



Leveraging Galaxy's Superpowers to Enhance Fermentation Innovation through the Siduri portal

Agnès Barnabé, Emilie Fernandez, Erwan Le Floch, Thomas Lacroix, Sophie Schbath, Valentin Loux

► To cite this version:

Agnès Barnabé, Emilie Fernandez, Erwan Le Floch, Thomas Lacroix, Sophie Schbath, et al.. Leveraging Galaxy's Superpowers to Enhance Fermentation Innovation through the Siduri portal. Galaxy Community Conference, Jun 2026, Clermont Ferrand (FR), France. <hal-05671477>

HAL Id: hal-05671477

<https://hal.science/view/index/docid/5671477>

Submitted on 26 Jun 2026

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➤ Leveraging Galaxy's Superpowers to Enhance Fermentation Innovation through the Siduri portal

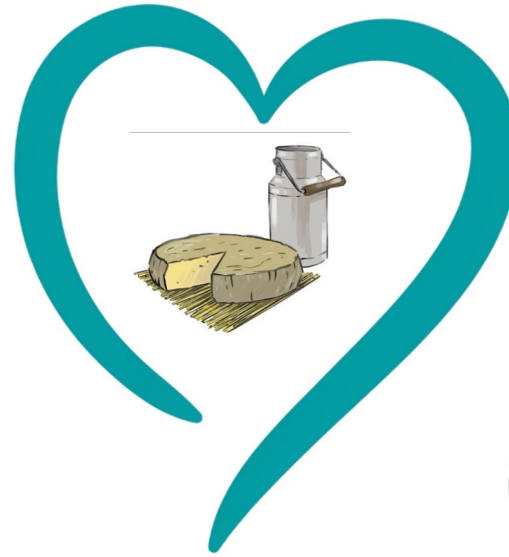
Agnès Barnabé

Ferments du Futur (US INRAE 1503)

Migale core Bioinformatics Facility, MaIAGE, INRAE Jouy-en-Josas

Everyone

Fish sauce
Vinegar
Miso **Wine**
Salami **Bread**
Sake **Cheese**
Kefir
Cider **Chocolate**
Kombucha
Pu-erh tea
Olives
Kvass
Gochujang



Coffee
Idli & dosa
Natto Tempeh
Cured ham **Injera**
Doenjang **Yogurt**
Pickles **Beer**
Kimchi
Soy sauce Rice wine
Sauerkraut

Fermentation



INRAE

Leveraging Galaxy's Superpowers to Enhance Fermentation Innovation through the Siduri portal

Agnès Barnabé – Ferments du Futur, Migale, INRAE Jouy-en-Josas

➤ Ferments du Futur (FdF)

7 INRAE research
platforms in a wide
range of expertise

6 academics projects
funded annually for
two years

10 years public/private
partnership to innovate
in fermentation
2022 - 2032



25 start-ups and food
industries involved
in private projects

One user-friendly portal to
rule them all

Siduri

➤ Challenge: massive and heterogeneous data

Projects with a wide range of topics



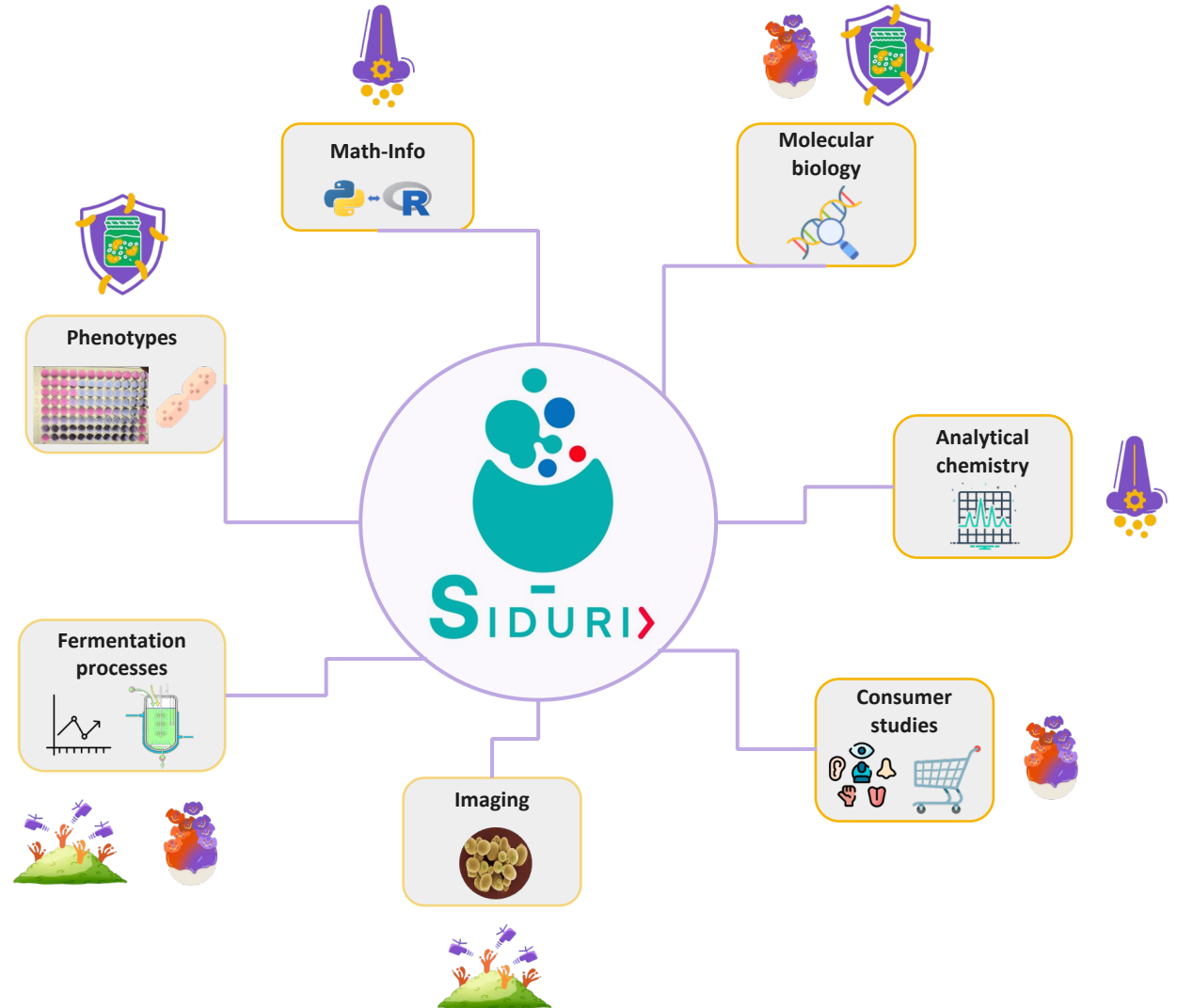
CapNoz : real-time monitoring of volatile compounds produced during fermentation

NIPPON : explore bio preservation strategies for plant-based food

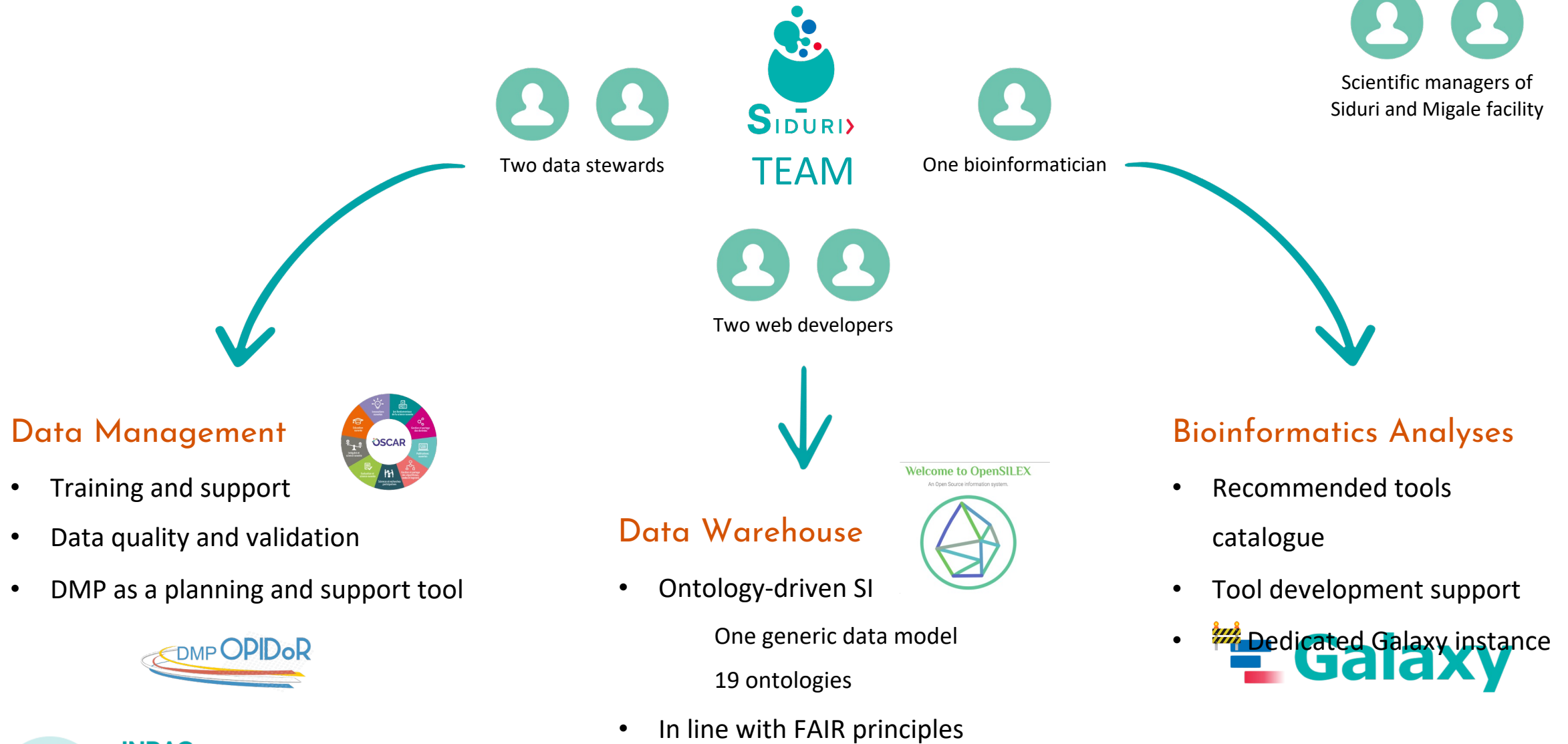


SSFsensors : innovative combination of sensors for controlling heterogeneities in Solid State Fermentations

BAMBI : bio production of microbial bio-colorants for consumer insights



➤ Siduri: a user-friendly portal for fermentation



➤ Bioinformatics catalogue



Guide expert and non-expert users to recommended tools and workflows for FdF data analyses

Analytical chemistry

- Quality control
- Molecules quantification
- Metabolites identification
- Alignment against spectral database
- ...



Molecular biology

- Quality control
- Assembly
- Functional annotation
- Metabolic pathway prediction
- Genome Scale Modeling



Consumer studies

Imaging

Phenotypes

Fermentation processes

Math-Info



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➤ Link Siduri to Galaxy Superpowers



No need for a superhero cape or mask



Just need API through BioBlend!

Siduri API via
Python client



Galaxy API via
BioBlend library

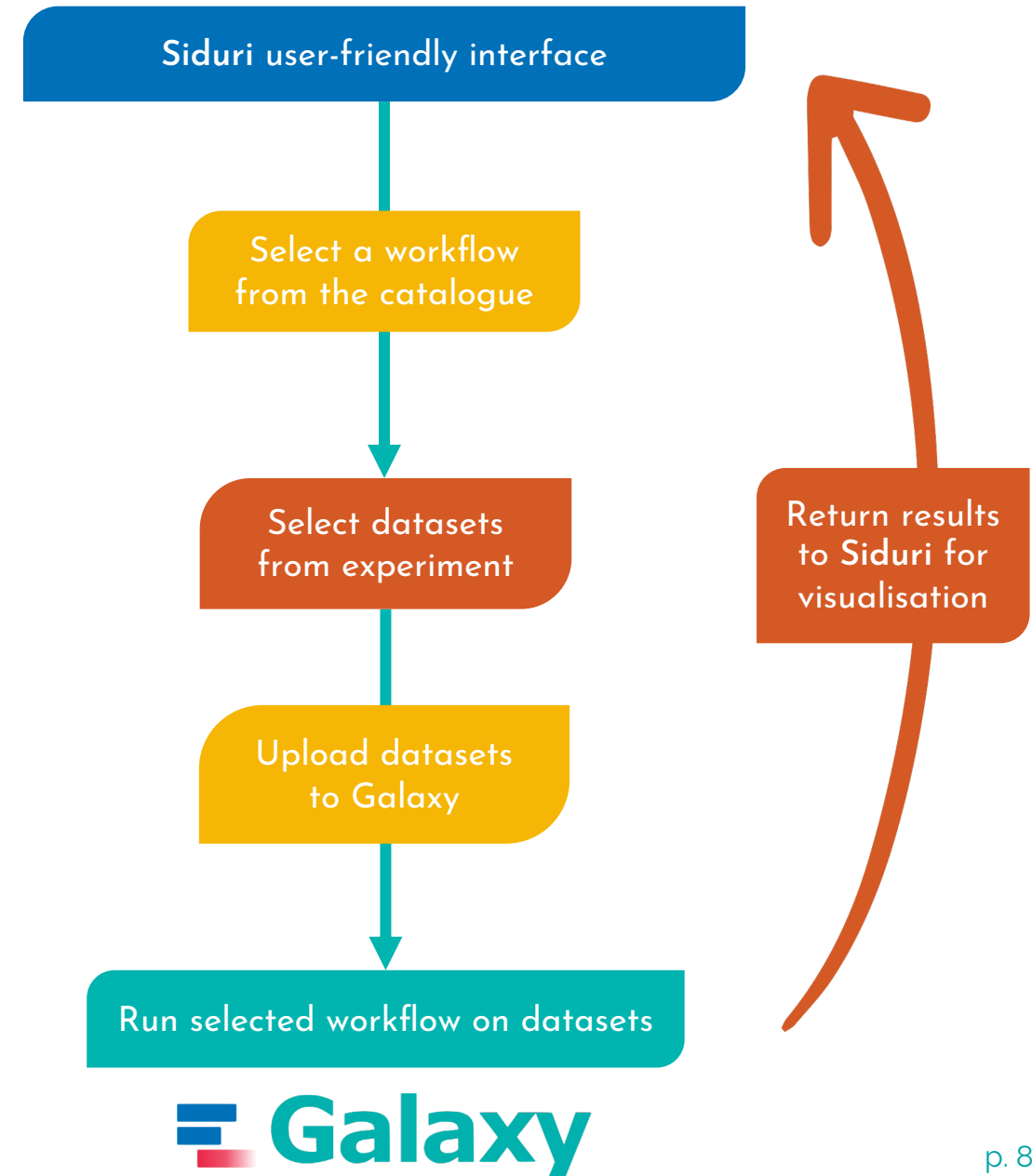
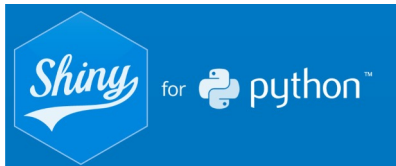


➤ Link Siduri to Galaxy Superpowers

The screenshot shows a web interface for Siduri. On the left is a sidebar with links: Projects & Experiments, Information, Data, About, and Tools. The main area is titled 'Data analysis catalogue' and contains two sections: 'Choose a dataset' with a 'DATASET URI' input field, and 'Select a workflow' with a 'WORKFLOW 1' dropdown menu. A teal 'Submit' button is at the bottom, with a red arrow pointing to it. The Siduri logo is in the top right corner.

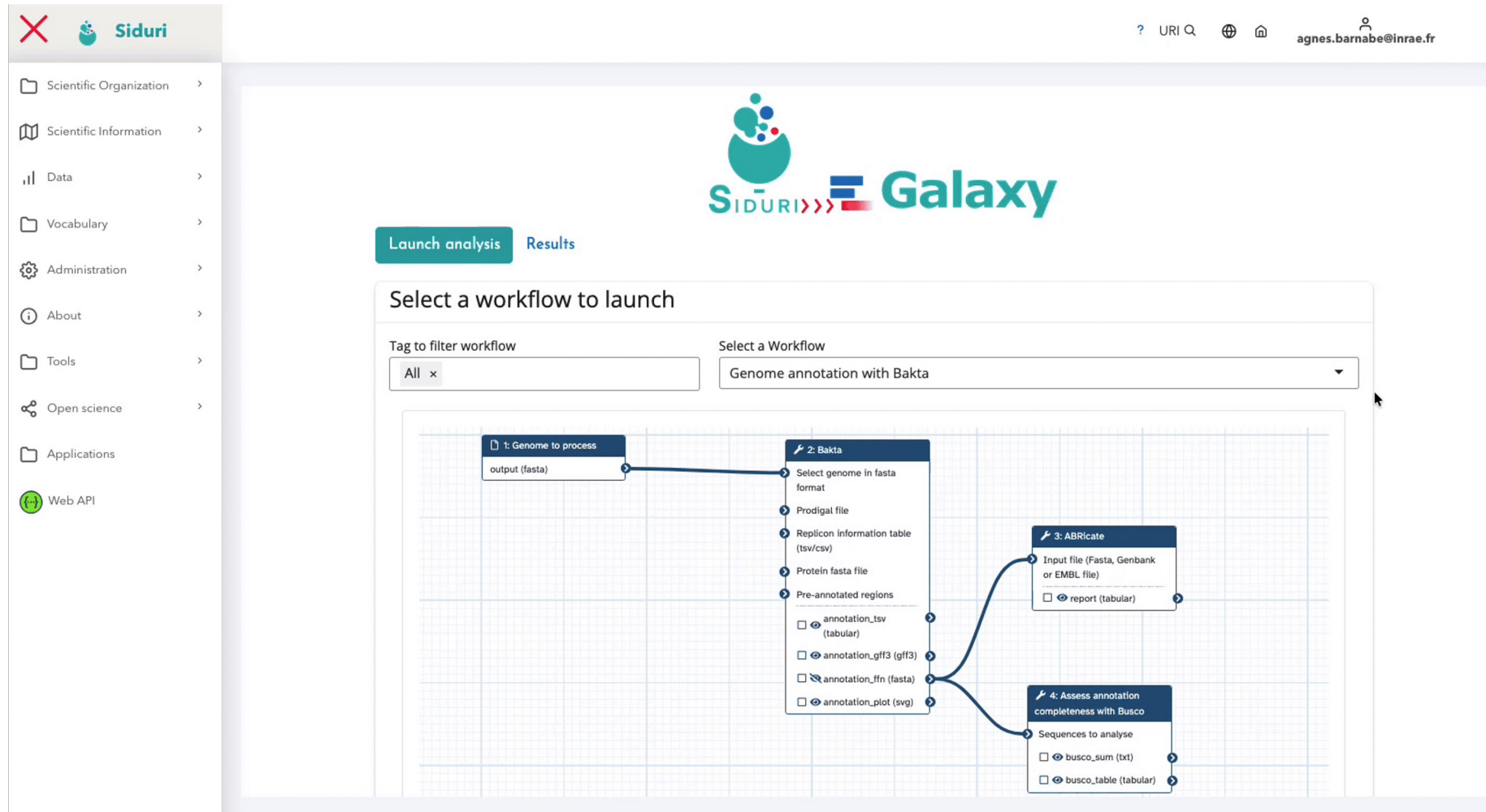
Siduri API via
Python client

Galaxy API via
BioBlend library



➤ Siduri-x-Galaxy

Select a workflow



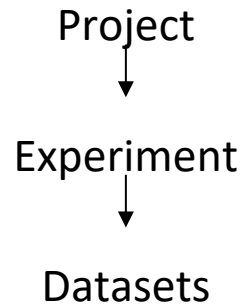
The screenshot displays the Siduri Galaxy web interface. On the left is a sidebar with navigation links: Scientific Organization, Scientific Information, Data, Vocabulary, Administration, About, Tools, Open science, Applications, and Web API. The main content area features the Siduri and Galaxy logos at the top. Below the logos are two tabs: 'Launch analysis' (active) and 'Results'. A section titled 'Select a workflow to launch' contains a 'Tag to filter workflow' dropdown set to 'All' and a 'Select a Workflow' dropdown set to 'Genome annotation with Bakta'. The workflow diagram is shown on a grid background. It starts with a box '1: Genome to process' with an output 'output (fasta)'. This connects to a larger box '2: Bakta' which contains several sub-steps: 'Select genome in fasta format', 'Prodigal file', 'Replicon information table (tsv/csv)', 'Protein fasta file', 'Pre-annotated regions', and a list of checkboxes for 'annotation_tsv (tabular)', 'annotation_gff3 (gff3)', 'annotation_fna (fasta)', and 'annotation_plot (svg)'. The output of the 'Bakta' box connects to two final boxes: '3: ABRicate' (with sub-steps 'Input file (Fasta, Genbank or EMBL file)' and 'report (tabular)') and '4: Assess annotation completeness with Busco' (with sub-steps 'Sequences to analyse', 'busco_sum (txt)', and 'busco_table (tabular)').

➤ Siduri-x-Galaxy

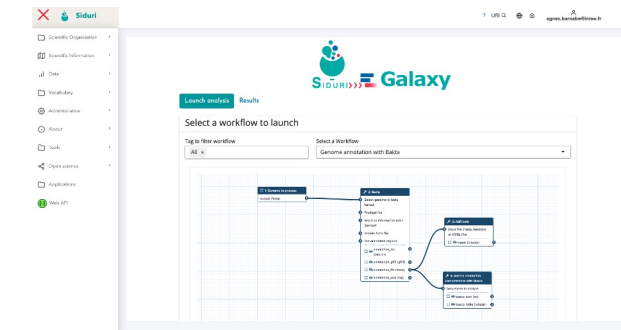
Select datasets

Provide inputs required by the selected workflow from **Siduri**

Siduri data structure



The screenshot displays the Siduri web interface. On the left is a sidebar menu with options: Scientific Organization, Scientific Information, Data, Vocabulary, Administration, About, Tools, Open science, Applications, and Web API. The main area shows a workflow diagram for 'Genome annotation with Bakta'. Below the diagram, there's a section titled 'Send dataset to Galaxy and launch selected workflow' which includes dropdowns for 'Select a project' (IBIS) and 'Select an experiment' (IBIS Genome-scale metabolic modeling), a text field for 'Galaxy history name', and a dropdown for 'data_input (fasta)' (GCF_025193525-1.fasta). A large orange button at the bottom says 'Send data and invoke workflow in Galaxy'.



➤ Siduri-x-Galaxy

Upload datasets then invoke the selected workflow

The screenshot displays the Siduri web portal interface. On the left is a sidebar menu with categories: Scientific Organization, Scientific Information, Data, Vocabulary, Administration, About, Tools, Open science, Applications, and Web API. The main content area shows a workflow diagram at the top. Below it, a modal dialog titled "Send data and invoke workflow" is active, displaying a progress indicator and the text "Sending data to Galaxy in history 'Annotation bakta'" and "Do not close the application!". In the background, the "Send dataset to Galaxy" form is visible, featuring dropdowns for "Select a project" (IBIS) and "Select an experiment" (IBIS Genome-scale metabolic modeling), a text field for "Galaxy history name" (Annotation bakta), and a section for "Inputs required by the workflow Genome annotation with Bakta" with a "Show help" link and a "data_input (fasta)" field containing "GCF_025193525-1.fasta". A large orange button at the bottom reads "Send data and invoke workflow to Galaxy". The top right of the page shows the user profile "agnes.barnabe@inrae.fr".



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➤ Siduri-x-Galaxy

Document: Publication, protocol, textual report...
Datafile: Elaborated data in non-tabular format

Explore histories with tag “Siduri” then upload datasets to Siduri

The screenshot displays the Siduri Galaxy web interface. On the left is a sidebar with navigation links: Scientific Organization, Scientific Information, Data, Vocabulary, Administration, About, Tools, Open science, Applications, and Web API. The main content area features the Siduri Galaxy logo at the top. Below the logo are buttons for 'Launch analysis' and 'Results'. The 'Show history content' section includes a 'Refresh histories' button, a toggle for 'Show datasets uploaded from Siduri', a dropdown menu for 'History name (with update date)' (currently showing 'Annotation bakta 2026-06-17'), another dropdown for 'Datasets in the history' (showing 'Bakta on dataset 1: Summary'), and two buttons: 'Download dataset locally' and 'Upload dataset to siduri-test.migale.inrae.fr'. The 'Visualize Galaxy dataset' section contains a table with dataset details and a text box with metadata.

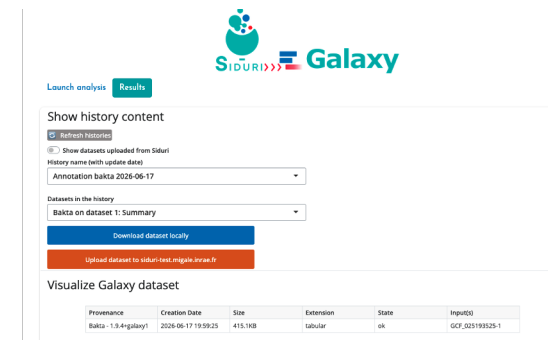
Provenance	Creation Date	Size	Extension	State	Input(s)
Bakta - 1.9.4+galaxy1	2026-06-17 19:59:25	415.1KB	tabular	ok	GCF_025193525-1

Annotated with Bakta
Software: v1.9.4
Database: v5.0, full
DOT: 10.1099/mgen.0.000685

➤ Siduri-x-Galaxy

Keep track of datasets provenance in Siduri

Upload Galaxy datasets as **Datafile** (non-tabular data) with rdf:type **Report**



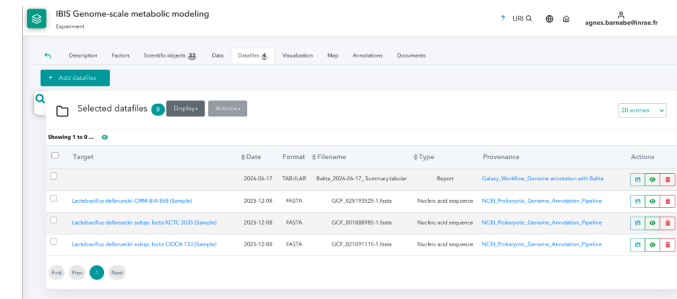
The screenshot shows the Siduri web interface for the experiment 'IBIS Genome-scale metabolic modeling'. The 'Datafiles' tab is active, showing a list of datafiles. The first datafile, 'Bakta_2026-06-17_Summary.tabular', is highlighted with a red box. The table columns are Target, Date, Format, Filename, Type, Provenance, and Actions.

Target	Date	Format	Filename	Type	Provenance	Actions
☐	2026-06-17	TABULAR	Bakta_2026-06-17_Summary.tabular	Report	Galaxy_Workflow_Genome annotation with Bakta	
☐ Lactobacillus delbrueckii CIRM-BIA 865 (Sample)	2025-12-08	FASTA	GCF_025193525-1.fasta	Nucleic acid sequence	NCBI_Prokaryotic_Genome_Annotation_Pipeline	
☐ Lactobacillus delbrueckii subsp. lactis KCTC 3035 (Sample)	2025-12-08	FASTA	GCF_001888985-1.fasta	Nucleic acid sequence	NCBI_Prokaryotic_Genome_Annotation_Pipeline	
☐ Lactobacillus delbrueckii subsp. lactis CIDCA 133 (Sample)	2025-12-08	FASTA	GCF_021091115-1.fasta	Nucleic acid sequence	NCBI_Prokaryotic_Genome_Annotation_Pipeline	

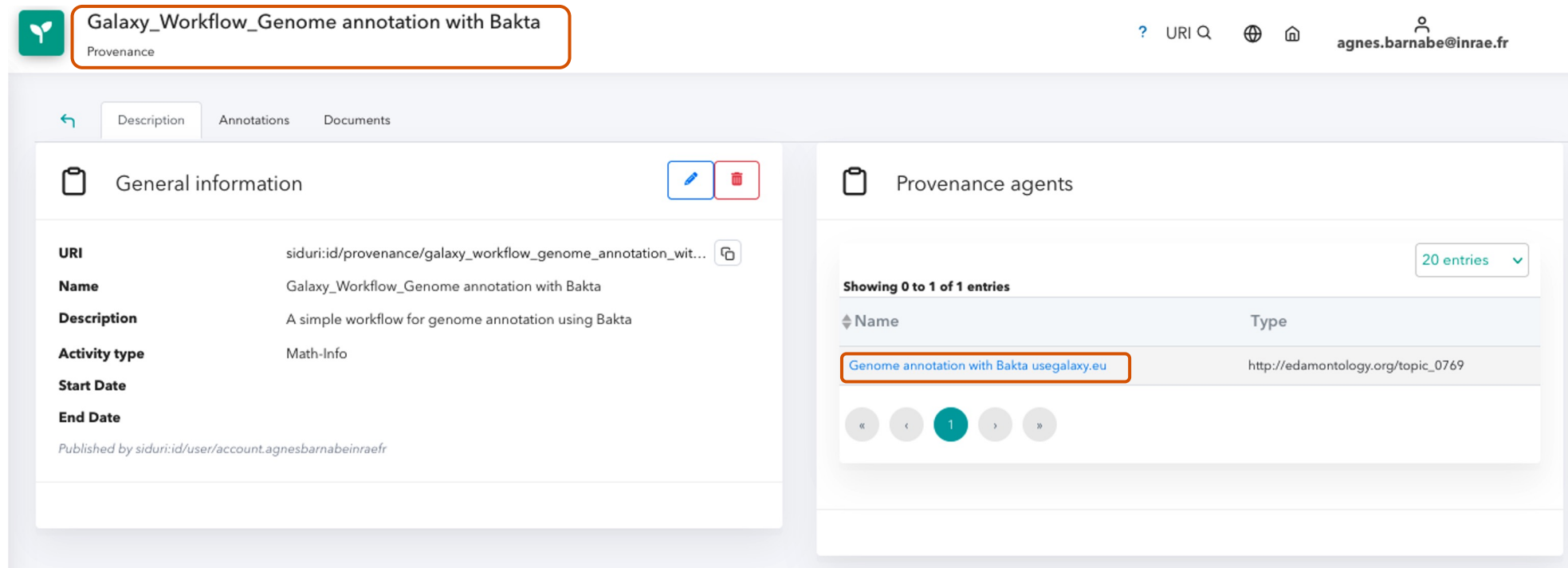
➤ Siduri-x-Galaxy

Keep track of datasets provenance in Siduri

Automatic creation of a **Provenance** with workflow metadata extracted from Galaxy based on **PROV** ontology and data model from **W3C** standard



Target	Date	Format	Filename	Type	Provenance	Actions
☐	2020-06-17	TSV/AR	Bakta_2020-06-17_Summary.tsv	Report	Galaxy_Workflow_Genome annotation with Bakta	View Download Delete
☐	2020-12-08	FASTA	GCF_020199225.1.fasta	Nucleic acid sequence	NCBI Prokaryotic Genome Annotation Pipeline	View Download Delete
☐	2020-12-08	FASTA	GCF_001888965.1.fasta	Nucleic acid sequence	NCBI Prokaryotic Genome Annotation Pipeline	View Download Delete
☐	2020-12-08	FASTA	GCF_020199155.1.fasta	Nucleic acid sequence	NCBI Prokaryotic Genome Annotation Pipeline	View Download Delete



Galaxy_Workflow_Genome annotation with Bakta
Provenance

URI: siduri.id/provenance/galaxy_workflow_genome_annotation_wit...

Name: Galaxy_Workflow_Genome annotation with Bakta

Description: A simple workflow for genome annotation using Bakta

Activity type: Math-Info

Start Date:

End Date:

Published by: siduri.id/user/account.agnesbarnabeinraefr

Provenance agents

Showing 0 to 1 of 1 entries

Name	Type
Genome annotation with Bakta usegalaxy.eu	http://edamontology.org/topic_0769



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➤ Siduri-x-Galaxy

Keep track of datasets provenance in Siduri

Automatic creation of a **Device** to describe the workflow in a specific Galaxy instance with it's unique ID as **attribute**

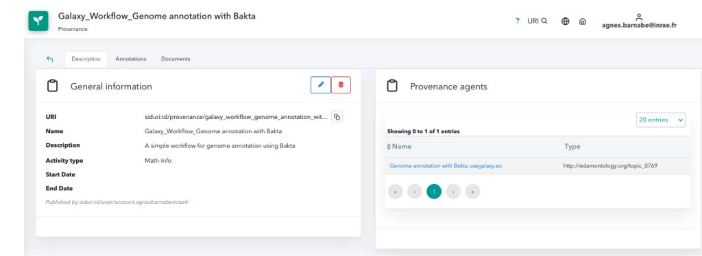
Genome annotation with Bakta usegalaxy.eu
Device

URI: siduri:device/genome_annotation_with_bakta_usegalaxyeu
Type: Workflow
Name: Genome annotation with Bakta usegalaxy.eu
Brand:
Constructor model:
Serial number:
Person in charge:
Start up:
Removal:
Description: A simple workflow for genome annotation using Bakta
Last calibration:
Last position:
Published on 18/06/2026, 00:06:42 by siduri:id/user/account.agnesbarnabeinraefr

Variables
No variable provided

Metadata

Attribute	Value
galaxy-id	992066b1b66bce26
galaxy-instance	https://usegalaxy.eu/workflows/run?id=992066b1b66bce26



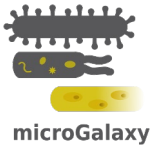
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➤ Achievements

Siduri-x-Galaxy

- Development of a Shiny Python to exchange datasets, explore histories and invoke workflows
- Identification of tools and workflows from *microGalaxy* and *workflow4metabolics* Galaxy Labs
- Automatic traceability of datasets provenance thanks to PROV data model implemented in Siduri



Contributions

- Release FdF developments (wrappers, workflows) to public catalogue and Galaxy project
- Involvement in working groups (Galaxy FR, ELIXIR Microbiome community, IFB Catalogue)



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> Perspectives

Short-term

- Deployment of a dedicated Galaxy instance on Migale infrastructure (IP constraints)
- **Unified user authentication** between Galaxy-FdF and Siduri
- Extension of available workflows to other data families (analytical chemistry, microbial metrics...)

Mid-term

- Improve **workflow execution and monitoring** from Siduri (work in progress)
- **CoFest idea**
 - An **upload plugin** for Galaxy that provides access to OpenSILEX data
 - Link advanced metadata to Galaxy history hidden from the interface





Acknowledgments

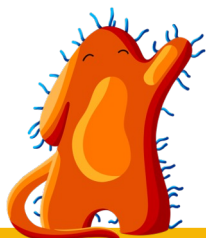
Ferments du Futur program

Siduri team (*Migale, INRAE*)

OpenSILEX team (*MISTEA, INRAE*)

GCC 2026 organizing and scientific program committee

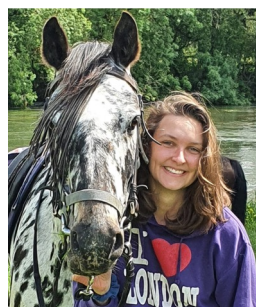




Get in touch!

If you have any question or if you are interested in
Ferments du Futur projects, OpenSILEX...

Join us during breaks or CoFest!



Agnès Barnabé
Bioinformatician

Django
A horse (remote only)

Valentin Loux
Scientific manager

