

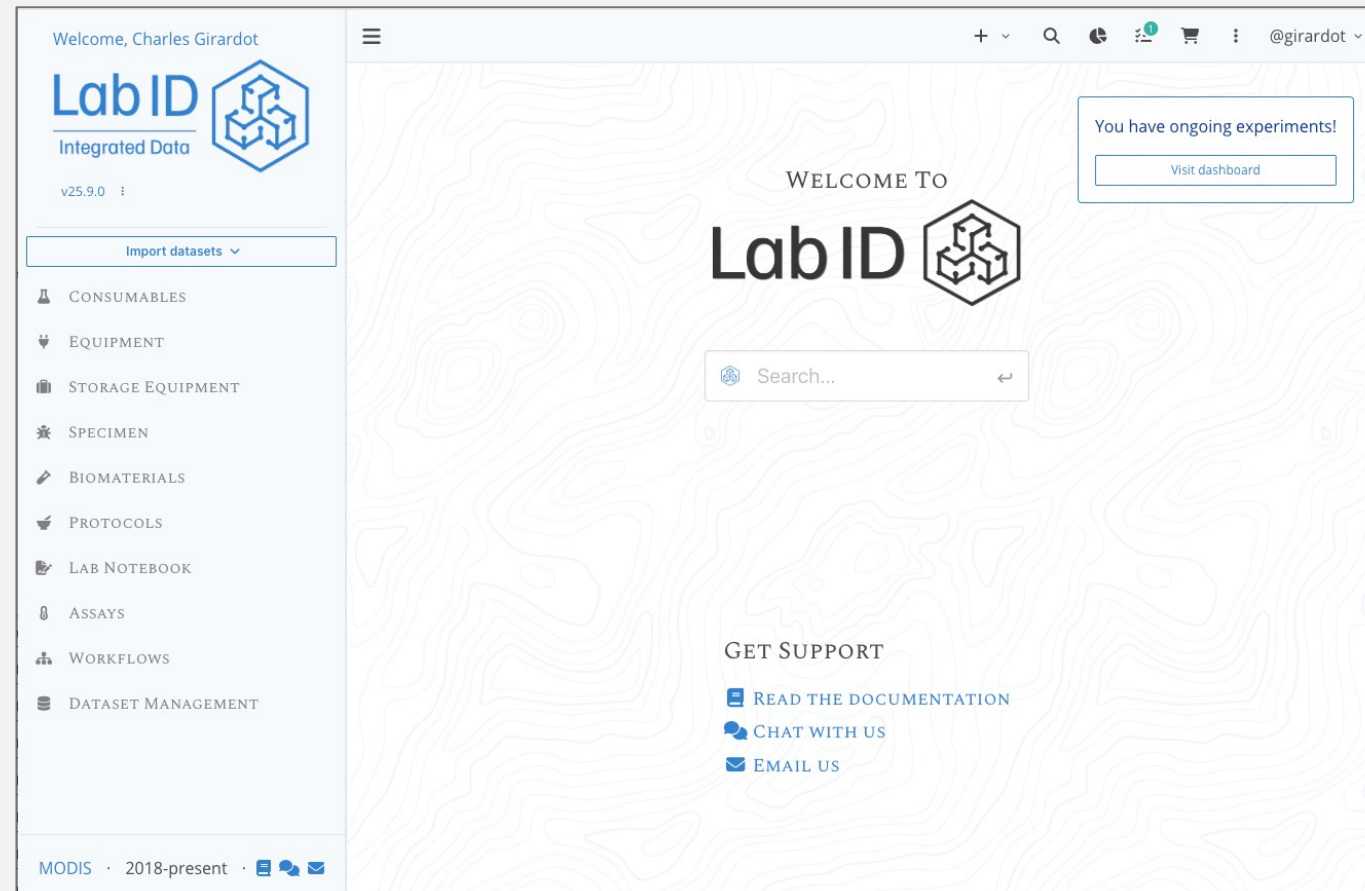
Data Management, Integration and FAIRification with LabID



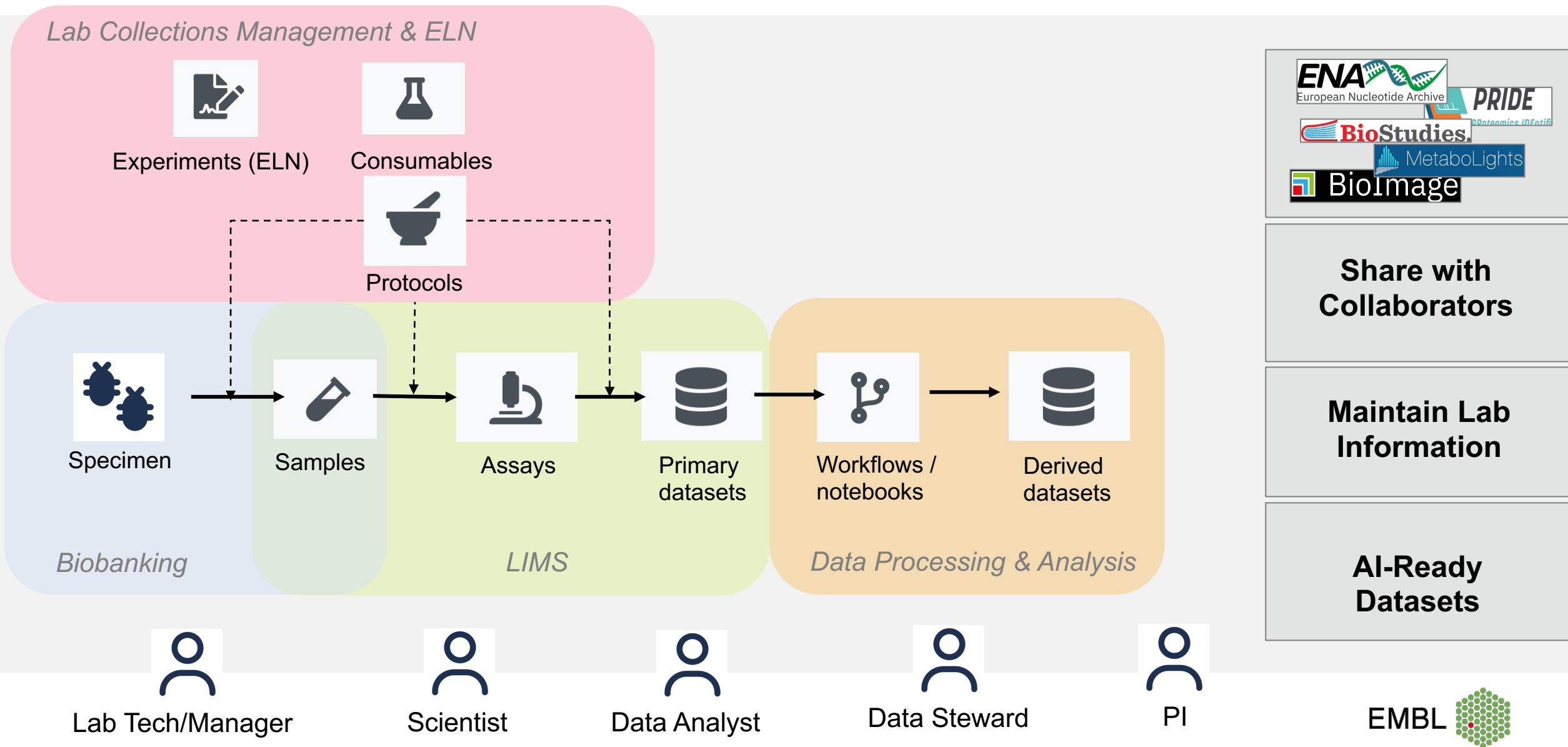
Charles Girardot
Multimodal Open Data Integration Support (MODIS)
Data Science Center

Lab Integrated Data: One-stop shop for managing all your data

- **FAIR** scientific Data Management solution
 - *Collect, Connect, Share Data & Metadata*
 - *Putting your DMP in practice*
- **Open Source**, developed by MODIS (EMBL)
 - ❖ <https://labintegrateddata.org/>
 - ❖ <https://gitlab.com/lab-integrated-data>



Capturing high-quality (meta)data from creation to dissemination



LabID articulates around 4 interconnected modules

Lab ID
Integrated Data



v26.9.0 ▾

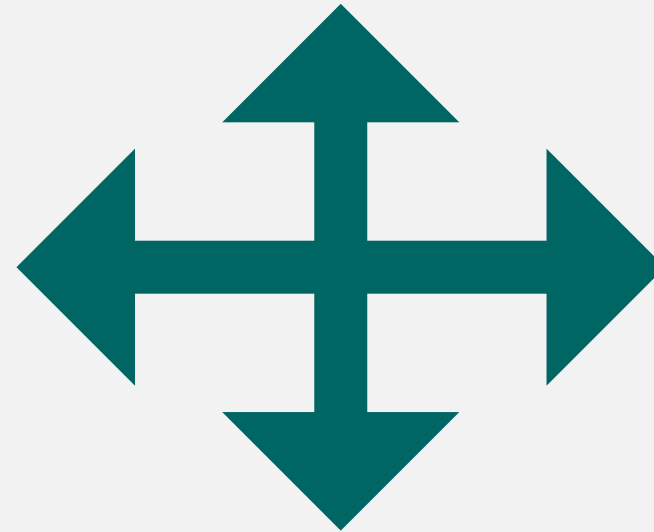
Import datasets ▾

- 🧴 CONSUMABLES
- 🔧 EQUIPMENT
- 📦 STORAGE EQUIPMENT
- 🧬 SPECIMEN
- 🔬 BIOMATERIALS
- 📋 PROTOCOLS
- 📓 LAB NOTEBOOK
- 🧪 ASSAYS
- 👥 WORKFLOWS
- 📊 DATASET MANAGEMENT

Lab Collection Management

(Consumables, Equipment, Storage)

Dataset Management
(Assays, Datasets, Workflows & Studies)



Electronic Lab Notebook (ELN)

(Project, Experiment & Protocols)

Biomaterial Management

(Sample & Specimen, Biobanking)

Unified representation across the software

ex : inventory of sequencers in the institute

Lab ID Integrated Data

development 81 v26.5.1

Import datasets

CONSUMABLES

EQUIPMENT

- Instrument Models
- Optical Components
- Store Items
- Centrifuges
- Microscopes
- IT Supplies
- Software
- Sequencer

EQUIPMENT / SEQUENCER

+ New Sequencer Search

1 2 1-10 of 11

GC

	Name	Code	Origin/Vendor	Stock locations	Responsible Person	Owned by Group
☐	GC - AVITI24 (Him and Mojo Jojo)	AV233002	Element Biosciences	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - GridION (Felonious Gru)	GXB01243	Oxford Nanopore Technologies	V106 Genomics Core Facility	@boulange	Genomics Core Facility
☐	GC - MiSeq i100 (OurSeq)	SH00428	Illumina	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - NextSeq 2000 (Blossom)	VH00558	Illumina	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - NextSeq 2000 (Bubbles)	VH00821	Illumina	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - NextSeq 2000 (Buttercup)	VH00531	Illumina	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - NovaSeq X plus (Titanic)	LH01019	Illumina	V109 Sequencing & Robotics	@boulange	Genomics Core Facility
☐	GC - PromethION 2 Integrated (P2i - Neferio)	p2i-00479	Oxford Nanopore Technologies	V106 Genomics Core Facility	@boulange	Genomics Core Facility
☐	GC - PromethION 2 Solo (P2 solo - Vector)	P2S-01321	Oxford Nanopore Technologies	V106 Genomics Core Facility	@boulange	Genomics Core Facility
☐	GC - PromethION P24 (Bob)	p24-753	Oxford Nanopore Technologies	V106 Genomics Core Facility	@boulange	Genomics Core Facility

➤ Customizable item types & properties

Specimen, the source of your samples

- **Specimen** are your living collections (fly lines, cell lines ...)
- **Samples** may derive from **Specimen**

EMBL Integrated Data v26.9.0

Import datasets

CONSUMABLES

EQUIPMENT

STORAGE EQUIPMENT

SPECIMEN

- TREC
- Cell Line
- Strain
- Fly Line
- Virus
- Cnidaria

	Name	Code	Stock locations	Protocol Code	Shipments	Collection Depth (m)	Country and/or Sea	BioSamples Acc.
☐	sample_2023-06-14T09:12:00Z_TREC_009-06-...	112557392	Box:C1, TREC 4C Cryobox 145 in TREC 4C Eurobox 31 i...	TARA_FM20	BiO5D plate 22/05/2026	0-3	Poland	https://www.ebi.ac.uk/bio
☐	sample_2023-11-08T13:46:00Z_TREC_028-05-0...	112556217	Box:D3, TREC 4C Cryobox 139 in TREC 4C Eurobox 31 ...	TARA_FM20	view 2 items	0-3	Spain	https://www.ebi.ac.uk/bio
☐	sample_2023-11-09T14:02:00Z_TREC_028-06-0...	112556235	Box:C3, TREC 4C Cryobox 139 in TREC 4C Eurobox 31 ...	TARA_FM20	BiO5D Plate 24.04.26	0-3	Spain	https://www.ebi.ac.uk/bio
☐	sample_2023-06-29T09:30:00Z_TREC_012-01-1...	112491101	Box:d1, TREC 4C Cryobox 108 in TREC 4C Eurobox 25 i...	SW_FM20	view 2 items	0-3	Estonia	https://www.ebi.ac.uk/bio
☐	sample_2023-06-30T07:05:00Z_TREC_012-07-...	112557936	Box:B3, TREC 4C Cryobox 144 in TREC 4C Eurobox 31 i...	TARA_FM20	Confocal Screen	0-3	Estonia	https://www.ebi.ac.uk/bio
☐	sample_2023-04-07T12:15:00Z_TREC_001-06-0...	112559508	Box:A4, TREC 4C Cryobox 138 in TREC 4C Eurobox 31 ...	TARA_FM20	Confocal Screen	0-3	France	https://www.ebi.ac.uk/bio
☐	sample_2023-04-08T08:55:00Z_TREC_001-03-...	112489202	Box:a2, TREC 4C Cryobox 112 in TREC 4C Eurobox 25 i...	SW_FM20	Confocal Screen	0-3	France	https://www.ebi.ac.uk/bio
☐	sample_2023-04-08T12:34:00Z_TREC_001-07-...	112559524	Box:D1, TREC 4C Cryobox 138 in TREC 4C Eurobox 31 i...	TARA_FM20	Confocal Screen	0-3	France	https://www.ebi.ac.uk/bio
☐	sample_2023-04-07T07:02:00Z_TREC_001-02-1...	112489119	Box:d2, TREC 4C Cryobox 112 in TREC 4C Eurobox 25 i...	SW_FM20	Confocal Screen	0-3	France	https://www.ebi.ac.uk/bio
☐	sample_2023-06-29T06:31:00Z_TREC_012-06-...	112557918	Box:C4, TREC 4C Cryobox 148 in TREC 4C Eurobox 31 ...	TARA_FM20	Confocal Screen	0-3	Estonia	https://www.ebi.ac.uk/bio

- Biobanking features like **stocks location** and **shipment tracking**

Samples derives from Specimen

include experimental information (protocol and/or experiment) and annotations

Embryos 0-1h yw 5 x 100ee

ID

4acba913-8e17-4d75-934c-231d8b0e9819

Name

Embryos 0-1h yw 5 x 100ee

Code

XYZ-3345

Project

Wonderful microscope project

Status

CREATED

Sample QC

PASSED

Organism

Drosophila melanogaster (Fly)

Material Type

whole organism (Whole Organism)

Description

—

Storage Locations

1. Tube A12-; Furlong Freezer 2 (-20) in V320 Furlong Laboratory

Locations paths

V320 Furlong Laboratory > Furlong Freezer 2 (-20) > Tube:-

Protocols

Fly Growth Protocol

Fly embryo collection

Sample Preparation

Is Control

✗ no

Is Single Cell

✗ no

Use Screen Position

✗ no

Sample Lineage

Derives from

Specimen

Specimen

yw, BEAF-32 330274/CyO; CP190 33903 RNAi

Children

RNA 0-1h yw 8 X aliquots 1ug/10ul

Link to ELN

Used in Experiments

yw RNA extraction for smth seq

Produced by Experiment

yw embryo collection for RNA extraction

Annotations

InitialTimePoint

egg laying

StrainOrLine

yw

Compound Dose

400 mg

IndividualGeneticCharacteristics

wild-type

Compound

ibuprofen

Age

0-1h

Attachments

Drag & Drop your files or [Browse](#)

Notes

Write a note

Add

Lineage Graph

Datasets (3)

Samples (6)

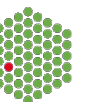
Specimen (1)

Everything

Find Element

Accumulate key information for FAIR data sharing and deposition

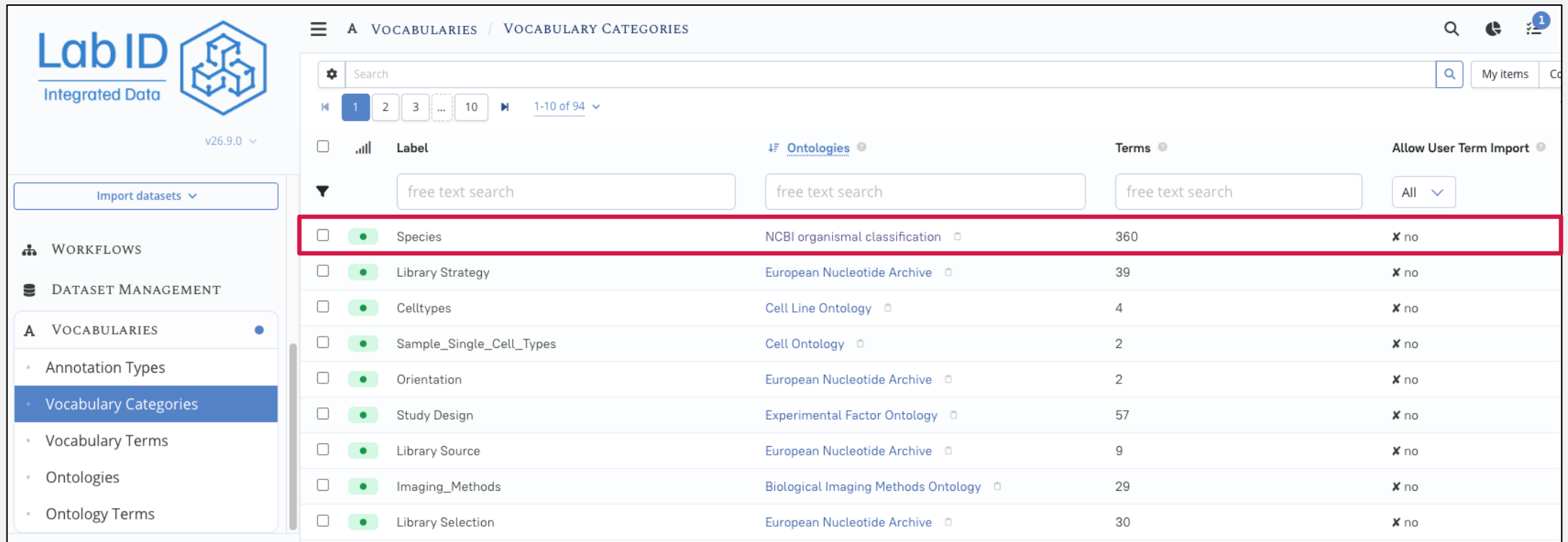
- **Experimental Variables as annotations**
 - Genotype
 - Cell Line
 - Developmental Stage
 - Treatments...
- **Controlled Vocabulary**
- **Protocols**
- **Lineage graph representing provenance**
 - biological vs technical replicates
 - collect metadata at the appropriate level
- **Connection to integrated ELN**

EMBL 

Integration with Ontologies

- Controlled Vocabulary locally defined can be mapped to Ontologies

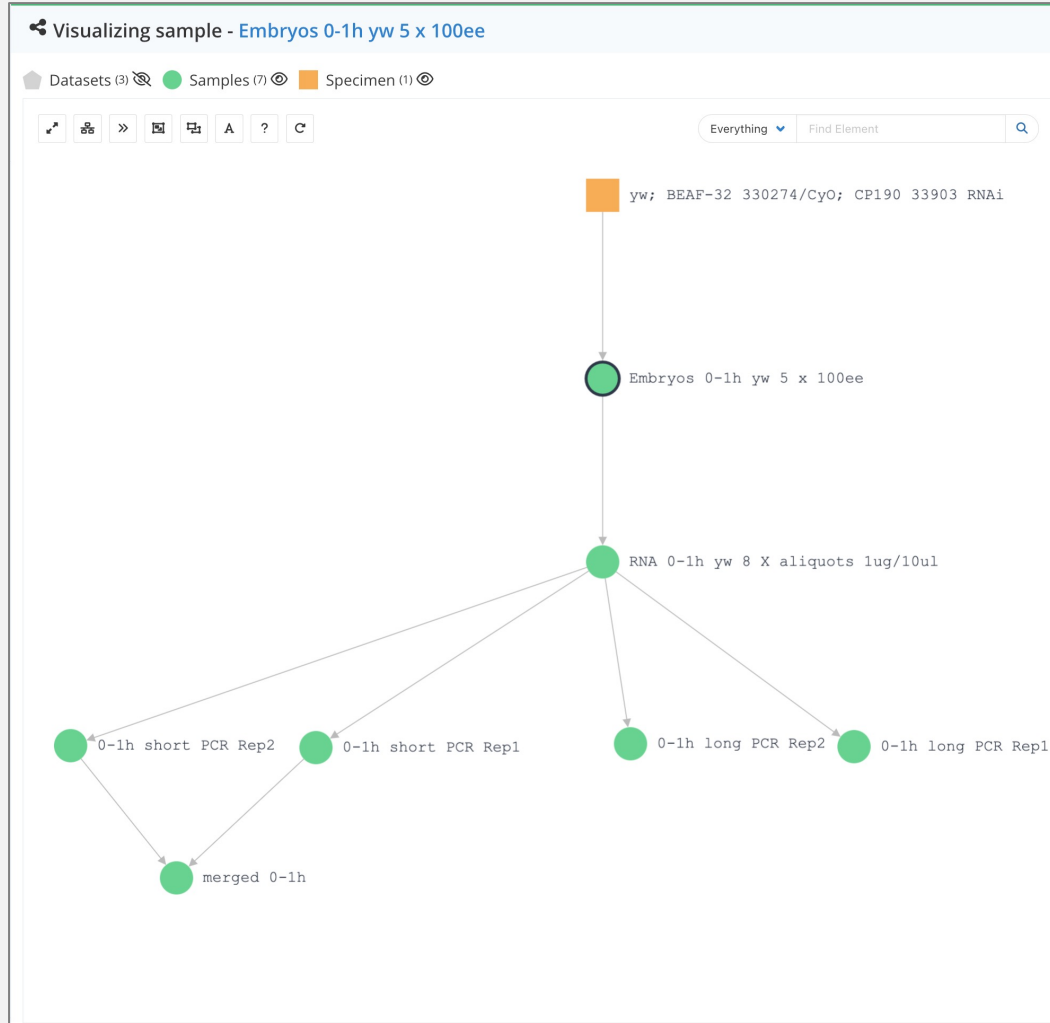
For example, the local “species” term category (used to e.g. describe a sample’s organism) is mapped to the NCBI Taxonomy



The screenshot displays the 'VOCABULARIES / VOCABULARY CATEGORIES' page in the Lab ID system. The interface includes a sidebar with navigation options like 'Import datasets', 'WORKFLOWS', 'DATASET MANAGEMENT', and 'VOCABULARIES'. The main area shows a table of vocabulary categories, each with a checkbox, a status indicator (green dot), a label, an ontology mapping, a term count, and an 'Allow User Term Import' toggle. The 'Species' category is highlighted with a red border.

☐	Label	Ontologies	Terms	Allow User Term Import
☐	Species	NCBI organismal classification	360	☒ no
☐	Library Strategy	European Nucleotide Archive	39	☒ no
☐	Celltypes	Cell Line Ontology	4	☒ no
☐	Sample_Single_Cell_Types	Cell Ontology	2	☒ no
☐	Orientation	European Nucleotide Archive	2	☒ no
☐	Study Design	Experimental Factor Ontology	57	☒ no
☐	Library Source	European Nucleotide Archive	9	☒ no
☐	Imaging_Methods	Biological Imaging Methods Ontology	29	☒ no
☐	Library Selection	European Nucleotide Archive	30	☒ no

Accurately reflect your sample processing workflow



- **Graphical Lineage** of relationships
- **Unlimited** step number
- **Merge & Split** supported

Sequencing library is a specialized sample type

➤ ENA-compliant metadata (values as controlled)

Import datasets

CONSUMABLES

EQUIPMENT

STORAGE EQUIPMENT

SPECIMEN

BIOMATERIALS

Sample

Sequencing Library

EM Sample

All

BIOMATERIALS / SEQUENCING LIBRARY

+ New Sequencing Library

Search

1 - 10 of 766

	Name	Material Type	Orientation	Selection	Source	Strategy
	free text search	free text search	free text search	free text search	free text search	free text search
☐	010INjwGV	polyA RNA (PolyA RNA)	5'-3'-3'-5' (5'-3'-3'-5')	cDNA_oligo_dT (cDNA_oligo_dT)	TRANSCRIPTOMIC (TRANSCRIPTOMIC)	RNA-Seq (RNA-Seq)
☐	011INjwGV	polyA RNA (PolyA RNA)	5'-3'-3'-5' (5'-3'-3'-5')	cDNA_oligo_dT (cDNA_oligo_dT)	TRANSCRIPTOMIC (TRANSCRIPTOMIC)	RNA-Seq (RNA-Seq)
☐	012INjwGV	polyA RNA (PolyA RNA)	5'-3'-3'-5' (5'-3'-3'-5')	cDNA_oligo_dT (cDNA_oligo_dT)	TRANSCRIPTOMIC (TRANSCRIPTOMIC)	RNA-Seq (RNA-Seq)

➤ Embedded support for Single Cell library information

☐	Is single cell sample	Name	Read Layout Cell Barcode Slot	Read Layout UMI Slot	Read Layout cDNA Slot	Library construction	Cell isolation
	Yes	free text search	free text search	free text search	free text search	10x multiome	free text search
☐	✓ yes	NPC2	read1/0/16	read1/15/8	read2/22/21	10x multiome	10X
☐	✓ yes	Neuron2	read1/0/16	read1/15/8	read2/22/21	10x multiome	10X
☐	✓ yes	NPC1	read1/0/16	read1/15/8	read2/22/21	10x multiome	10X
☐	✓ yes	Neuron1	read1/0/16	read1/15/8	read2/22/21	10x multiome	10X

Describe protocols with details and share with your lab

The screenshot displays the Lab ID Integrated Data web application. On the left is a sidebar with a navigation menu including CONSUMABLES, EQUIPMENT, STORAGE EQUIPMENT, SPECIMEN, BIOMATERIALS, PROTOCOLS (highlighted with a red box), LAB NOTEBOOK, ASSAYS, WORKFLOWS, and DATASET MANAGEMENT. The main content area shows a protocol titled 'Fixation and staining - version 2'. At the top of this section are buttons for Edit, Copy URL, Clone (highlighted with a red box), Derive Lab Note, PDF, and Delete. Below the title is a 'Summary' section with the text 'Fixation in 3.7 % PFA in 100 % EtOH, staining with DAPI and Phalloidin'. The main body of the protocol is titled 'Fixation and Staining of sponges in PFA' and contains a bulleted list of steps: gemmules are grown in glass bottom dishes; under the hood: prepare fixative (3.7 % (P)FA [37 % stock solution], 100 % ice-cold EtOH, e.g.: 720 uL EtOH + 80 uL PFA); remove all of the FLW from the sponges; add 200 uL of the fixative directly to the glass bottom (sponges should be covered) (otherwise, use more fixative --> 1 mL); incubate for 30 min - 1 h at 4 oC; wash 3 x with 5 mL PBS (keep third washing step for 10 min); remove PBS; add 200 uL of staining solution (e.g.: DAPI, Phalloidin, antibody staining). At the bottom is an 'Item details' section with fields for ID (1f76b3b6-1f8a-4e8a-8bad-211e868df7c3), Type (LABELING), Parent protocol (Fixation and staining), and Modified (2023-10-27 18:16:23).

- **Protocols are cooking recipes**
- **Rich text** formatting
- Embed **tables and images**
- **Attach** documents e.g. excel table
- Export to **PDF**
- **Protocols** may be **versioned** ("Clone")
- **Protocols** act as templates for **Experiments**

An experiment is an entry in your ELN

Fixation and staining of sponges in PFA

- bottom dishes
- ive
- solution]

PFA

sponges

ctly to the glass bottom (sponges should be covered)

tive --> 1 mL

pC

or 10 min

n

tbody staining

1f76b3b6-1f8a-4e8a-8bad-211e868df7c3

LABELING

Fixation and staining

2023-10-27 18:16:23

Lab ID
Integrated Data
v26.1.1

Import datasets

- CONSUMABLES
- EQUIPMENT
- STORAGE EQUIPMENT
- SPECIMEN
- BIOMATERIALS
- PROTOCOLS
- LAB NOTEBOOK**
 - Projects
 - Experiment
- Studies
- ASSAYS
- WORKFLOWS
- DATASET MANAGEMENT

EXPERIMENTS

Fixation and staining - version 2 - 2023-10-27 18:22:52

Project: Wonderful microscope project

Estimated Completion Date: 2023-11-03

Status: (in progress)

Created on: 2023-10-27 18:22:52

Fixation and Staining of sponges in PFA

- gemmules are grown in glass bottom dishes
- under the hood: prepare fixative
 - 3.7 % (P)FA [37 % stock solution]
 - 100 % ice-cold EtOH
 - e.g.: 720 uL EtOH + 80 uL PFA
- remove all of the FLW from the sponges
- add 200 uL of the fixative directly to the glass bottom (sponges should be covered)
 - otherwise, use more fixative --> 1 mL

It worked

Item details

ID	c6208f09-1a4c-43c1-838b-34685912bb7
Deleted	no
Summary	—
Start date	2023-10-27
Completed	—
Frozen	no

Linked items (5)

- 0-Nitrophenyl β-D-Galacto-Pyranoside
- 0.3% alcian blue in 70% ethanol
- 10 mM Alexa Fluor™ 405 NHS Ester in DMSO
- AatII
- Accl

Attachments (2)

- Experiments grouped into **Projects**
- Experiment may consume Samples (*Input Samples*) and produce Samples (*Output Samples*)
- Experiments have a **life-cycle**: **Frozen experiment** are electronically **timestamped**

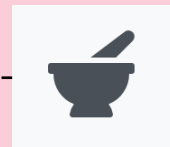
Lab Collections Management & ELN



Experiments (ELN)



Consumables



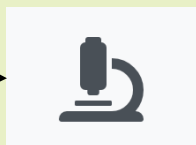
Protocols



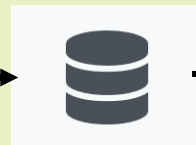
Specimen



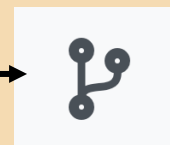
Samples



Assays



Primary
datasets



Workflows /
notebooks



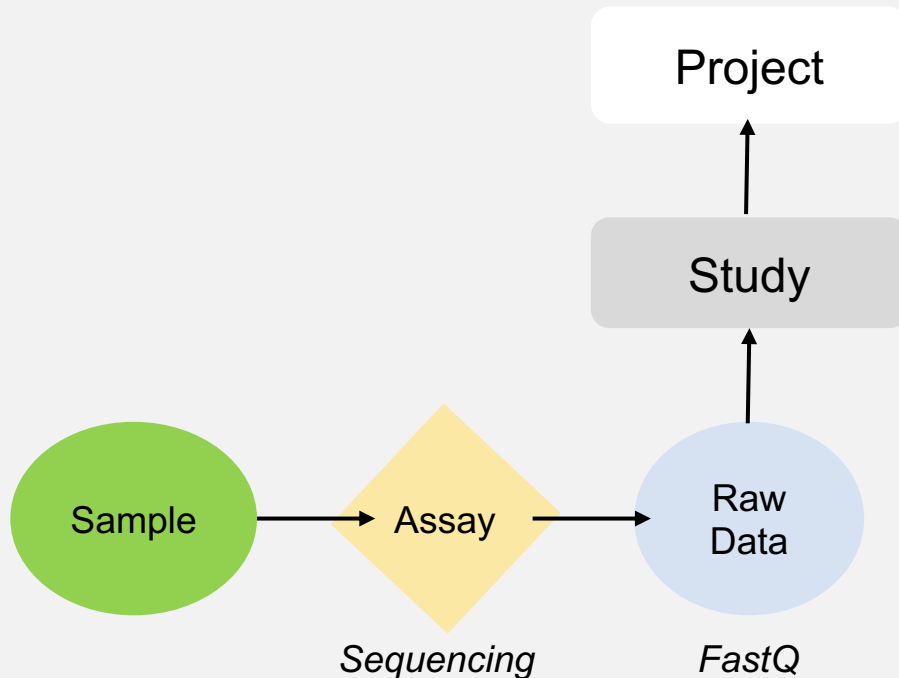
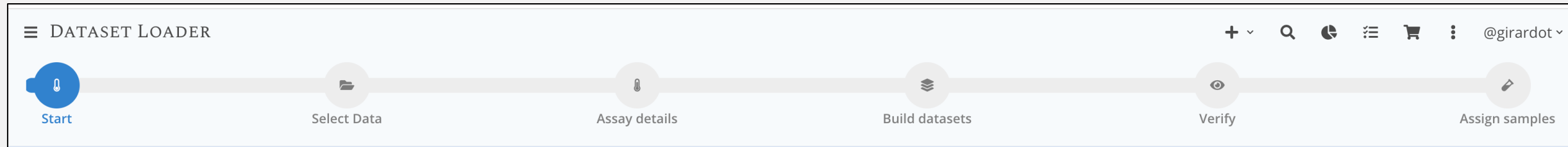
Derived
datasets

Biobanking

LIMS

Data Processing & Analysis

Connecting datasets with samples at data registration



- An **Assay** uses samples and generates Raw data by **running an instrument**
- **Datasets** are organized into **Studies** that belong to **Projects**
- General support for **all types of assay**
- **Specialized support** for Sequencing, Light & Electron Microscopy

Assay view

ex: sequencing assay

Lab ID

Integrated Data

development 81 v26.5.1

Import datasets

CONSUMABLES

EQUIPMENT

STORAGE EQUIPMENT

SPECIMEN

BIOMATERIALS

PROTOCOLS

LAB NOTEBOOK

ASSAYS

Generic

Illumina Sequencing

Nanopore Sequencing

AVITI Sequencing

Light Microscopy

Light Microscopy Screen

Transmission EM

Volume EM

ASSAYS / ILLUMINA SEQUENCING

23KCKNLT3_lane1

Edit Not your data? Clone Send to S3 Sync with Galaxy Delete

Assay Details

Registered Managed

Name23KCKNLT3_lane1

IDc8334d0e-ffe8-48b2-84b0-86aa4f05bc13

StateREGISTEREDIs TemplateX no

Multiplexed✓ yesNr. of samples5

StudiesFrag-C for Ramile and Vale (hearts and cardio-organoids)

Run directory/g/funcgen/base/labid-data/dev/g/furlong/STOCKS/Data/Assay/sequencing/2026/2026-04-29-23KCKNLT3

Linked datasessions2026_04_29_13_31_42.90_golov

Description—

ProtocolList—

Run Parameters

InstrumentGC - NovaSeq X plus (Titanic)

Sequencer Session20260424_LH01019_0022_B23KCKNLT3

Flowcell23KCKNLT3Flowcell version—

Lane1

Run typePaired-End

Run mode61-8-8-61Read length—

Annotations0

Pick an annotation type to add

Lineage Graph

Assays (1) Datasets (5) Samples (5)

samples

5 datasets

23KCKNLT3_lane1

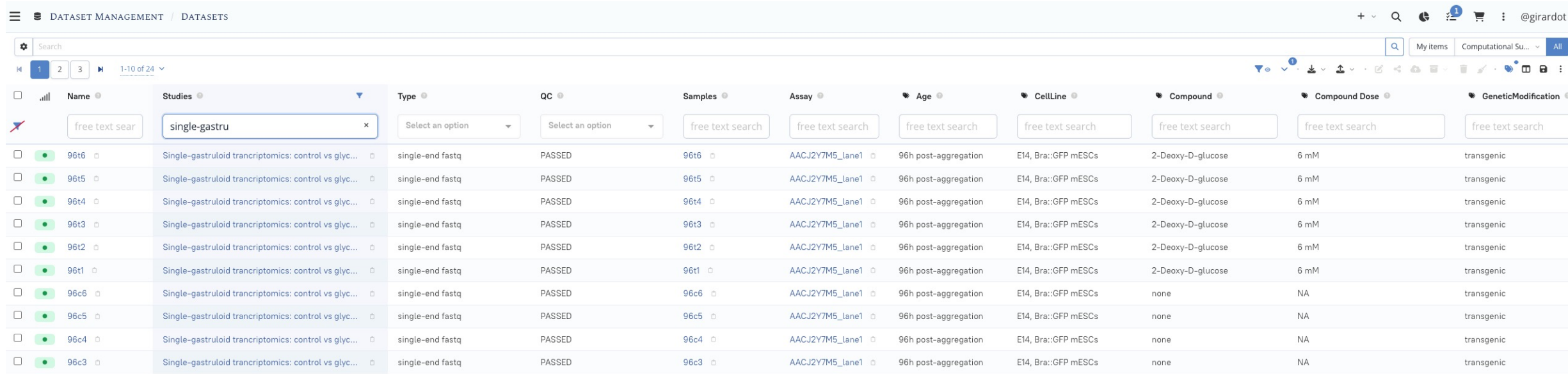
Notes0

Write a note

Add

With references to instrument, samples & datasets

“Datasets” as flexible data-units



Name	Studies	Type	QC	Samples	Assay	Age	CellLine	Compound	Compound Dose	GeneticModification
96t6	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t6	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96t5	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t5	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96t4	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t4	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96t3	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t3	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96t2	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t2	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96t1	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96t1	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	2-Deoxy-D-glucose	6 mM	transgenic
96c6	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96c6	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	none	NA	transgenic
96c5	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96c5	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	none	NA	transgenic
96c4	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96c4	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	none	NA	transgenic
96c3	Single-gastruloid transcriptomics: control vs glyc...	single-end fastq	PASSED	96c3	AACJ2Y7M5_lane1	96h post-aggregation	E14, Bra::GFP mESCs	none	NA	transgenic

- Datasets can be **accessed and filtered by** assays, studies, projects, samples or annotations
- A **Dataset** is made of **file(s) and/or folder(s)**
 - ex: paired-end fastq dataset with 2 files
- Dataset, Datafile & Datafile Copy are all *annotable*, separately

Standard-compliant metadata for (EBI) submission

ENA Library Information including single-cell support

Sequencing Library Preparation			
Library Kit Type	10x 3' v3.1	Orientation	5'-3'-3'-5' (5'-3'-3'-5')
Barcode	GTCCTTCGGC CTGTGCATGA		
Source	TRANSCRIPTOMIC SINGLE CELL (RNA-seq of coding RNA from single cells or RNA-seq of non coding RNA from single cells)	Strategy	ssRNA-seq (ssRNA-seq)
Selection	cDNA_oligo_dT (cDNA_oligo_dT)	RT Primer Type	oligo-dT
Library Strand	NA	End Bias	3 prime end bias

Single-Cell Sample			
Single Cell Type	normal cell	Cell Number	12927
Single Cell Library Construction	10x 3' v3	Single Cell Isolation	10X

Study Design, Exp Factor & Contributors

Name	Bait-capture based single molecule footprinting of Sox2 degran mESC line
Project	Genetic_variation
Design	biological replicate , genetic modification design , strain or line design
PubMed ID	—
Description	Bait-capture based Single Molecule Footprinting (SMF) data. SMF data is obtained by treating extracted nuclei with a GpC and a CpG methyltransferase, where binding of proteins on DNA, e.g. nucleosomes and transcription factors (TFs), leave behind unmethylated cytosines as footprints. Data in this experiment comprises SMF data obtained from a previously reported Sox2 degran mESC line (see PMID: 33318687). Sequencing libraries were prepared using Agilent Sure-Select Mouse Methyl-Seq kit, enriching the sample for cis-regulatory regions of the mouse genome prior to library preparation. Thus, these data contain high coverage accessibility information at regulatory loci in different cell types.
Nr. of datasets	7
Archives	—
Experimental Factors & Required Annotations	7
Contributors	3

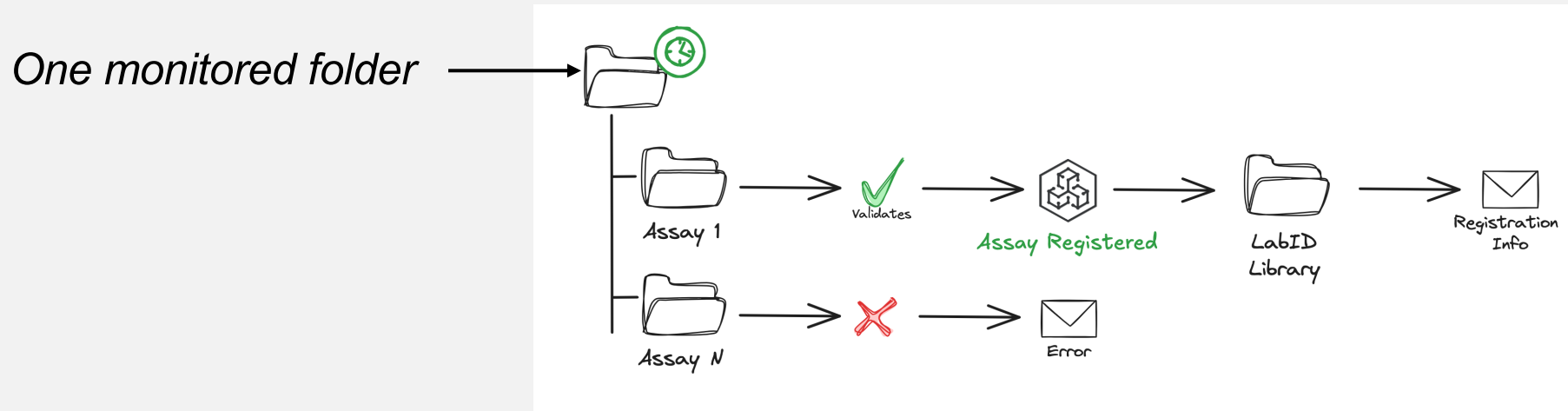
</> XML

MAGE-TAB



✓ 180+ studies submitted to date

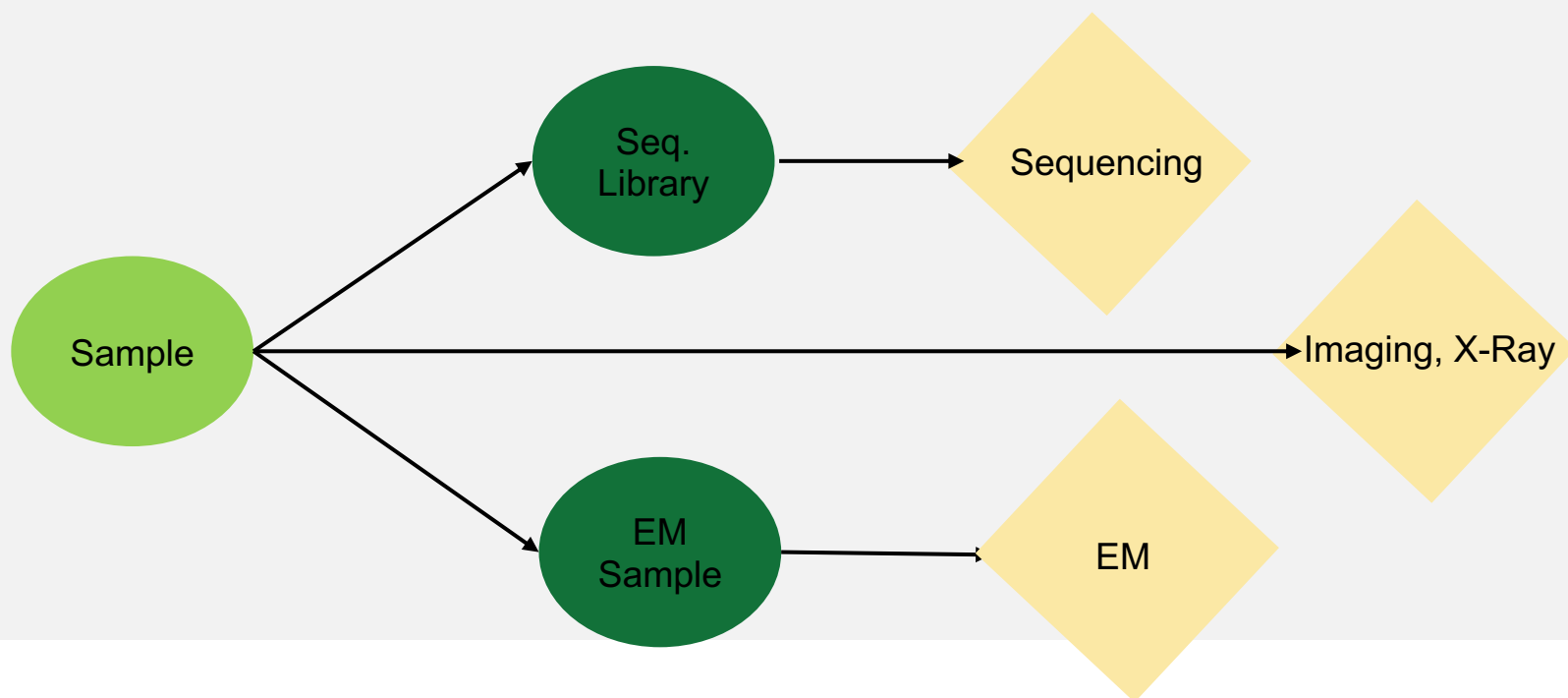
Data Registration Automation



- ✓ Automate (primary) data registration in well defined scenarios (e.g. experiment type, project)
- ✓ Registration only happens after successful content validation
 - ✓ Data structure, Naming convention (as defined in DMP)
 - ✓ Rule enforcement e.g. samples must already exist...
- ✓ Similar assays are registered the same way
- ✓ Metadata Extraction
- ✓ Plugin approach

Supporting multi-modal & multi-site projects

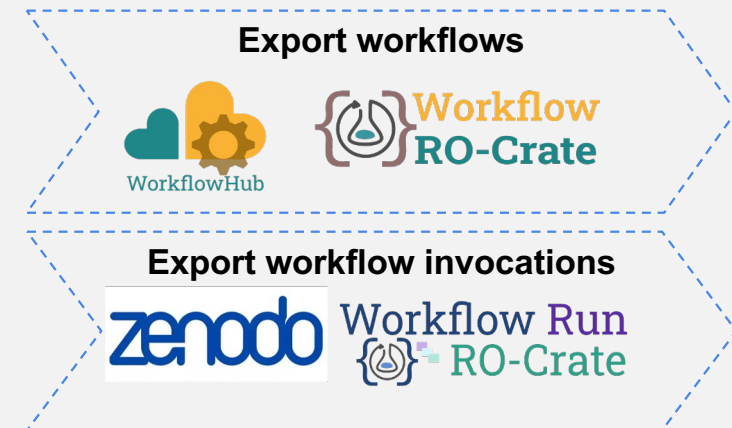
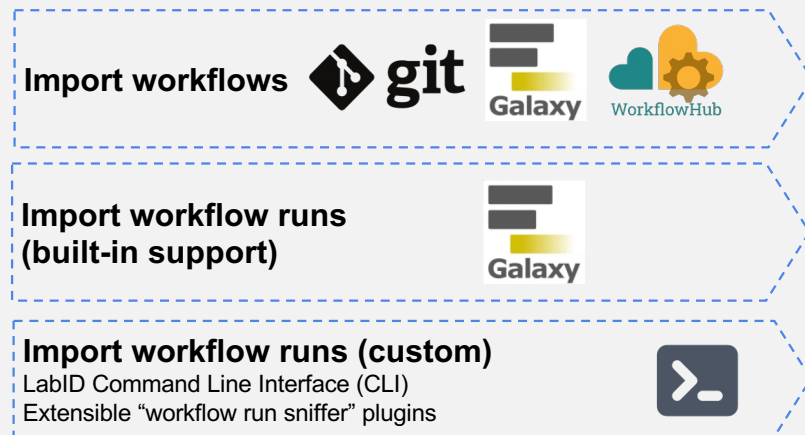
- Projects frequently look at samples using different modalities
- Spatial-omics associate sequencing and image datasets
- Correctly linking multi-modal datasets to their common origin is key
- Data generated at different sites



Interoperability with workflow ecosystem

LabID supports the concept of

- **Workflow:** from simple script to popular WMS (Galaxy, Nextflow, Snakemake...)
- **Workflow Run** to capture execution of a specific workflow version with metadata



Straightforward data processing using Galaxy Workflow

ATAC-seq of wildtype or Dppa2 knockout ESC upon release c

[Sync with Galaxy](#)

Item details

ID: 2735409c-3cc2-47a9-a7d7-799c7eb70695

Project: VC20_007 CnR in Dppa2KO

Design: biological replicate, genotype design

PubMed ID:

Description: Chromatin accessibility was assayed in *wildtype* or *Dppa2* knockout ESC after 26 days of release of the trigger imposed by epigenetic editing. Samples were collected in two clonal *knockout* and *wildtype* lines after sorting at FACS of cells which maintained a repressive Esg1-tdTomato (TOMneg) reporter expression after 26 days of DOX washout (release of the trigger).

Nr. of datasets: 4

Archives

Modified: 2021-05-11 11:56:49

Modified by: girardot

Created: 2021-05-05 14:34:19

Created by: carlini

Owner: carlini

Owned by Group: Hackett Group

Permissions

	View	Edit	Delete
Groups			
Hackett Group	✓	✓	
Users			
carlini	✓	✓	✓
girardot	✓	✓	

Datasets

Name	Description	Type	QC	Samples
KOB67dWTOMneg_HG7WLBGXG_1		paired-end fastq	PASSED	KOB6_26dDW_TOI
KOC7dWTOMneg_HG7WLBGXG_1		paired-end fastq	PASSED	KOC7_26dDW_TOI
WT126dDW_HG7WLBGXG_1		paired-end fastq	PASSED	WT1_26dDW
WT226dDW_HG7WLBGXG_1		paired-end fastq	PASSED	WT2_26dDW

No data duplication

Galaxy

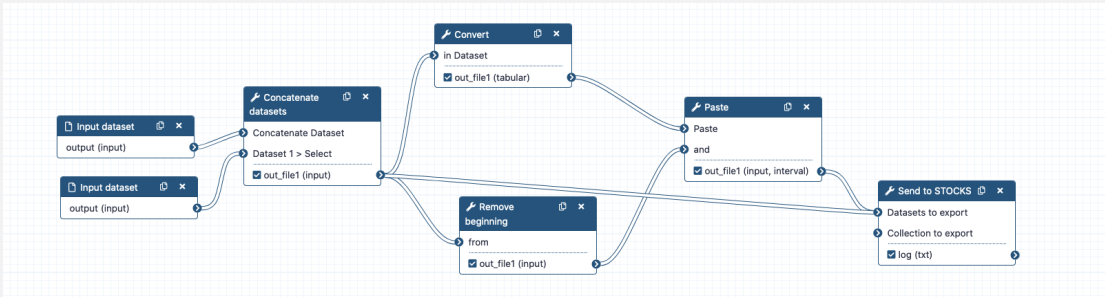
Workflow Visualize Shared Data Admin Help User

Libraries / Hackett Lab / VC20_007 ATAC-seq Dppa2KO

Name	Description	Type	Size	Updated	State
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_1_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	845.3 MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_2_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	847.1 MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_3_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	241.6 MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_4_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	242.5 MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_5_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_6_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	421.1 MB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_7_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	1.1 GB	a year ago	Manage
HG7WLBGXG_VC20_006-VC20_007_20x002698-1-1_Carlini_Jane1KOB67dWTOMneg_8_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	1.1 GB	a year ago	Manage

<https://galaxy.embl.de>

Start ATAC-seq Standard WF



All jobs executed on ITS HPC

WF Run Metadata + Link

Processed Data

Online Doc & Training Material

- Discover by theme
 - ELN
 - Lab Inventory
 - Sample Management
 - Dataset & Assays
 - Advanced topics
- Presentations & recorded videos
- Hands-on material that can be run independently
- Separate server for training

The screenshot displays the LabID Documentation website. The 'Training' tab in the top navigation bar is highlighted with a red box. The left sidebar lists various topics under 'Training', including 'Agenda', 'Electronic Lab Notebook', 'Collection Management', 'Sample Management', 'Dataset & Assay Management', 'Galaxy Sync', and 'Command Line Interface'. The main content area shows the 'Foreword' section, which includes a 'Use a training instance' box with instructions on how to access the training environment. Below this, the 'Summary' section is titled 'Electronic Lab Notebook (ELN) and Lab Collections' and contains a table of training modules.

Title	Topics	Duration	Link
Overview	Inventory, Sample & Data Management, Concepts	8min	
Electronic Lab Notebook (ELN)			
Presentation			
1 - Explore Lab Notes	Create a note & explore functionalities	25min	Go
2 - Explore Protocols	Create a protocol & derive a lab note	15min	Go
3 - Explore Permissions & Lifecycle	Understand the different status of an experiment	10min	Go
Lab Collection Management			
Presentation	Consumable, Equipment & Storage Equipment		
1 - Create, Browse and Edit Items	Create collection items & explore functionalities	45min	Go

Thank you

Multimodal Open Data Integration Support (MODIS) part of EMBL Data-Science Center



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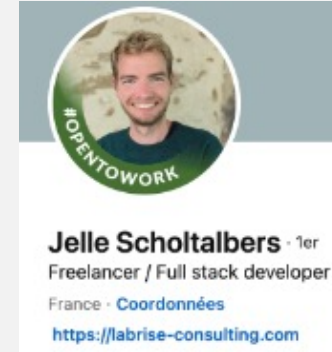
Matthias Monfort

Web Developer / Workflow Management



Marco Wetter

Full Stack Developer



Join LabID on Slack

Contact : modis@embl.de