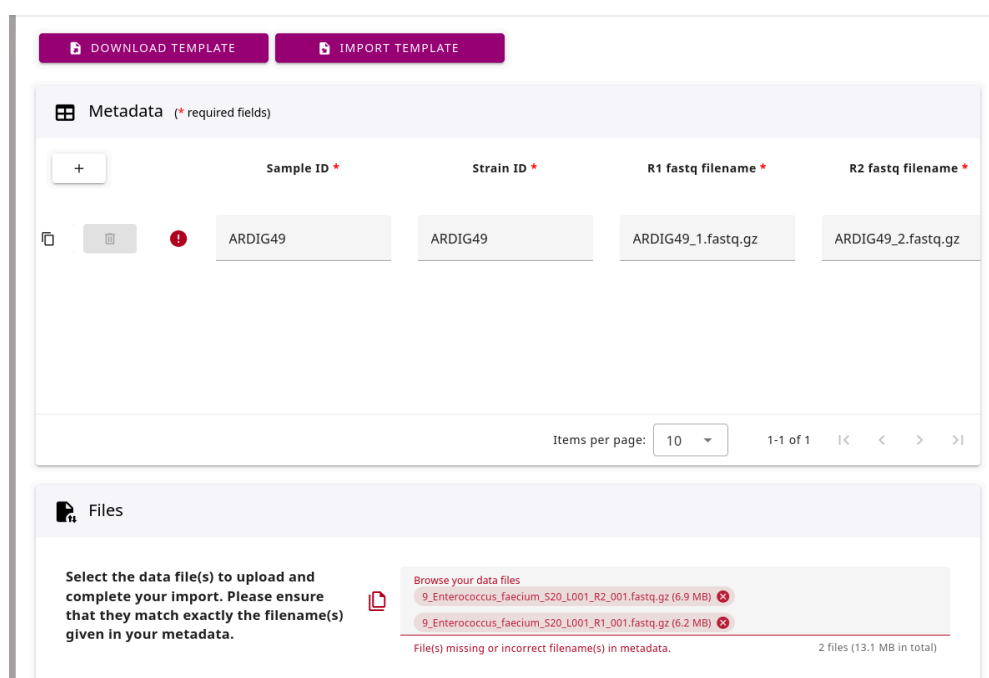


| A           | B           | C                   | D                   | E                  | F             | G               | H              | I                               | J         | K         | L          | M                | N                | O                | P              |
|-------------|-------------|---------------------|---------------------|--------------------|---------------|-----------------|----------------|---------------------------------|-----------|-----------|------------|------------------|------------------|------------------|----------------|
| 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-Fr | Le Kremlin | 2019-03-01       |                  |                  |                |

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.**



**DOWNLOAD TEMPLATE** **IMPORT TEMPLATE**

**Metadata** (\* required fields)



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

Items per page: 10 1-1 of 1 < >

**Files**

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

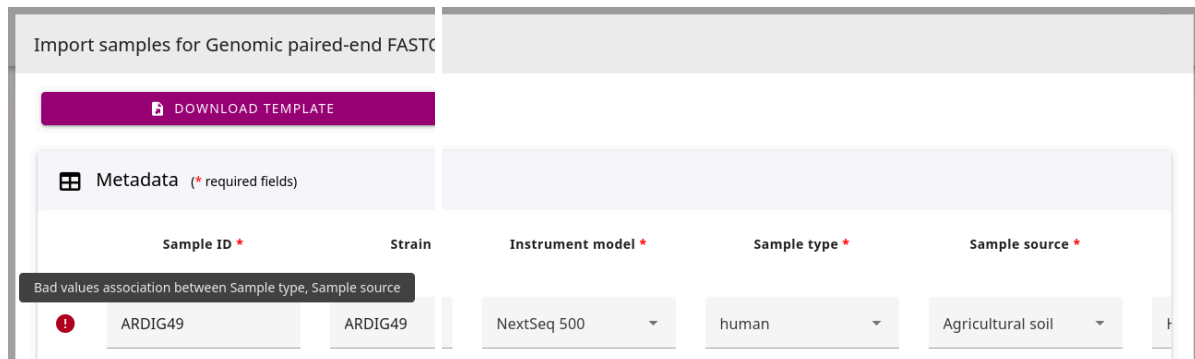
Browse your data files

- 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)

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”.



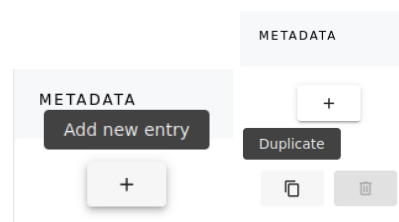
Import samples for Genomic paired-end FASTQ

[DOWNLOAD TEMPLATE](#)

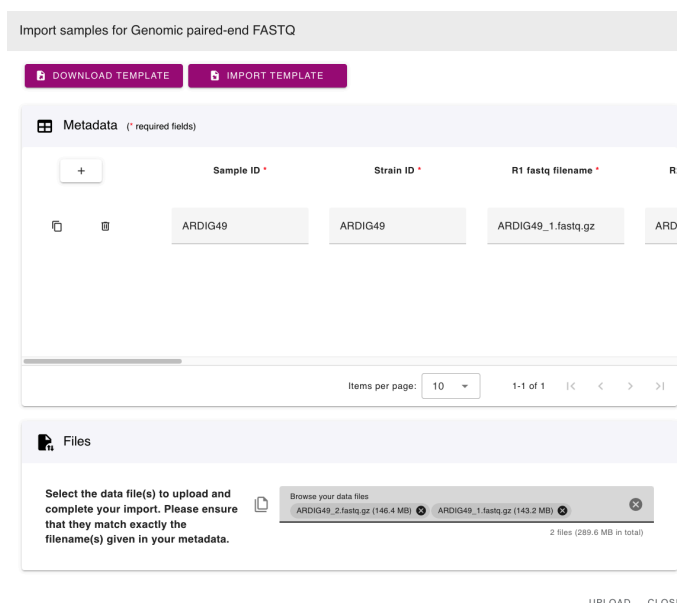
**Metadata** (\* required fields)

| Sample ID *   | Strain  | Instrument model * | Sample type * | Sample source *   |
|---|---------|--------------------|---------------|-------------------|
| Bad values association between Sample type, Sample source |         |                    |               |                   |
| ARDIG49   | ARDIG49 | NextSeq 500        | human         | 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.



Import samples for Genomic paired-end FASTQ

[DOWNLOAD TEMPLATE](#) [IMPORT TEMPLATE](#)

**Metadata** (\* required fields)

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

Items per page: 10 1-1 of 1

**Files**

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

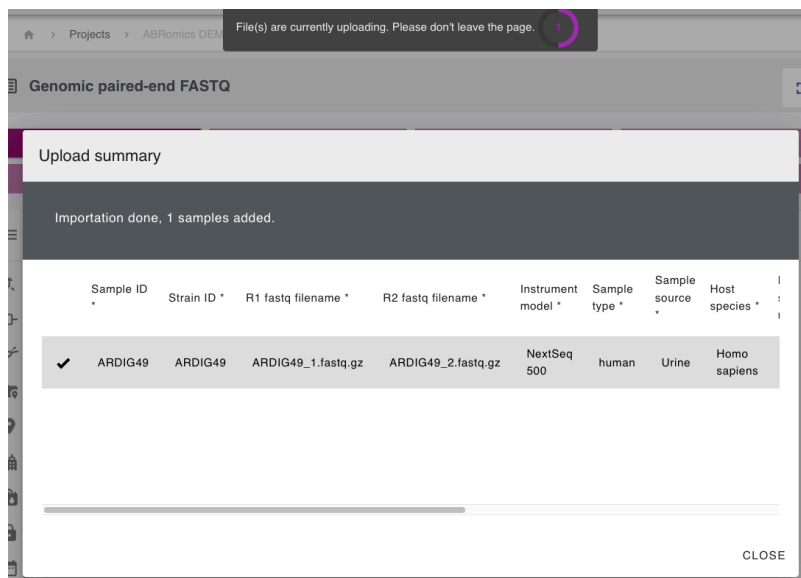
Browse your data files

ARDIG49\_2.fastq.gz (146.4 MB) ARDIG49\_1.fastq.gz (143.2 MB)

2 files (289.6 MB in total)

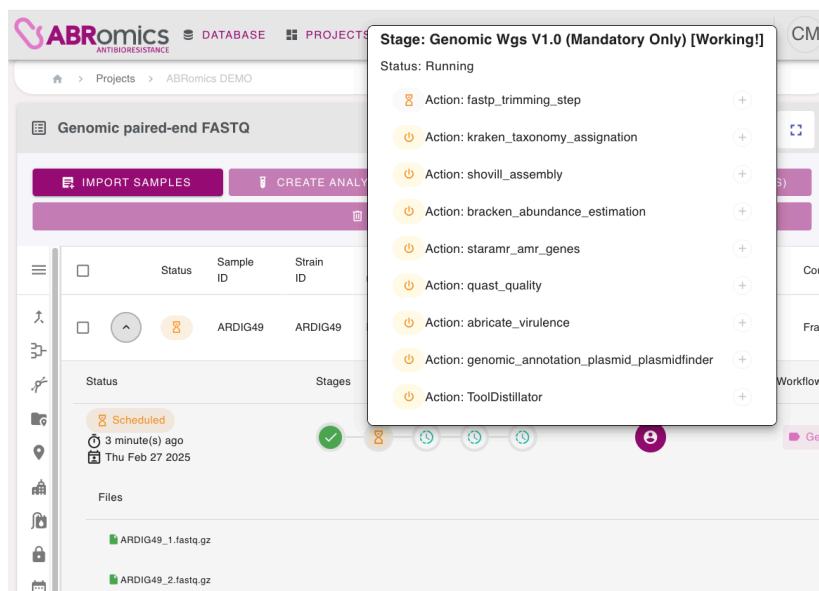
[UPLOAD](#) [CLOSE](#)

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

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

✓

Action: fastp\_trimming\_step

+

✓

Action: kraken\_taxonomy\_assignment

+

✓

Action: shovill\_assembly

+

✓

Action: bracken\_abundance\_estimation

+

⏸

Action: staramr\_amr\_genes

+

⏸

Action: quast\_quality

+

⏸

Action: abricate\_virulence

+

⏸

Action: genomic\_annotation\_plasmid\_plasmidfinder

+

⏸

Action: ToolDistillator

+

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

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

| Status   | Stages  | Created by | Workflow                                     |
|--|---|------------|--|
| <div>⏸ Downloading Json Results</div> <div>⌚ 21 minute(s) ago</div> <div>📅 Thu Feb 27 2025</div> | <div> <div>✓</div> <div>✓</div> <div>⏸</div> <div>⌚</div> <div>⌚</div> </div> <div> Stage: Downloading<br/>Status: Running </div> | Ⓜ          | Genomic WGS v1.0 (mandatory only) [working!] |

Files

📄 ARDIG49\_1.fastq.gz

📄 ARDIG49\_2.fastq.gz

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.

| Status | Sample ID | Strain ID | Instrument model | Sample type | Sample source  | Host species | Microorganism scientific name | Country | Region | Place | Collected date |
|--------|-----------|-----------|------------------|-------------|----------------|--------------|-------------------------------|---------|--------|-------|----------------|
| ✓      | test      | testB     | 454 GS           | human       | Bone and joint | Homo sapiens | Campylobacter jejuni          | Fiji    |        |       | 2007           |

| Status  | Stages  | Created by | Workflow  |
|---|---|------------|---|
| <div>✓ Ready To Report</div> <div>⌚ 00:18:24</div> <div>📅 Wed Nov 13 2024</div> | <div> <div>✓</div> <div>✓</div> <div>✓</div> <div>✓</div> <div>📄</div> </div> | Ⓜ          | Copy of abromics_beta_test_genomic_without_annotation_andnorecentrifuge_1.0 |
| <div>✓ Ready To Report</div> <div>⌚ 00:41:41</div> <div>📅 Wed Oct 30 2024</div> | <div> <div>✓</div> <div>✓</div> <div>✓</div> <div>✓</div> <div>📄</div> </div> | Ⓜ          | Genomic WGS - QC, taxonomy, assembly and AMR annotation                     |

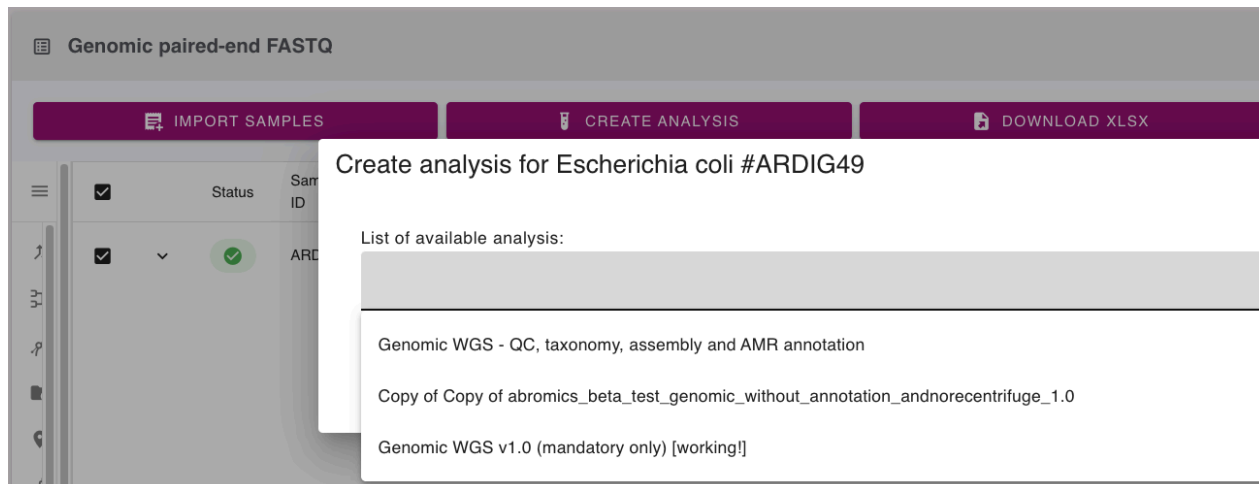
Files

📄 sub\_r1\_2.fastq.gz

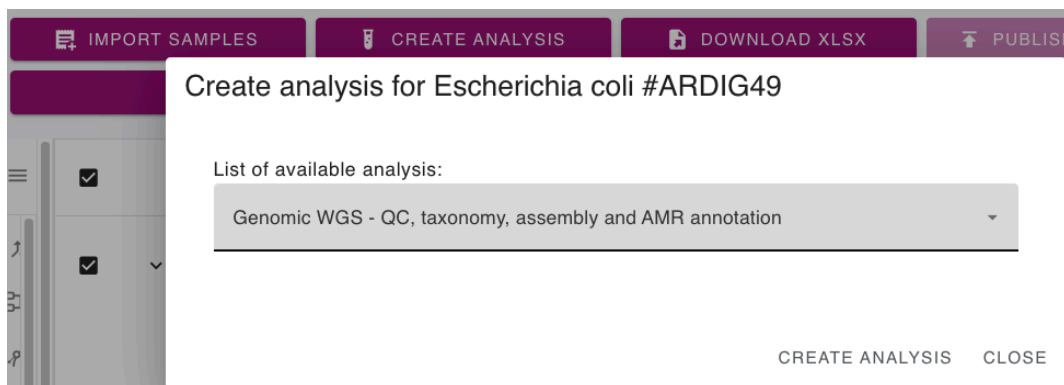
📄 sub\_r2\_2.fastq.gz



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



**Status**


 **Creating Invocation**

 19 second(s) ago  
 Fri Nov 29 2024


**Status**



 **Scheduled**

 40 second(s) ago  
 Fri Nov 29 2024



☐ ^  ARDIG49 ARDIG49

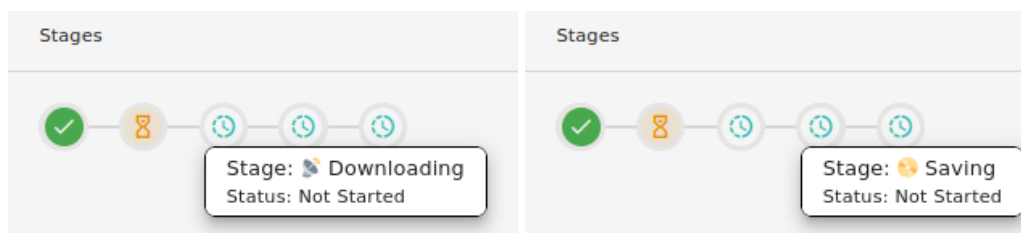
**Status**

 **Error**

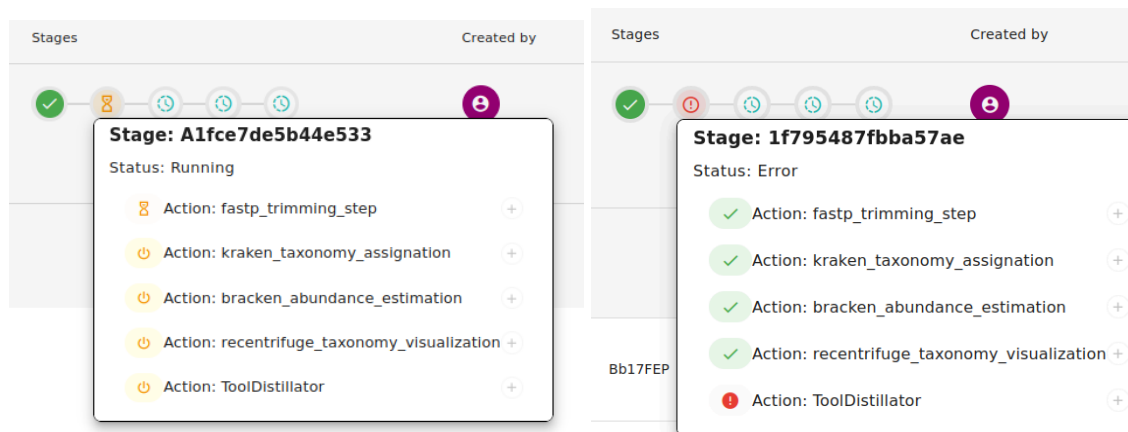
 1 day(s) ago  
 Thu Nov 28 2024

**Stages**



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.

Project details: TEST2, animal, Anus, Bos taurus, Streptococcus agalactiae, Antarctica

Status: Ready To Report (00:43:06, Fri Aug 29 2025) | Anomalies found

Stages: Progress bar with 5 green checkmarks. A tooltip for the final stage shows 'Stage: Ready To Report' and 'Status: Error'. An 'Open report' button is visible.

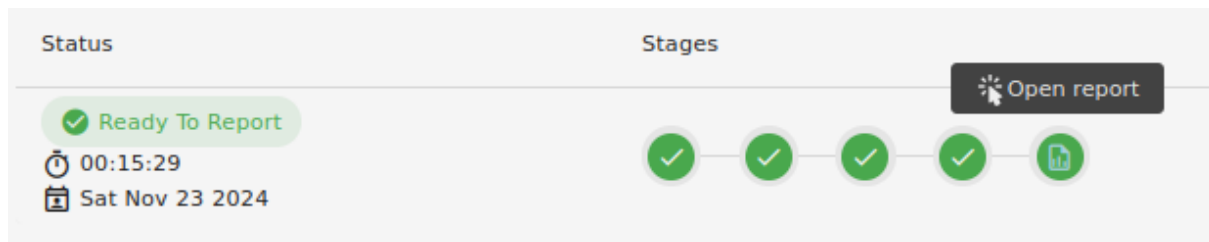
| Microorganism scientific name | Country    | Region | Place | Collected date |
|-------------------------------|------------|--------|-------|----------------|
| Streptococcus agalactiae      | Antarctica |        |       | 2011           |

**One or more analysis has detected a different bacterial species.**

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.



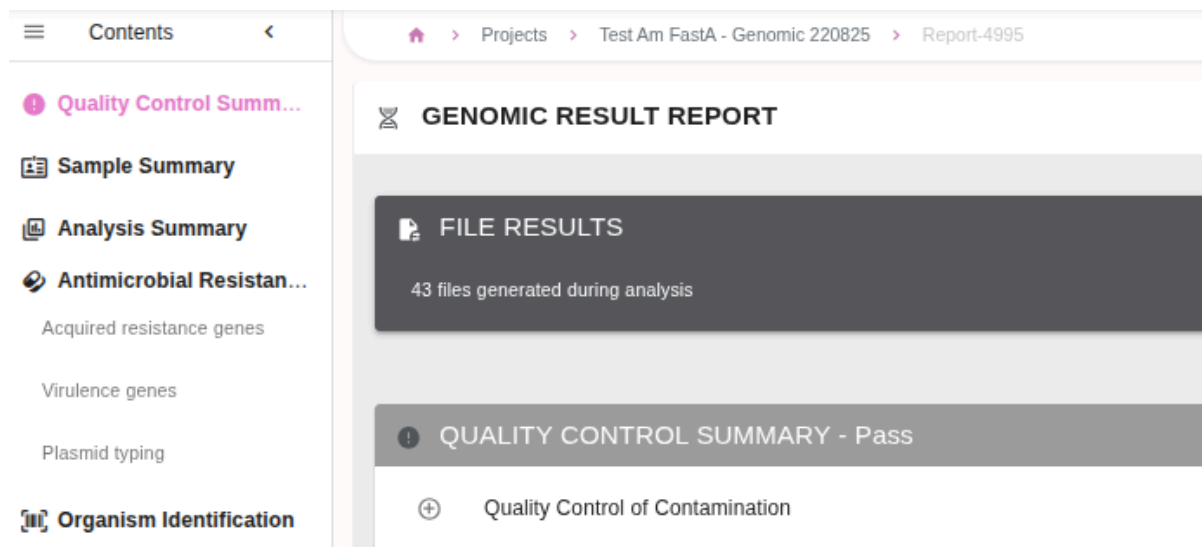
The screenshot displays the ABRomics interface for a completed analysis. On the left, under the 'Status' header, a green pill-shaped button indicates 'Ready To Report'. Below this, a clock icon shows a duration of '00:15:29' and a calendar icon shows the date 'Sat Nov 23 2024'. On the right, under the 'Stages' header, a horizontal sequence of five green circular icons with white checkmarks represents the progress of the analysis. To the right of the stages, a dark grey button with a document icon and the text 'Open report' is visible.

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.

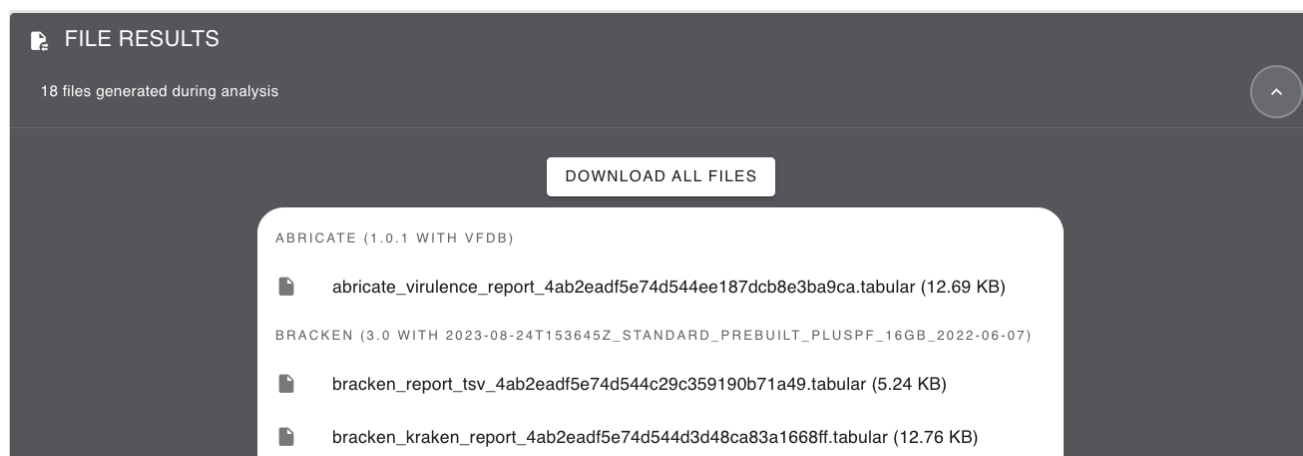
On the left side of this page a *Table of Content* is available to access easily the section you want without scrolling the overall report:




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.






- **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.


**QUALITY CONTROL SUMMARY - Pass**



**Quality Control of Reads**


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


**Pass**



**Quality Control of Contamination**


Bracken 1st hit reads assessment passed. (values tested: Top species detected: 100.0% reads)


**Pass**


---

Bracken 1st hit species assessment passed. (values tested: Sample metadata and the species detected with the most reads)


**Pass**


---



CheckM2 completeness assessment passed. (values tested: Completeness: 100.0)


**Pass**


---

CheckM2 contamination number assessment passed. (values tested: Contamination: 0.08)


**Pass**



**Quality Control of Assembly**


CheckM2 genome size flag assessment passed. (values tested: Assembled genome size: 5122973)


**Pass**


---

QUAST average coverage depth assessment passed. (values tested: Average coverage depth: 211.0)


**Pass**


---

QUAST and CheckM2 N50 assessment passed. (values tested: N50 for a 0bp base: 1, N50 for a 200bp base: 1)


**Pass**

---

QUAST contigs number assessment passed. (values tested: #Contigs >= 0bp: 358, #Contigs >= 200bp: 224)


**Pass**

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

| ANALYSIS SUMMARY   |                  |
|--|------------------|
| Isolate identified as  | Escherichia coli |
| Sequence type (ST)   | 131              |
| Number of genes with known resistance to target antibiotics  | 16               |
| <b>List of target antibiotics:</b> <ul style="list-style-type: none"> <li>• Ampicillin</li> <li>• Erythromycin and Azithromycin</li> <li>• Kanamycin</li> <li>• Streptomycin</li> <li>• Sulfisoxazole</li> <li>• Trimethoprim</li> </ul> |                  |

- **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  |             |              |              |             |                 |               |        |                           |                                 |
|--|-------------|--------------|--------------|-------------|-----------------|---------------|--------|---------------------------|---------------------------------|
| <b>Acquired resistance genes</b><br>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          | Target                          |
| blaTEM-1B  | 861         | 100          | 100          | contig00036 | 670             | 1530          | +      | Beta-lactam               | Amc<br>Amf<br>Cep<br>Pip<br>Tic |
| blaTEM-1B  | 861         | 100          | 100          | contig00036 | 670             | 1530          | +      | Beta-lactam               | Amc<br>Amf<br>Cep<br>Pip<br>Tic |
| dfrA17   | 474         | 100          | 100          | contig00062 | 8591            | 9064          | -      | Folate pathway antagonist | Trim                            |


| <b>Virulence genes</b><br>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   | # Accession |
| espL1  | 1899        | 95.05        | 100          | contig00001 | 225642          | 227540        | -      | (espL1)<br>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)<br>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: *mist 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

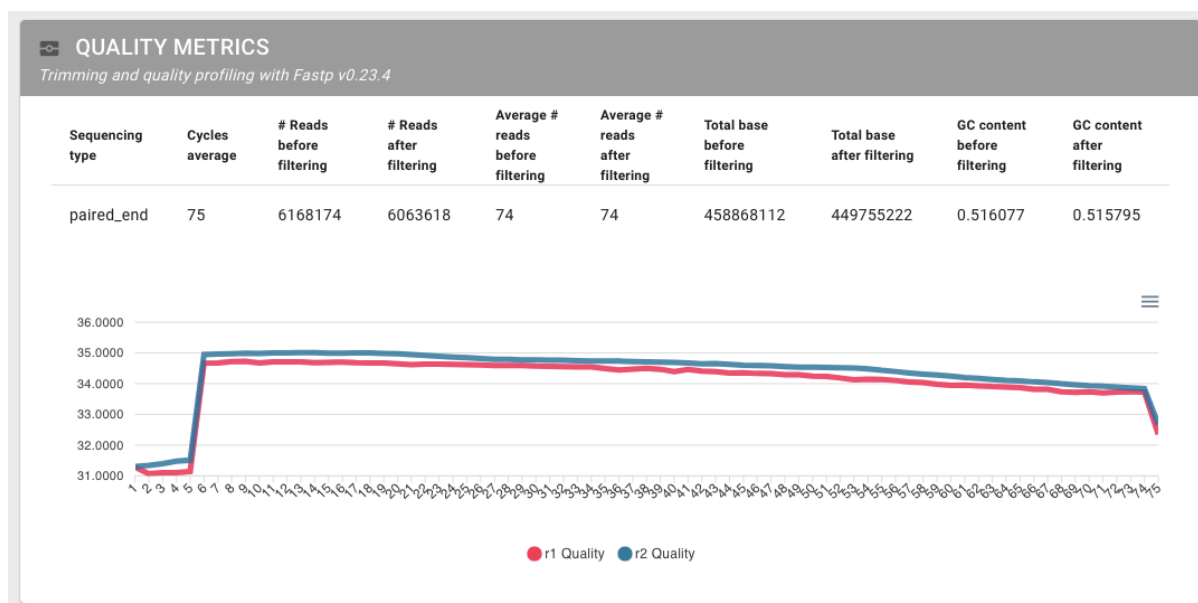
purA

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.

Genomic paired-end FASTQ

IMPORT SAMPLES

CREATE ANALYSIS

DOWNLOAD XLSX

PUBLISH SAMPLE(S)

DELETE SAMPLE(S)

Filters list

Sample type

Sample source

Host species

Microorganism scientific name

Country

Place

Class of antibiotic

Permission

Collected date

Search

Sample ID

Strain ID

| Status                                       | Sample ID | Strain ID | Instrument model    | Sample type | Sample source | Host species | Microorganism scientific name |
|--|-----------|-----------|---------------------|-------------|---------------|--------------|-------------------------------|
| <div><div></div><div></div><div></div></div> | CIP110464 | NIPH1669  | Illumina HiSeq 2000 | human       | Blood         | Homo sapiens | Acinetobacter baumannii       |
| <div><div></div><div></div><div></div></div> | CIP110436 | NIPH528   | Illumina HiSeq 2000 | human       | Urine         | Homo sapiens | Acinetobacter baumannii       |
| <div><div></div><div></div><div></div></div> | CIP110435 | NIPH527   | Illumina HiSeq 2000 | human       | Urine         | Homo sapiens | Acinetobacter baumannii       |
| <div><div></div><div></div><div></div></div> | T20-Cu8   | T20-Cu8   | Illumina HiSeq 2000 | human       | Not Collected | Homo sapiens | Acinetobacter baumannii       |
| <div><div></div><div></div><div></div></div> | K19M7     | K19M7     | Illumina HiSeq 2000 | human       | Wound         | Homo sapiens | Acinetobacter baumannii       |

You can select samples either one by one by clicking on the checkbox at the beginning of a row in the sample collection table or by 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"<sup>2</sup>, MLST result "Sequence type"<sup>3</sup>, "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".

IMPORT SAMPLES

CREATE ANALYSIS

DOWNLOAD XLSX

PUBLISH SAMPLE(S)

DELETE SAMPLE(S)

Q Search

Urine Germany

ID Sample ID

ID Strain ID

|                          | Status         | Sample ID | Strain ID  | Instrument model    | Sample type | Sample source | Host species | Microorganism scientific name | Country |
|--------------------------|----------------|-----------|------------|---------------------|-------------|---------------|--------------|-------------------------------|---------|
| <input type="checkbox"/> | ▼ <div>✓</div> | K19M15    | K19M15     | Illumina HiSeq 2000 | human       | Urine         | Homo sapiens | Acinetobacter baumannii       | Germany |
| <input type="checkbox"/> | ▼ <div>✓</div> | CIP64.1   | ATCC 17904 | Illumina HiSeq 2000 | human       | Urine         | Homo sapiens | Acinetobacter baumannii       | 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.

Sample source

Select source

☐ Blood ( 4 )
☐ Feces ( 14 )
☐ Urine ( 1 )

<sup>2</sup> The filter "Microorganism scientific name", in this case, corresponds to the name of the taxonomy detected with the highest percentage of reads.

<sup>3</sup> 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.

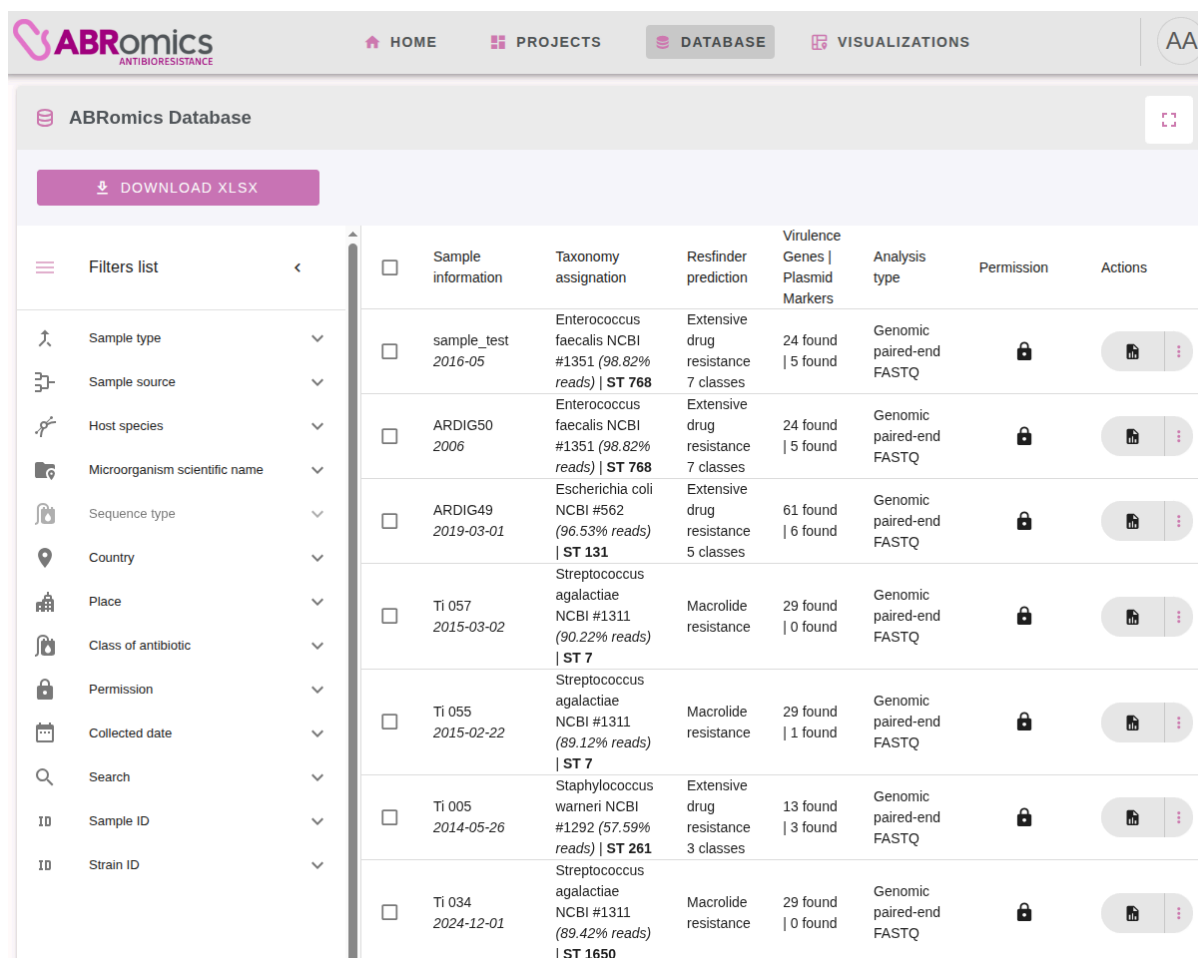
| Class of antibiotic   | Count  |
|---|--------|
| <input type="checkbox"/> Aminoglycoside   | ( 25 ) |
| <input type="checkbox"/> Aminoglycoside, Quinolone  | ( 2 )  |
| <input type="checkbox"/> Amphenicol   | ( 14 ) |
| <input type="checkbox"/> Amphenicol, Folate pathway antagonist, Quaternary Ammonium Compound, Quinolone | ( 3 )  |
| <input type="checkbox"/> Amphenicol, Lincosamide, Oxazolidinone, Pleuromutilin, Streptogramin A         | ( 1 )  |
| <input type="checkbox"/> Amphenicol, Oxazolidinone  | ( 5 )  |

|   |               |
|---|---------------|
| <input type="checkbox"/> ERS163 / 7935   Chile ESBLEcoli_Chile   2019     | identified    |
| <input type="checkbox"/> FRC1894   France (Dole) Données test BEBP   2023 | Not available |

## 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.



| Filters list                  |   | Sample information                              | Taxonomy assignation   | Resfinder prediction                   | Virulence Genes   Plasmid Markers | Analysis type            | Permission | Actions |
|-------------------------------|---|---|--|--|-----------------------------------|--------------------------|------------|---------|
| Sample type                   | ▼ | <input type="checkbox"/> sample_test<br>2016-05 | Enterococcus faecalis NCBI #1351 (98.82% reads)   ST 768     | Extensive drug resistance<br>7 classes | 24 found<br>  5 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Sample source                 | ▼ | <input type="checkbox"/> ARDIG50<br>2006        | Enterococcus faecalis NCBI #1351 (98.82% reads)   ST 768     | Extensive drug resistance<br>7 classes | 24 found<br>  5 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Host species                  | ▼ | <input type="checkbox"/> ARDIG49<br>2019-03-01  | Escherichia coli NCBI #562 (96.53% reads)   ST 131           | Extensive drug resistance<br>5 classes | 61 found<br>  6 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Microorganism scientific name | ▼ | <input type="checkbox"/> Ti 057<br>2015-03-02   | Streptococcus agalactiae NCBI #1311 (90.22% reads)   ST 7    | Macrolide resistance                   | 29 found<br>  0 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Sequence type                 | ▼ | <input type="checkbox"/> Ti 055<br>2015-02-22   | Streptococcus agalactiae NCBI #1311 (89.12% reads)   ST 7    | Macrolide resistance                   | 29 found<br>  1 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Country                       | ▼ | <input type="checkbox"/> Ti 005<br>2014-05-26   | Staphylococcus warneri NCBI #1292 (57.59% reads)   ST 261    | Extensive drug resistance<br>3 classes | 13 found<br>  3 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Place                         | ▼ | <input type="checkbox"/> Ti 034<br>2024-12-01   | Streptococcus agalactiae NCBI #1311 (89.42% reads)   ST 1650 | Macrolide resistance                   | 29 found<br>  0 found             | Genomic paired-end FASTQ | 🔒          | 📄 ⋮     |
| Class of antibiotic           | ▼ |   |  |  |                                   |                          |            |         |
| Permission                    | ▼ |   |  |  |                                   |                          |            |         |
| Collected date                | ▼ |   |  |  |                                   |                          |            |         |
| Search                        | ▼ |   |  |  |                                   |                          |            |         |
| Sample ID                     | ▼ |   |  |  |                                   |                          |            |         |
| Strain ID                     | ▼ |   |  |  |                                   |                          |            |         |

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;

|  |   |
|--|---|
| No resistance detected                 | <b>10 Genes detected:</b><br>Aminoglycoside (3)<br>Folate pathway antagonist (2)<br>Beta-lactam (1)<br>Lincosamide, Macrolide, Streptogramin B (1)<br>Macrolide (1)<br>Quaternary Ammonium Compound (1)<br>Peroxide (1) |
| Extensive drug resistance<br>7 classes |   |
| Extensive drug resistance<br>7 classes |   |

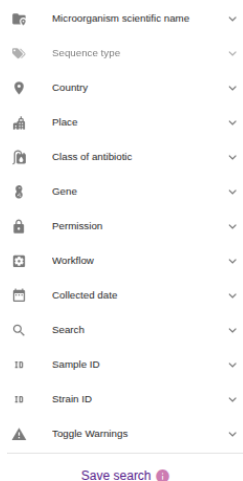
- **Virulence genes | Plasmid markers:**

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                | <b>Plasmid markers found:</b><br>IncI1-(Alpha) (+)<br>IncY (+)<br>IncX4 (+)<br>ColpEC648 (+)<br>Col(pHAD28) (+)<br>IncFIA(HI1) (+) | 🔒          |
| 61 found   6 found                |  | 🔒          |
| 61 found   0 found                |  | 🔒          |
| 61 found   0 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:



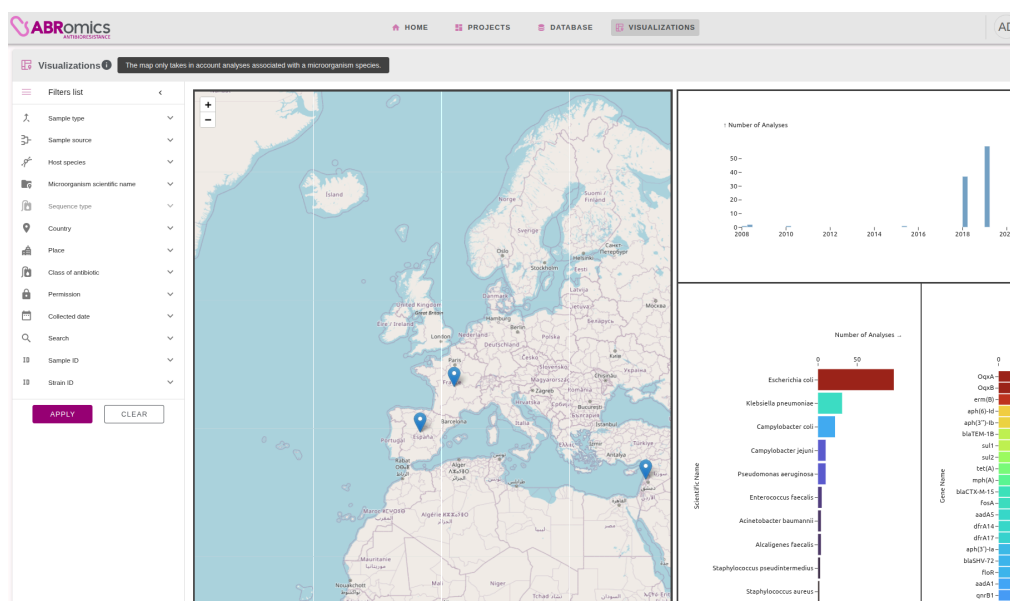
- You can filter out according to sample metadata: "Sample type", "Sample source", "Host species", "Country", "Place", "Collected date", "Sample ID", "Strain ID";

- Or according to analyses results: "Microorganism scientific name"<sup>4</sup>, MLST result "Sequence type"<sup>5</sup>, "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.



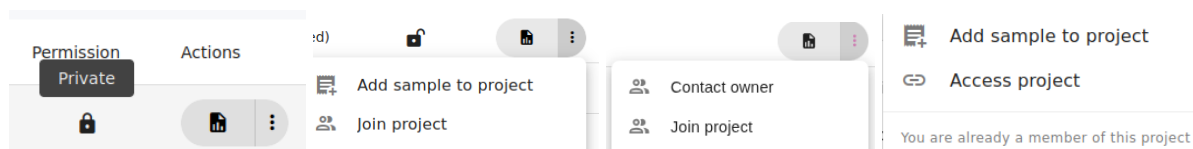
<sup>4</sup> The filter "Microorganism scientific name", in this case, corresponds to the name of the taxonomy chosen by the user who completed metadata information and uploaded the sample.

<sup>5</sup> The filter "Sequence type" can only be used if a "Microorganism scientific name" is selected.



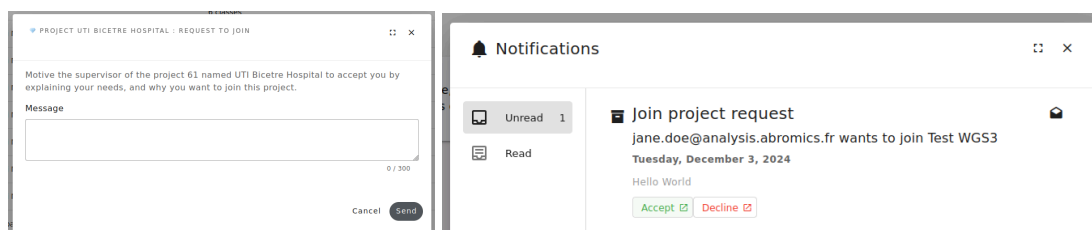
The “map” view in “VISUALIZATIONS”, the third main page of ABRomics, shows the locations of samples according to their “country” metadata. Hovering over a country will highlight the corresponding number of samples and the three most represented antibiotic classes in the detected AMR genes of these samples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

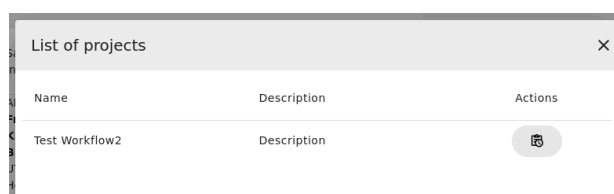
You can also use the ABRomics analyses “Database” page to request access to a project. By clicking on the kebab menu icon (3 dots) in the “Actions” column and then clicking on “Join project” a pop-up enables you to write a message to the project supervisor. The supervisor will then receive a notification 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.

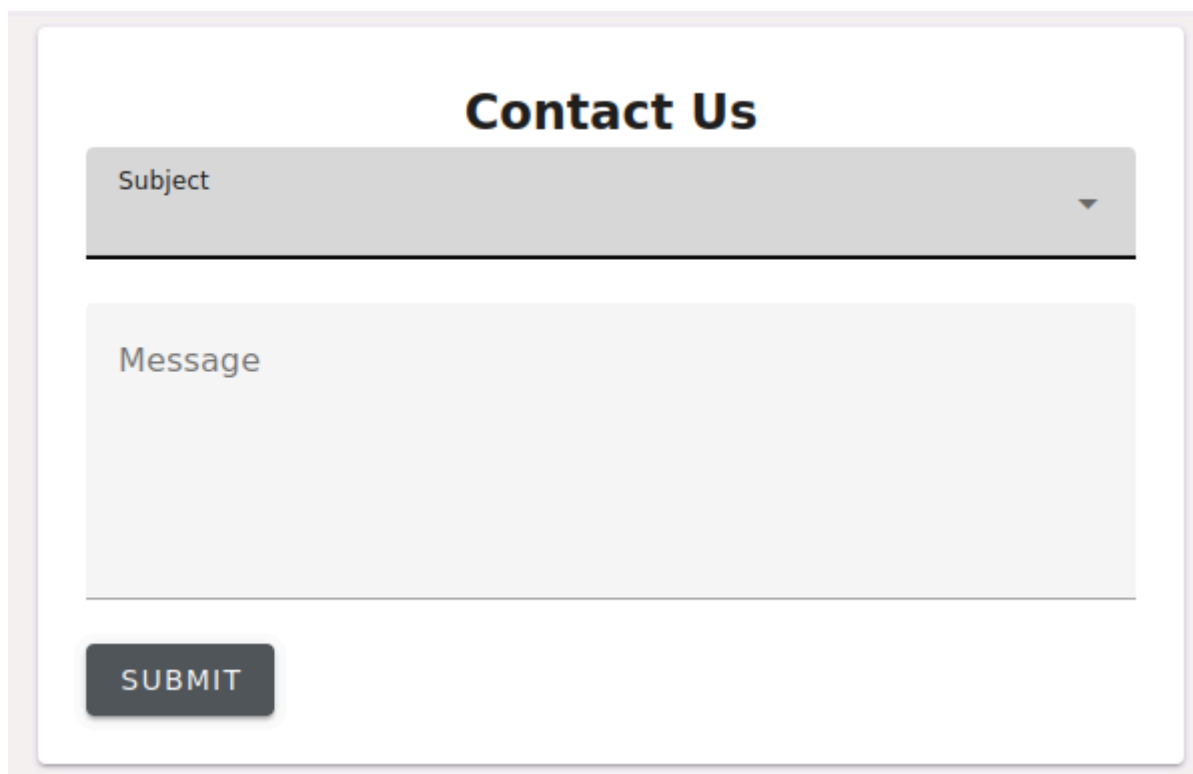
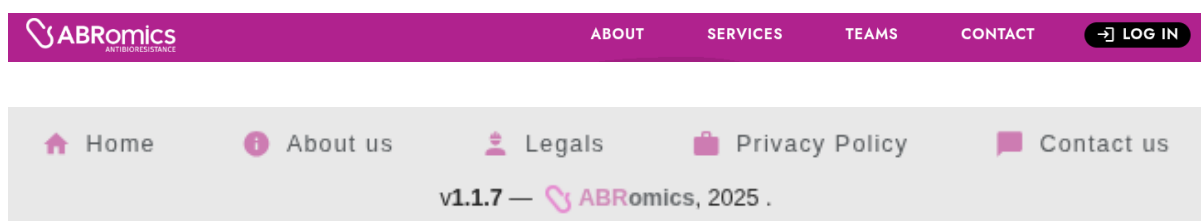
## CONTACT US

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

[abromics-support@groupe.france-bioinformatique.fr](mailto:abromics-support@groupe.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.

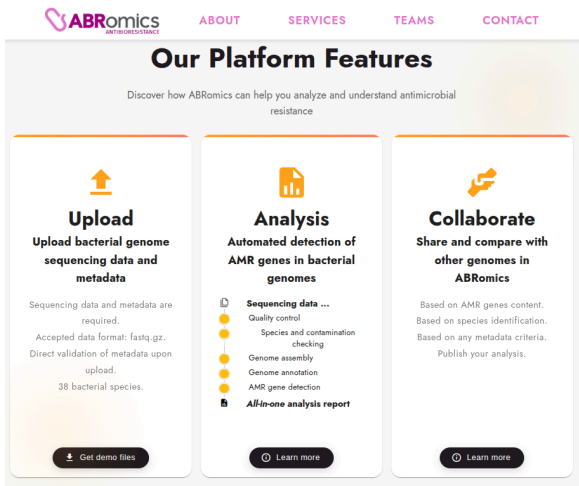
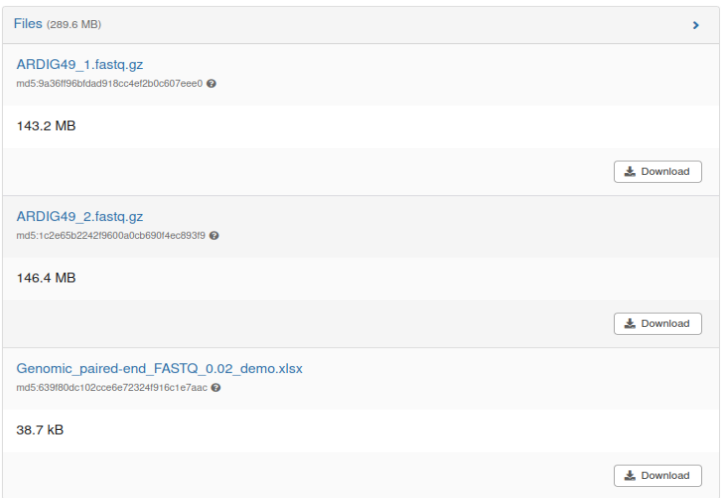
The image shows a 'Contact Us' form with a title 'Contact Us' in bold. Below the title is a dropdown menu labeled 'Subject' with a downward arrow. Underneath is a large text area labeled 'Message'. At the bottom left of the form is a dark grey button labeled 'SUBMIT'.

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

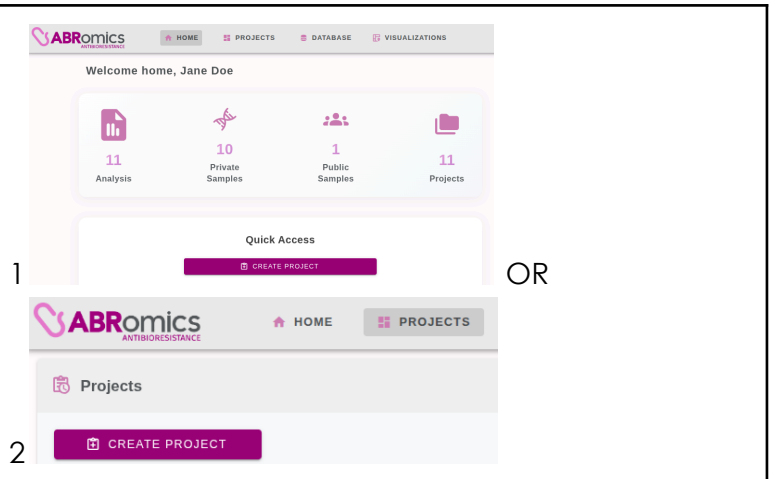
### How to use demo files

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

|  |  |
|--|--|
| <p>You can find the demo files on the ABRomics analysis homepage (<a href="https://analysis.abromics.fr/">https://analysis.abromics.fr/</a>) by clicking on the <b>“GET THE DEMO FILES”</b> button.</p>  |    |
| <p>You will be redirected to <a href="https://www.abromics.fr/abromics-platform/metadata-referential/">https://www.abromics.fr/abromics-platform/metadata-referential/</a> web page, where you can find FASTQ or FASTA demo files* :</p> <p>Click on <b>“Download the Demo files”</b> on the left (fastQ file format)</p>  | <h3>Overview</h3> <p>The <b>ABRomics analyses platform</b> is designed to analyze the AMR genes content of bacterial samples using two types of data:</p> <ul style="list-style-type: none"> <li>→ <b>Genomic paired-end FASTQ files</b></li> <li>→ <b>Genomic FASTA files</b></li> </ul> <ul style="list-style-type: none"> <li>→ Download the <b>Metadata referentials</b></li> <li>→ Download the <b>Metadata referentials</b></li> <li>→ Download the <b>Demo files</b></li> <li>→ Download the <b>Demo files</b></li> </ul> |
| <p>You will be redirected to <a href="https://zenodo.org/records/14366711">https://zenodo.org/records/14366711</a> where you can find a description of the files and the <b>download links under the “Files” section</b> of the page.</p> <p>ARDIG49_1.fastq.gz is the <b>R1 input file</b> and ARDIG49_2.fastq.gz is the <b>R2 input file</b>.</p> <p>Genomic_paired-end_FASTQ_0.02_demo.xlsx is the demo <b>metadata template</b>.</p> | <h3>Files</h3>   |

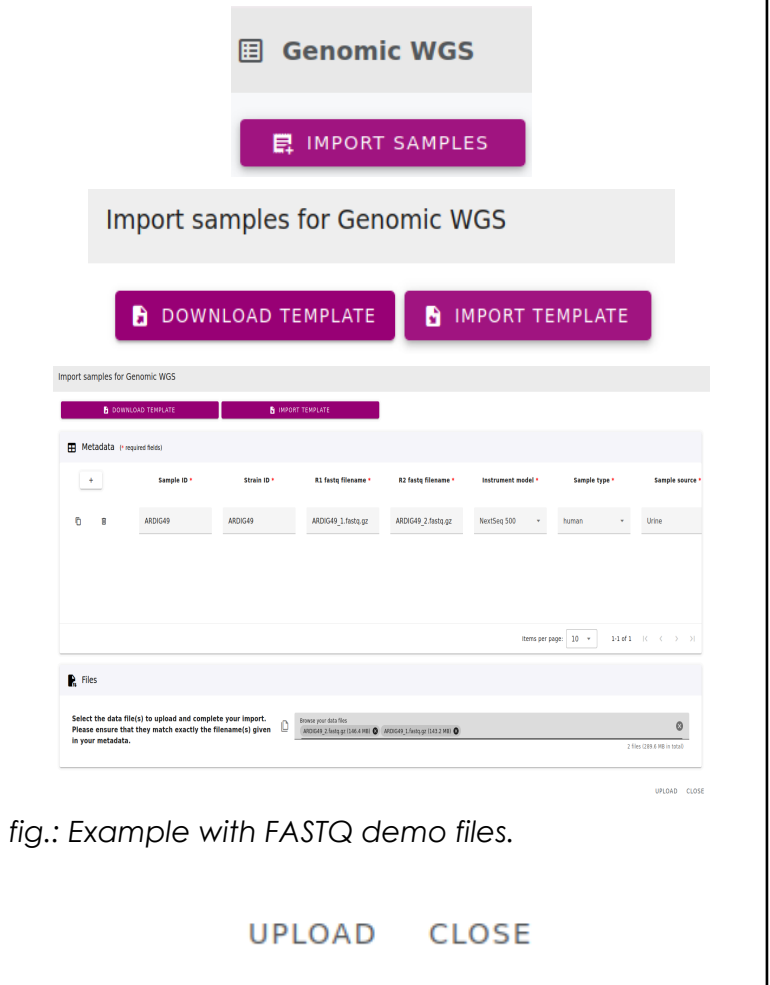
Follow the steps described in section **"PROJECTS & PROJECT MANAGEMENT"** to create your demo project\*

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

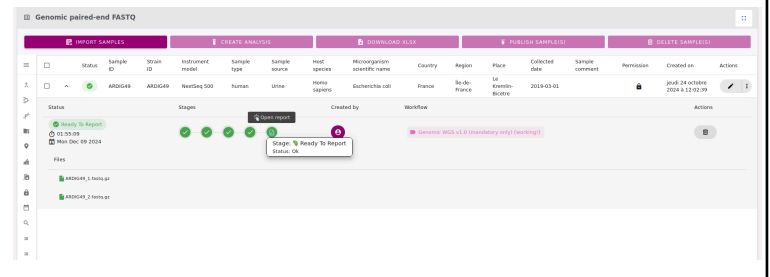


Follow the steps described in section **"Upload a sample & metadata validation"** and upload the demo sample by importing the demo metadata template and the demo raw data files.

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.



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           |
|--------------------------------------|---|------------------|---|---------------------------|
| <b>Sample ID</b>                     | ID of the sample  | <b>mandatory</b> | Sample ID must be unique in the whole document  | Free text                 |
| <b>Strain ID</b>                     | Name of the isolated strain   | <b>mandatory</b> | Strain ID must be unique in the whole document  | Free text                 |
| <b>R1 fastq filename</b>             | Name of the fastq forward file  | <b>mandatory</b> | The filename must end by ".fastq.gz"  | Free text                 |
| <b>R2 fastq filename</b>             | Name of the fastq reverse file  | <b>mandatory</b> | The filename must end by ".fastq.gz"  | Free text                 |
| <b>Instrument model</b>              | The sequencing instrument model used in the experiment                          | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Sample type</b>                   | Indicate if the sample is collected on human, on animal or in an environment    | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Sample source</b>                 | Site of isolation of the sample   | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Host species</b>                  | Species of the host   | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Microorganism scientific name</b> | Scientific name of the isolated microorganism                                   | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Country</b>                       | Name of the country in which the sample has been collected                      | <b>mandatory</b> | Country english full name   | See "Fields values" (*)   |
| <b>Region</b>                        | Region where the sample has been collected                                      | optional         | <b>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".</b> |                           |
| <b>Place</b>                         | Place where the sample has been collected                                       | optional         |   |                           |
| <b>Collected date</b>                | The date of sampling  | <b>mandatory</b> | Must be a valid full date. For example: 07/10/2024  | Must be a valid full date |
| <b>Travel countries</b>              | 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" (*)   |
| <b>Accession number</b>              | Accession numbers associated with the sample                                    | optional         | Multiple values should be split by ','  | Free text                 |
| <b>Sample comment</b>                | 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           |
|--------------------------------------|--|------------------|---|---------------------------|
| <b>Sample ID</b>                     | ID of the sample   | <b>mandatory</b> | Sample ID must be unique in the whole document  | Free text                 |
| <b>Strain ID</b>                     | Name of the isolated strain  | <b>mandatory</b> | Strain ID must be unique in the whole document  | Free text                 |
| <b>Fasta filename</b>                | Name of the fasta file   | <b>mandatory</b> | The filename must end by ".fasta"   | Free text                 |
| <b>Instrument model</b>              | The sequencing instrument model used in the experiment                           | optional         | One of the accepted values  | See "Fields values" (*)   |
| <b>Assembly method</b>               | Method used to assembly raw reads to a final fasta file                          | optional         | Free text   | Free text                 |
| <b>Sample type</b>                   | Indicate if the sample is collected on human, on animal or in an environment     | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Sample source</b>                 | Site of isolation of the sample  | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Host species</b>                  | Species of the host  | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Microorganism scientific name</b> | Scientific name of the isolated microorganism                                    | <b>mandatory</b> | One of the accepted values  | See "Fields values" (*)   |
| <b>Country</b>                       | Name of the country in which the sample has been collected                       | <b>mandatory</b> | Country english full name   | See "Fields values" (*)   |
| <b>Region</b>                        | Region where the sample has been collected                                       | optional         | <b>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".</b> |                           |
| <b>Place</b>                         | Place where the sample has been collected  | optional         |   |                           |
| <b>Collected date</b>                | The date of sampling   | <b>mandatory</b> | Must be a valid full date. For example: 07/10/2024  | Must be a valid full date |
| <b>Travel countries</b>              | 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" (*)   |
| <b>Accession number</b>              | Accession numbers associated with the sample                                     | optional         | Multiple values should be split by ';'.   | Free text                 |
| <b>Sample comment</b>                | Any comments on the sample.  | optional         | Free text   | Free text                 |

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