Part 1

The Basics of Benchling

An introduction to our **Laboratory Information Management System** (LIMS)

Reach out when struggling with Benchling:

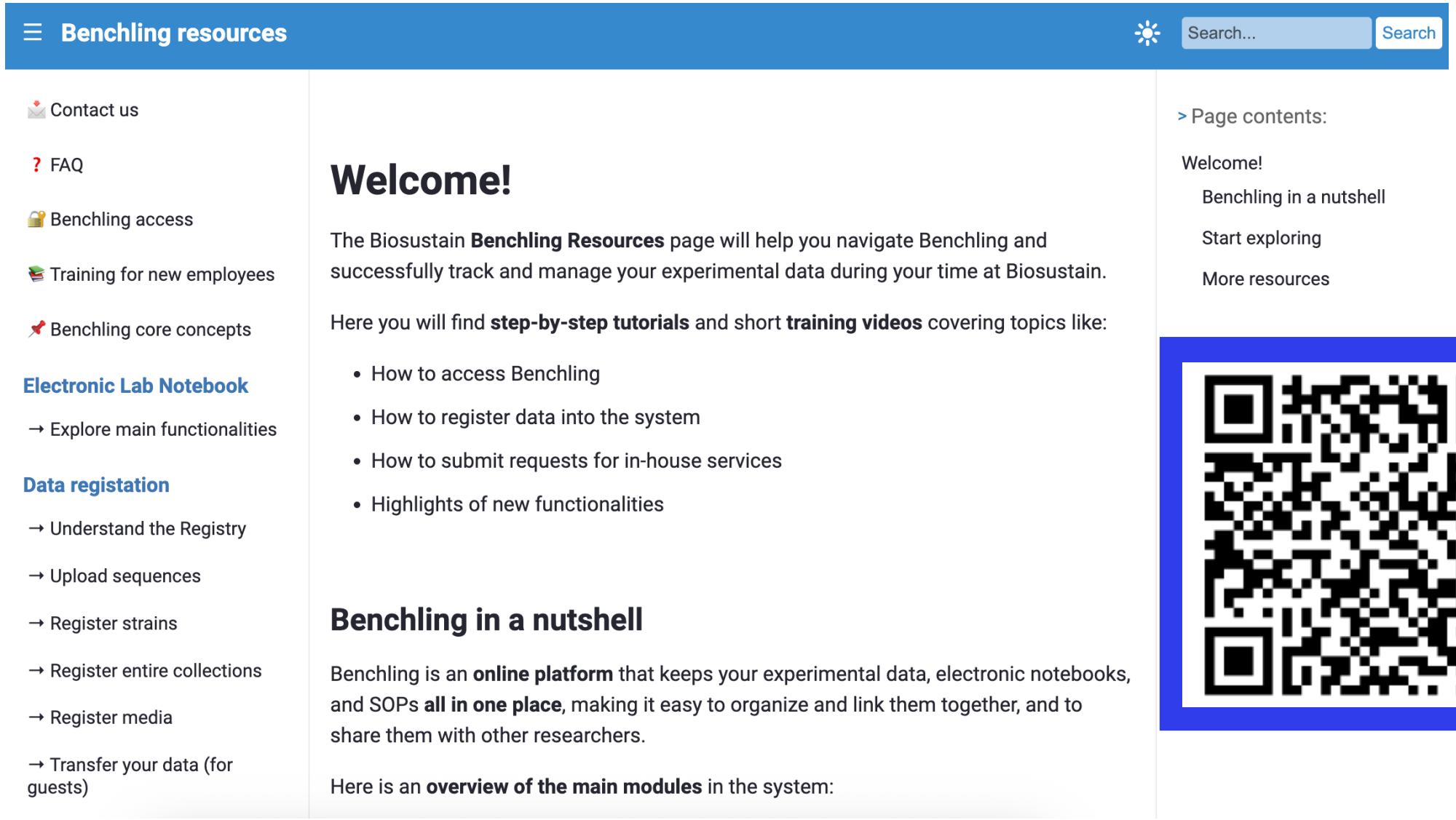
Biosustain Benchling support
lims_support@biosustain.dtu.dk

Access Benchling:

biosustain.benchling.com

(login with DTU credentials)

Check out our new Benchling Resources wiki



Check out our new Benchling Resources wiki

📩 Contact us

❓ FAQ

🔐 Benchling access

📚 Training for new employees

📌 Benchling core concepts

Data registation

→ Understand the Registry

→ Upload sequences

→ Register strains

→ Register entire collections

→ Register media

→ Transfer your data (for guests)

New functionalities

→ Try out Plate Maps

Electronic Lab Notebook

→ Explore main functionalities

In-house services

→ Order lab materials

→ Submit samples for analysis to DNA Foundry and PPP

→ Submit samples for analysis to Analytics (new Workflows)

→ Execute Analytics Workflows (for analysts only)

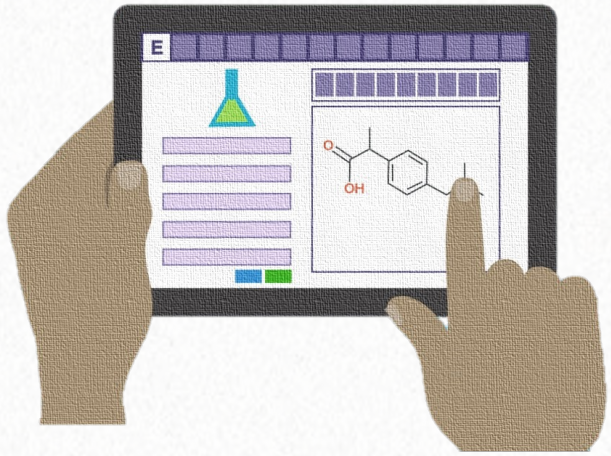
Agenda

- Introduction to Benchling and best practices — ~ 30 min
- Hands-on — ~ 15 min

Agenda

Introduction to Benchling and best practices	~ 30 min
Hands-on	~ 15 min

What is a LIMS?



What is a LIMS?

L.I.M.S = Laboratory Information Management System

- It **keeps track of laboratory data** associated with samples and experiments
- At Biosustain, we use **Benchling**, a Cloud-based platform

biosustain.benchling.com

Main functionalities

ELN

- Experiment notes
- Registration of samples

Samples storage

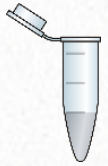
- Samples transfer in boxes/plates

Molecular Biology tool

- Import of sequences
- Plasmid design and annotation

Requests

- Samples submission for analysis
- Lab material order request



Working with Benchling

Benefits

- Facilitates **passing over** of projects
- Foster **collaboration**
- Promotes data capture in a **defined place** preventing its loss
- Make knowledge **findable**
- Promotes the adoption of **common practices** across research groups

Working with Benchling

Obstacles

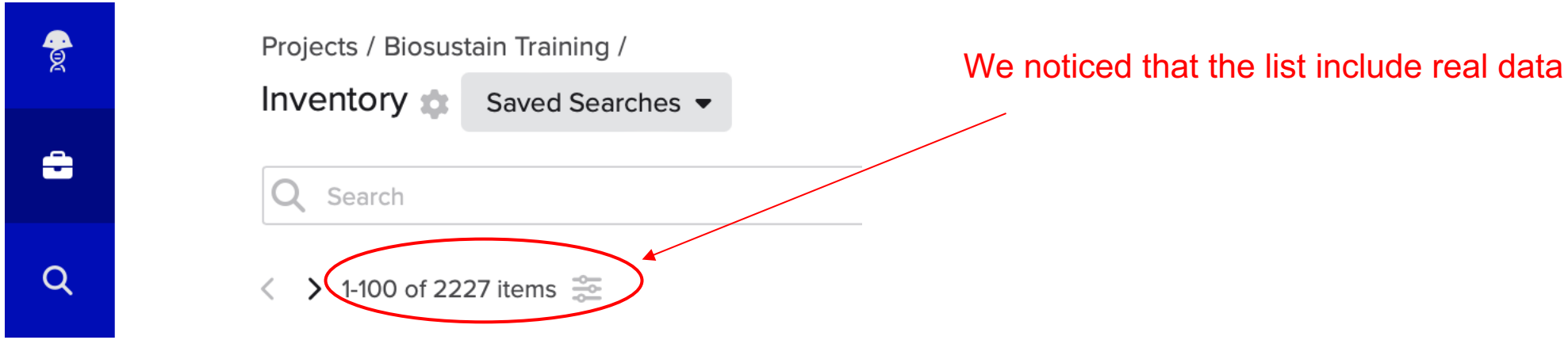
- Adapting to a **new way of working**
- **Software limitations** and “pain points”
- **Learning curve**
  - Many functionalities
  - Complex / confusing data model

Good practices

- ✓ Record all necessary information to make your experiment **clear to others** and reproducible
- ✓ Register important data (strains, media, plasmids…)
- ✓ Keep your project folders organized and use **clear names** and **descriptions**

Good practices

- ✓ Make sure **not** to save relevant data in the **Biosustain Training** project folder



Good practices

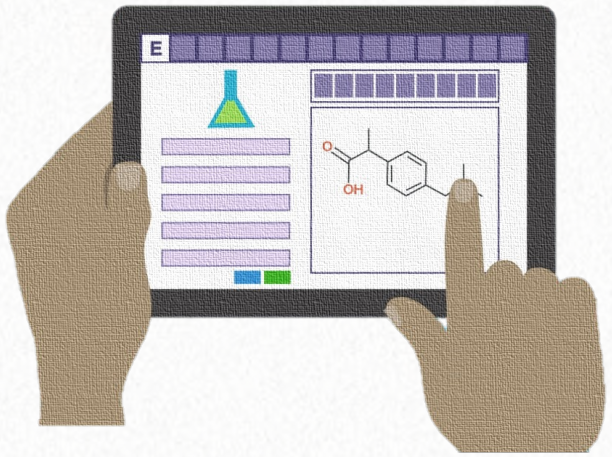
- ✓ Reach out when struggling using the platform
- ✓ There might be a **quicker** and **easier** way to do what you are doing !

Submit your questions to
lims_support@biosustain.dtu.dk

Get hands-on Benchling support

Mondays 13:00 -14:00 (Room 222)

Getting started



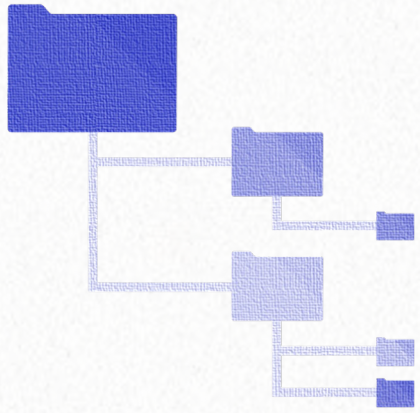
Step 1: Create your project folder

Step 2: Create your experiment ELN & register samples

Step 3: Navigate through your data

Step 1:

Create your project folder



Project folder

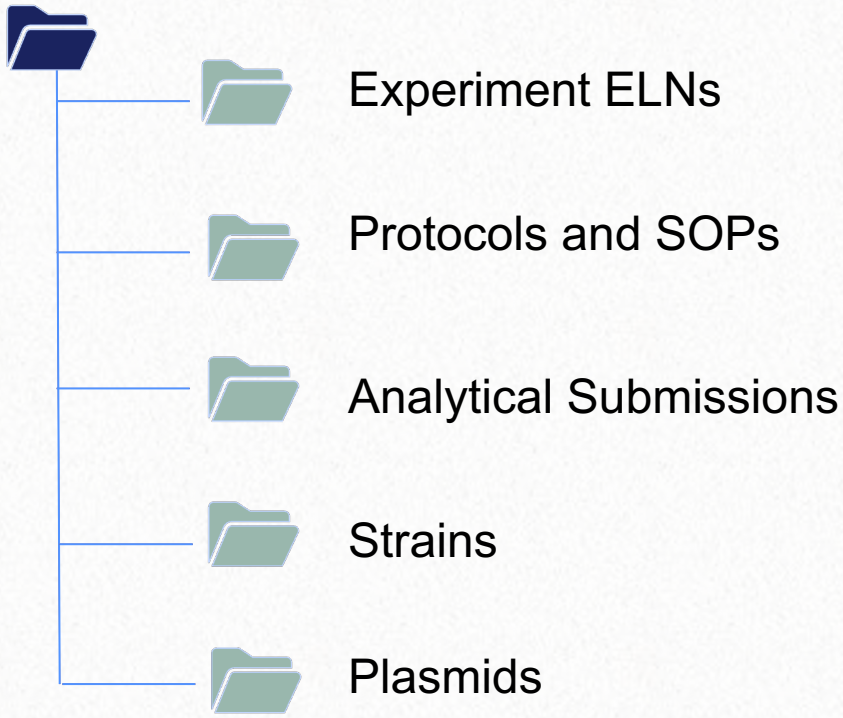
Your Project folder will contain:

- ✓ your Electronic Notebook pages (called “**Entries**”)
- ✓ your registry items (called “**Entities**”) strains, plasmids,…

Example of folder structure

Project folder

Subfolders

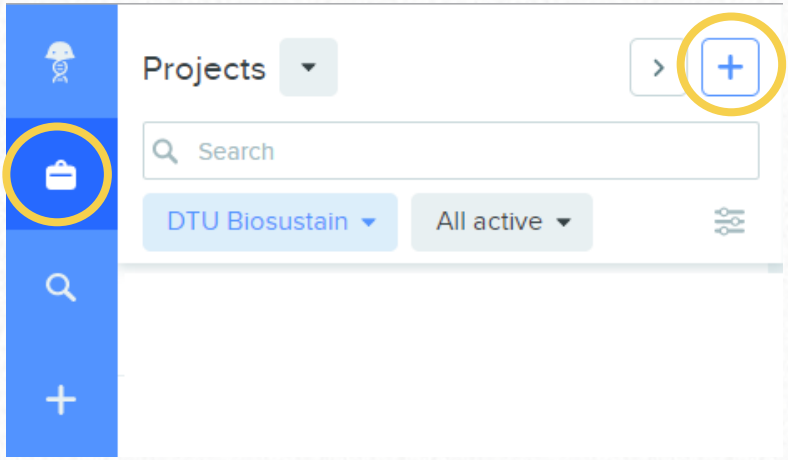


Project folder

To create a New Project:

- Click on the “Project” icon
- Click on the “+” icon

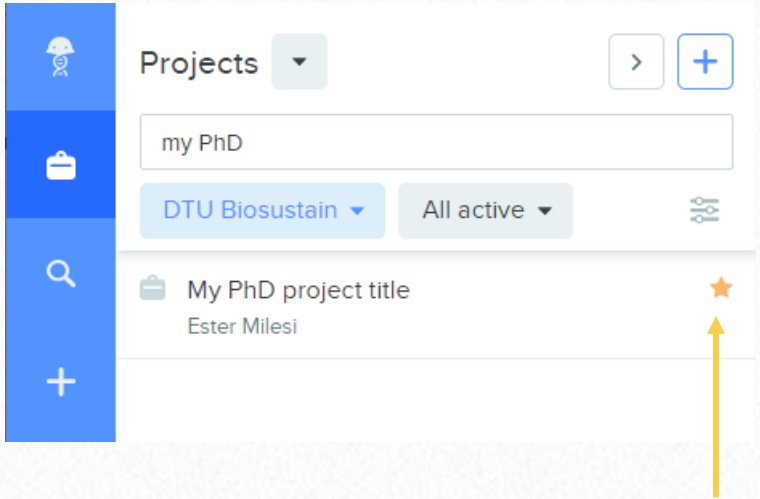
- Give the folder a clear name (e.g., your PhD project title)



Project folder

Star ★ your Project:

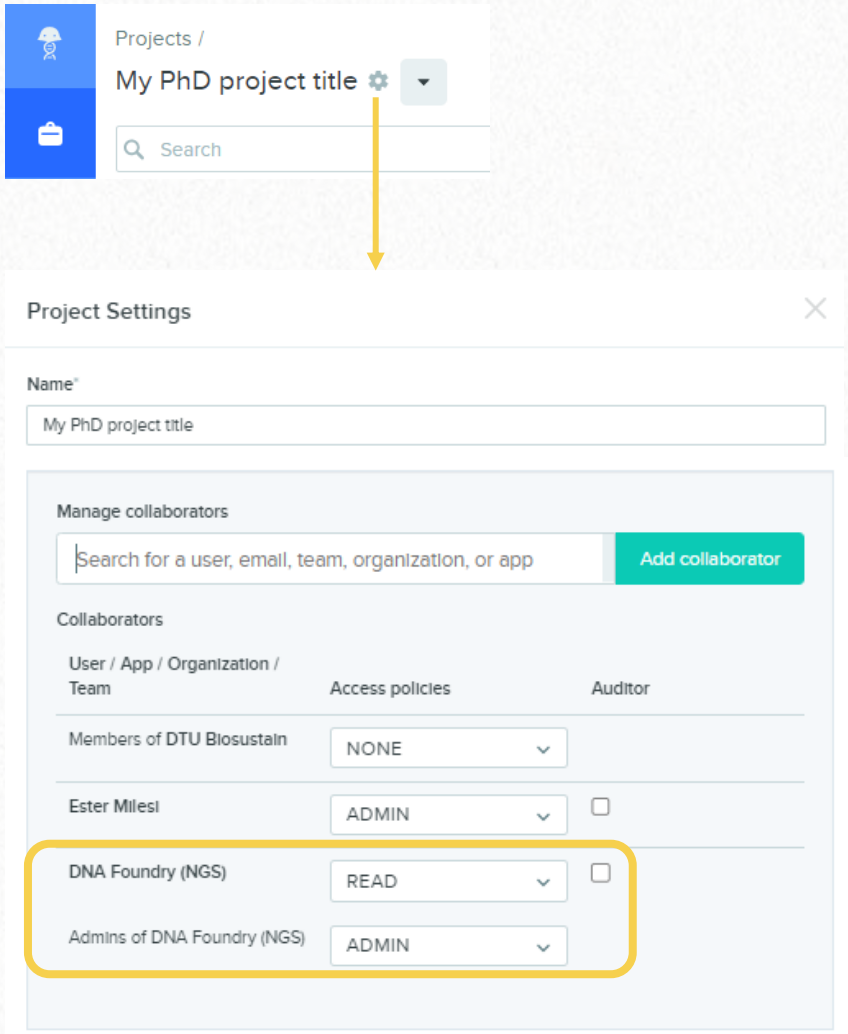
- This way, it will appear on top of every other Project that you have access to



Project folder

Give access to your team

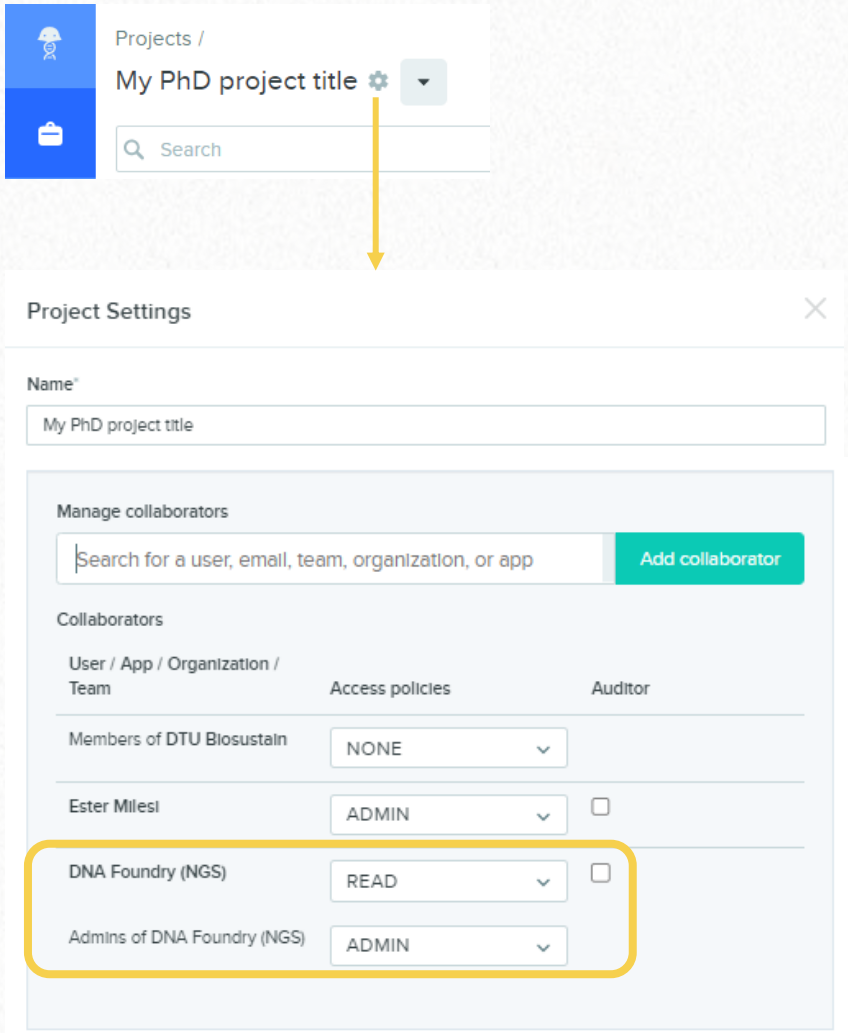
- Almost all Research groups have a **Benchling Team**
- When possible, add **your Team** among the collaborators of the Project



Project folder

Benefits

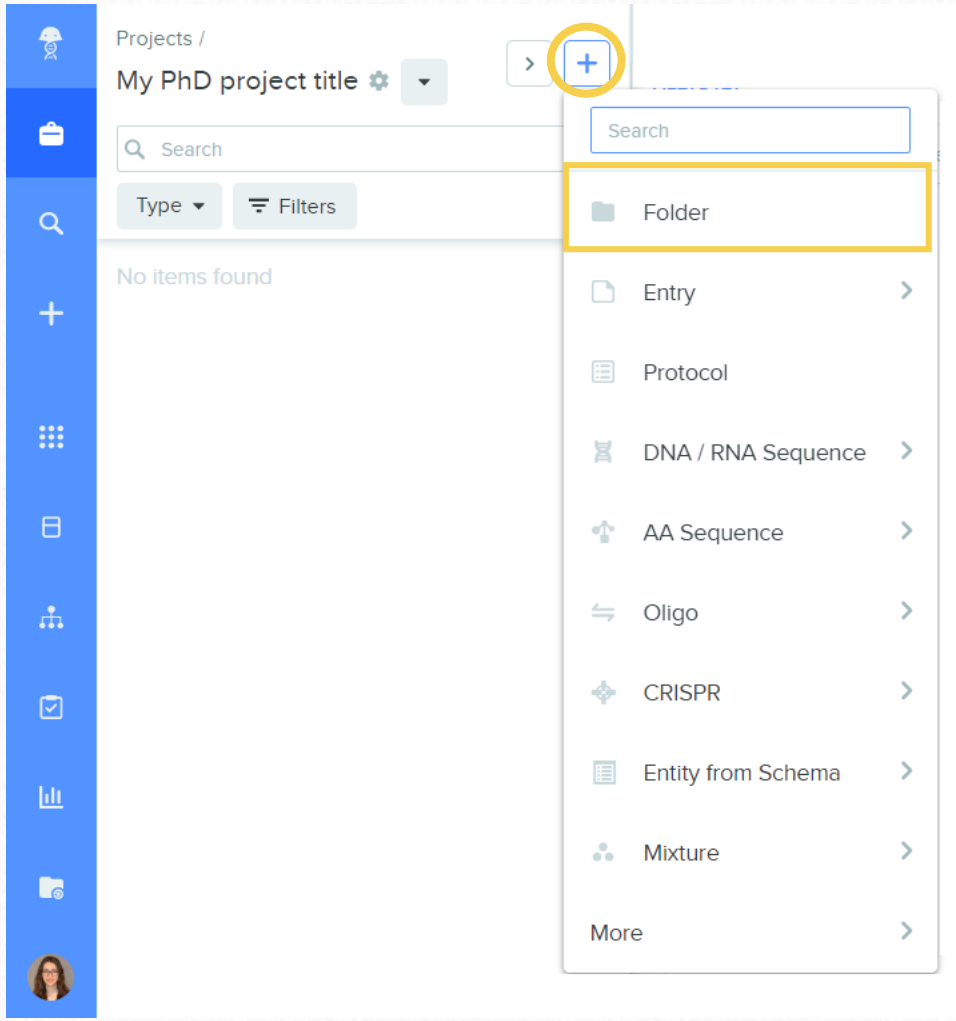
- ✓ You don’t have to add each member one-by-one
- ✓ When new researchers join the Team, **they get automatically access to all shared Project folders**



Creating subfolders

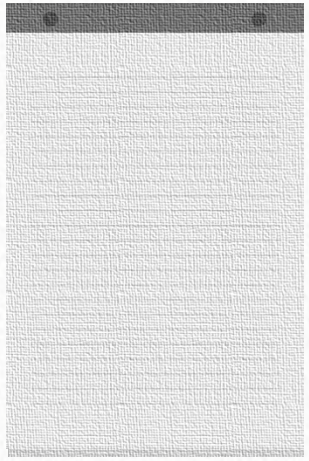
To create a subfolder:

- Enter your newly created Project
- Click on the “+” icon
- Select “Folder”



Step 2:

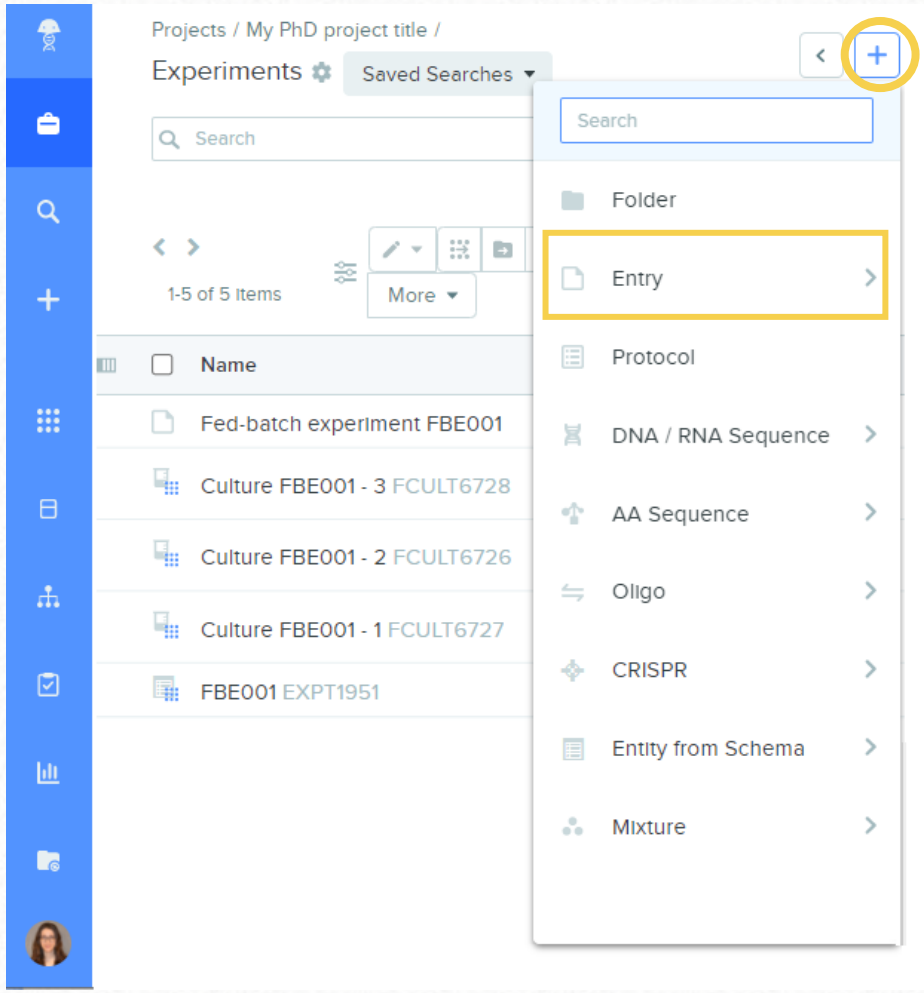
Create your experiment ELN & create samples



Electronic notebook

To create a new Entry:

- Go to the relevant folder (e.g., “Experiments”)
- Click on the “+” icon
- Select “Entry”



Electronic notebook

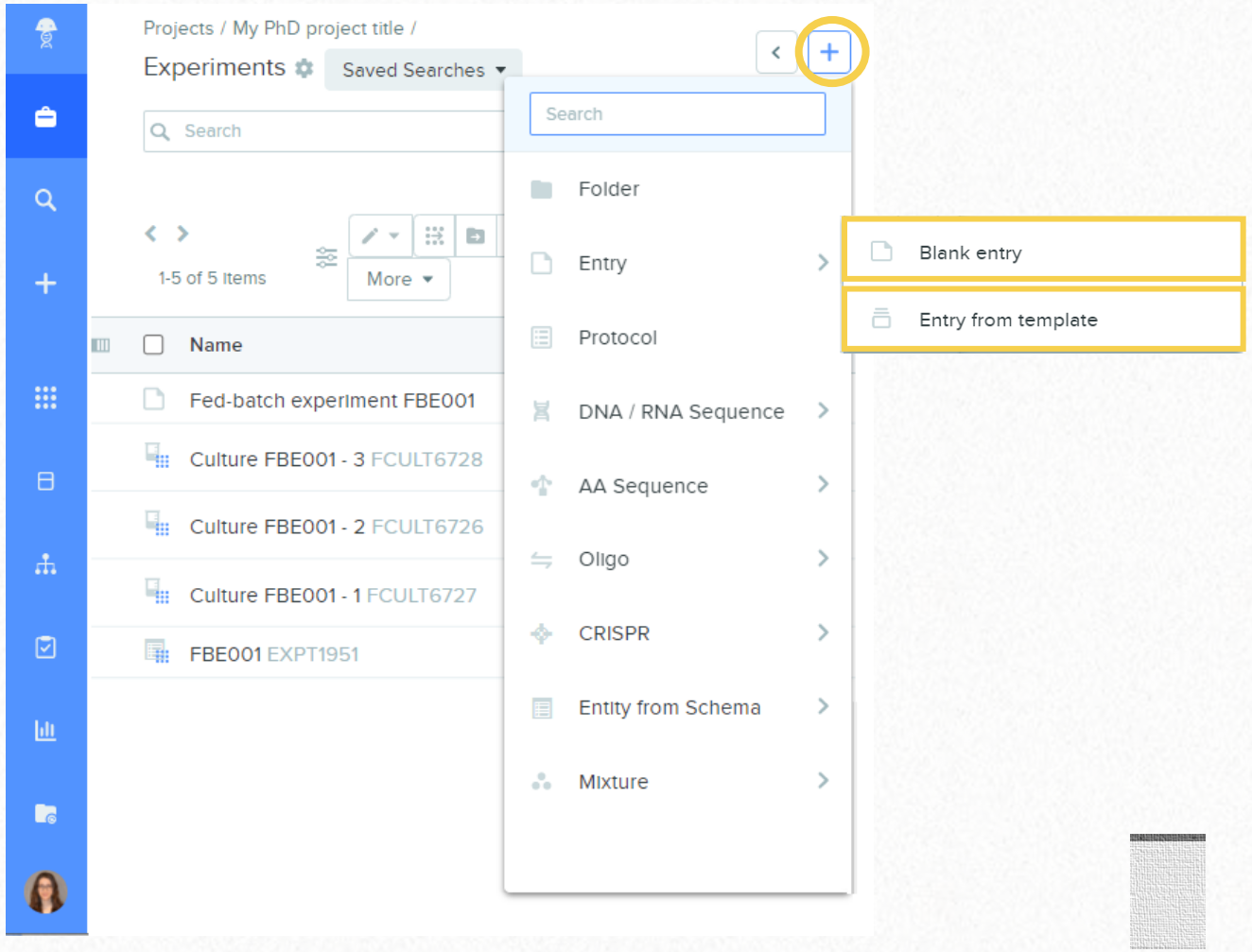
Option 1:

Blank entry

Option 2:

New Entry from Template

--- you can create your own!

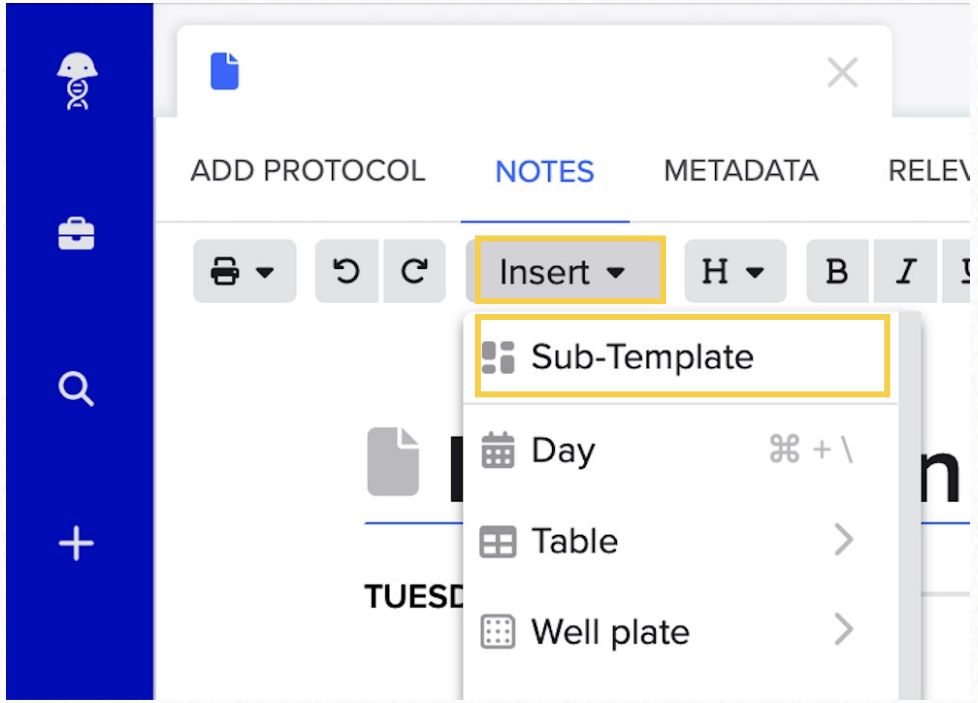


Electronic notebook

Option 3:

Blank entry + Sub-Template

--- you can create your own!

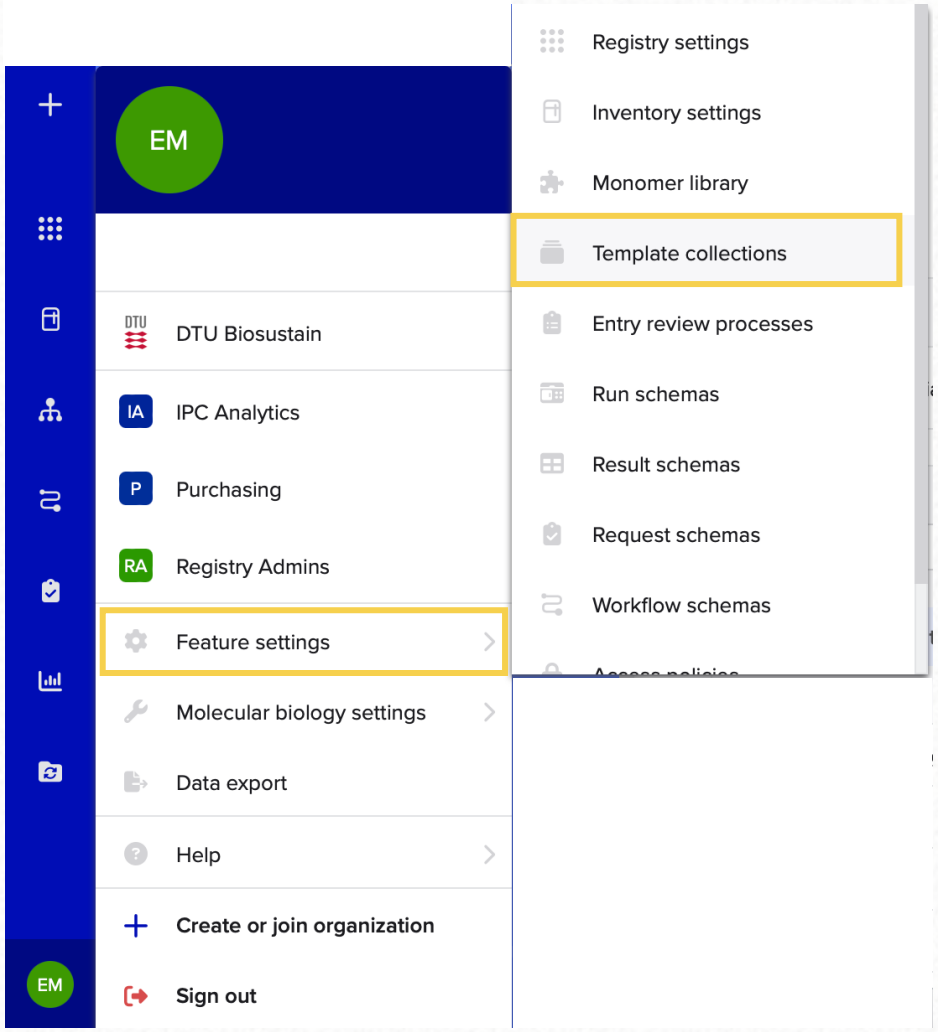


Electronic notebook

To create a Template or a Sub-template:

- Go to your profile
- Go to Feature settings
- Go to Template collections

Create your own!



Electronic notebook

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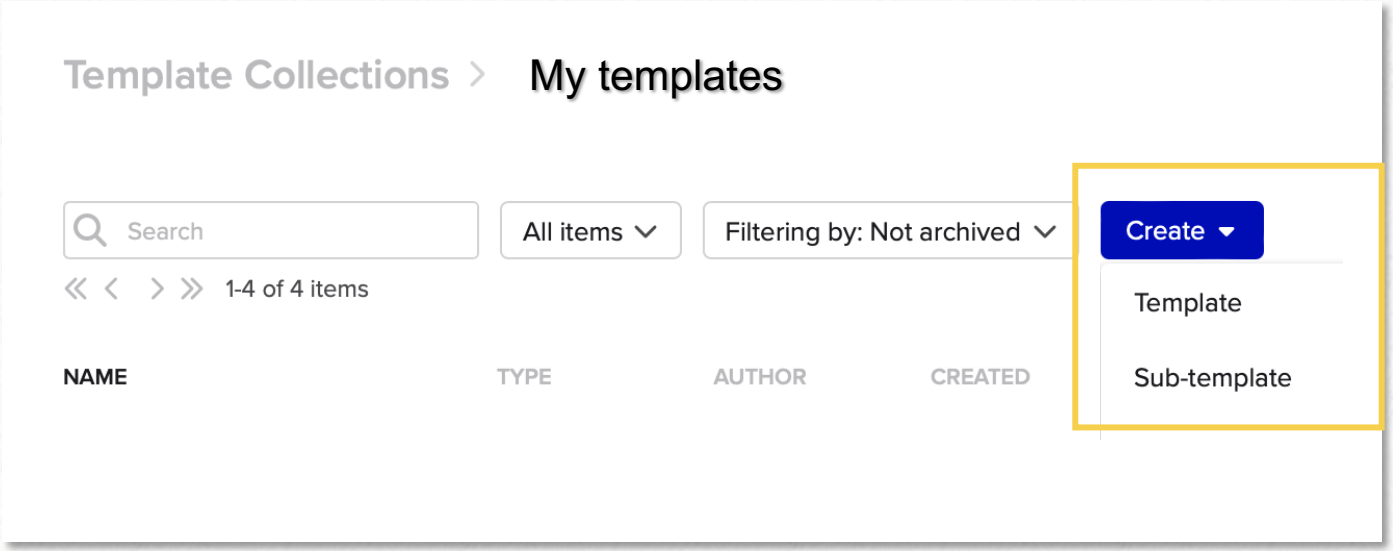
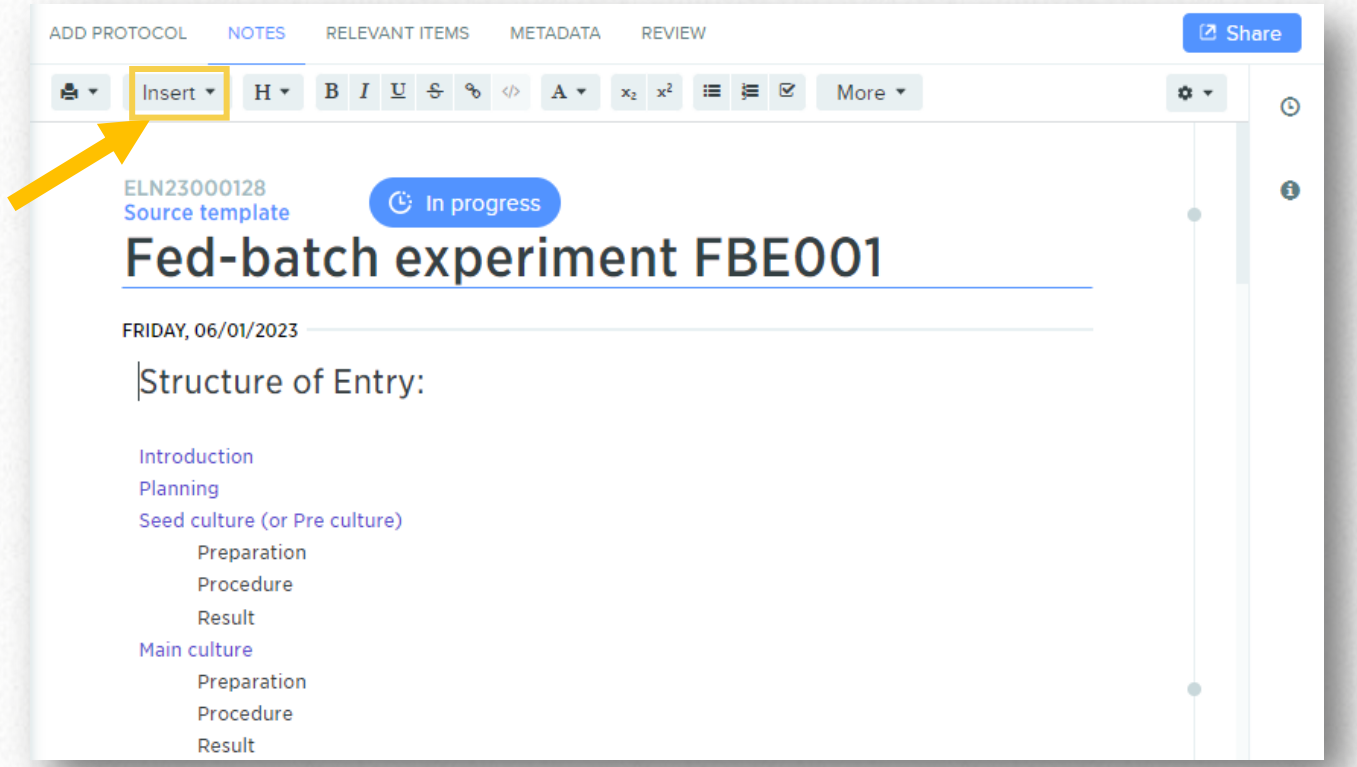


Electronic notebook

In your Entry you can:

- Take **notes**
- Add **attachments/files**
- Create **tables**

Click on **Insert** to see the whole list of options

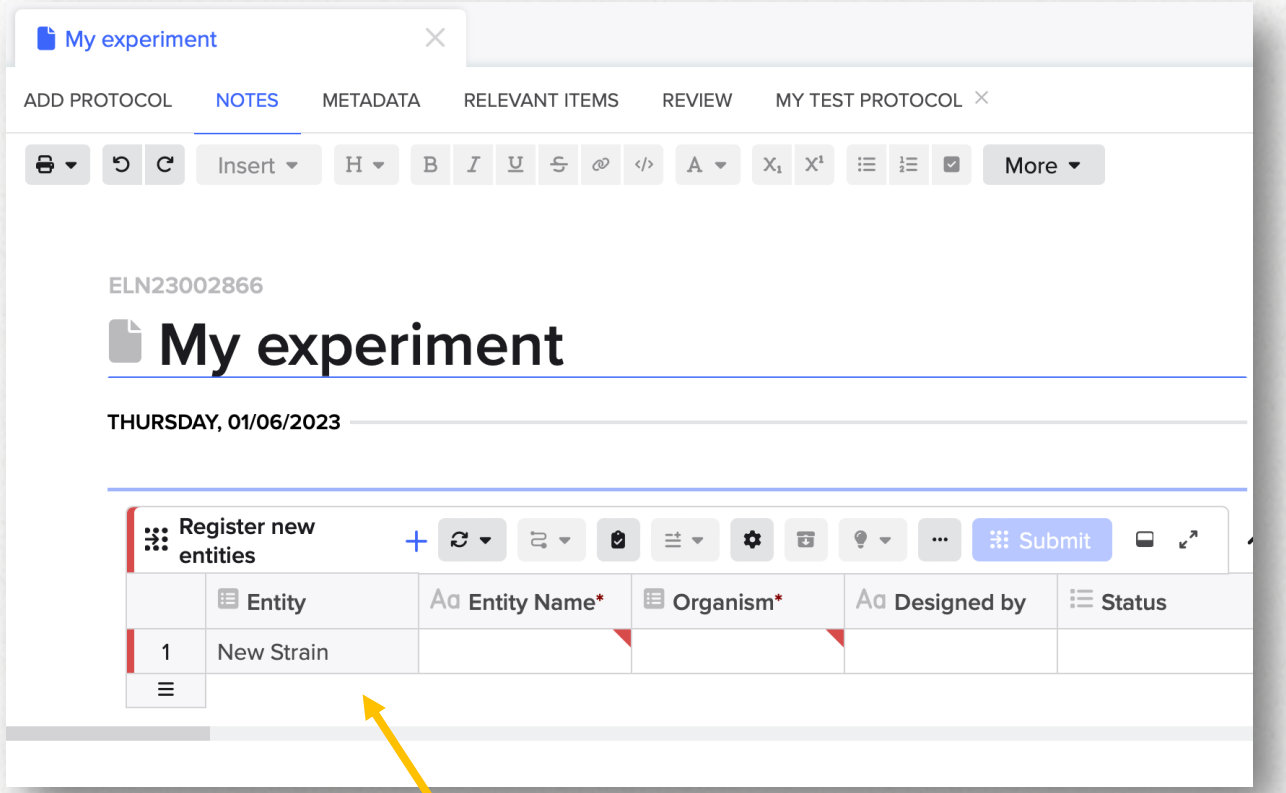


Electronic notebook

In your Entry you can:

- Register strains, media, etc. using **Registration tables**
- Assign **storage location** to registered entities

= more of this in the *Hands-on*



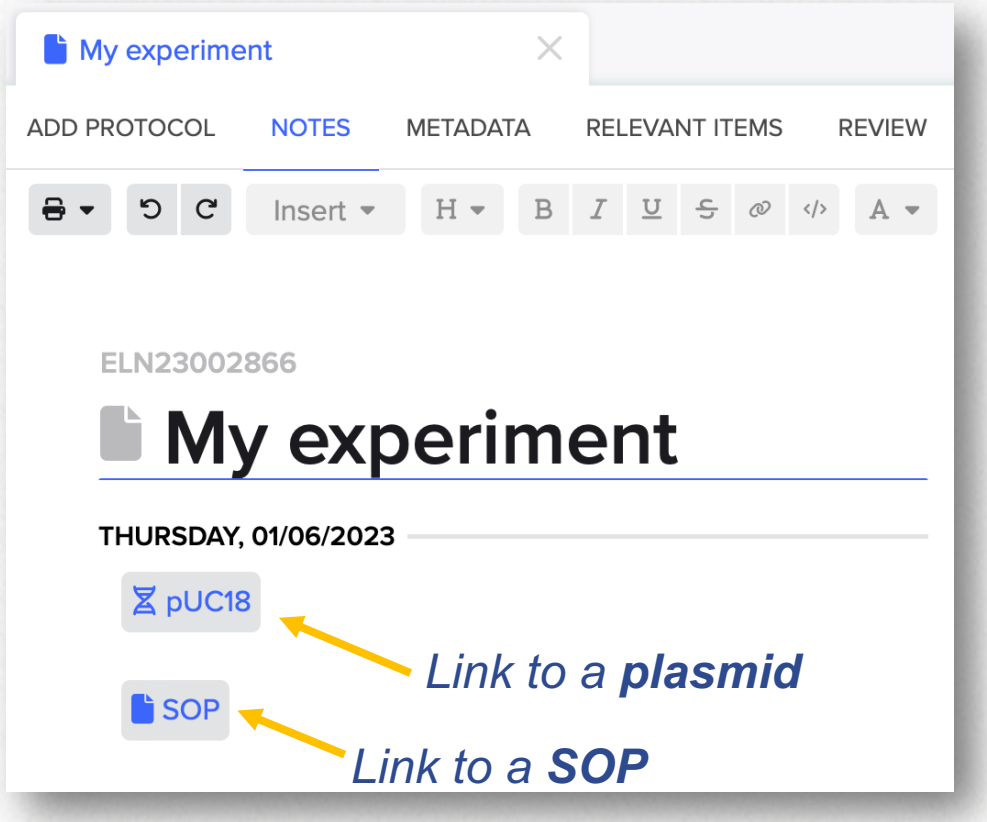
*A **Registration table** for strains*

Electronic notebook

In your Entry you can:

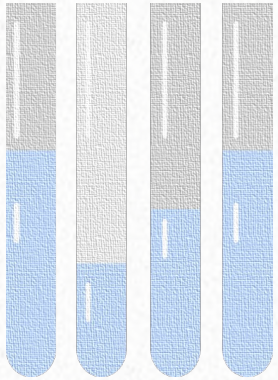
- Tag your plasmids, sequences, etc. (everything that you create)
- Tag another ELN or SOP

To tag an object, type @...



Step 3:

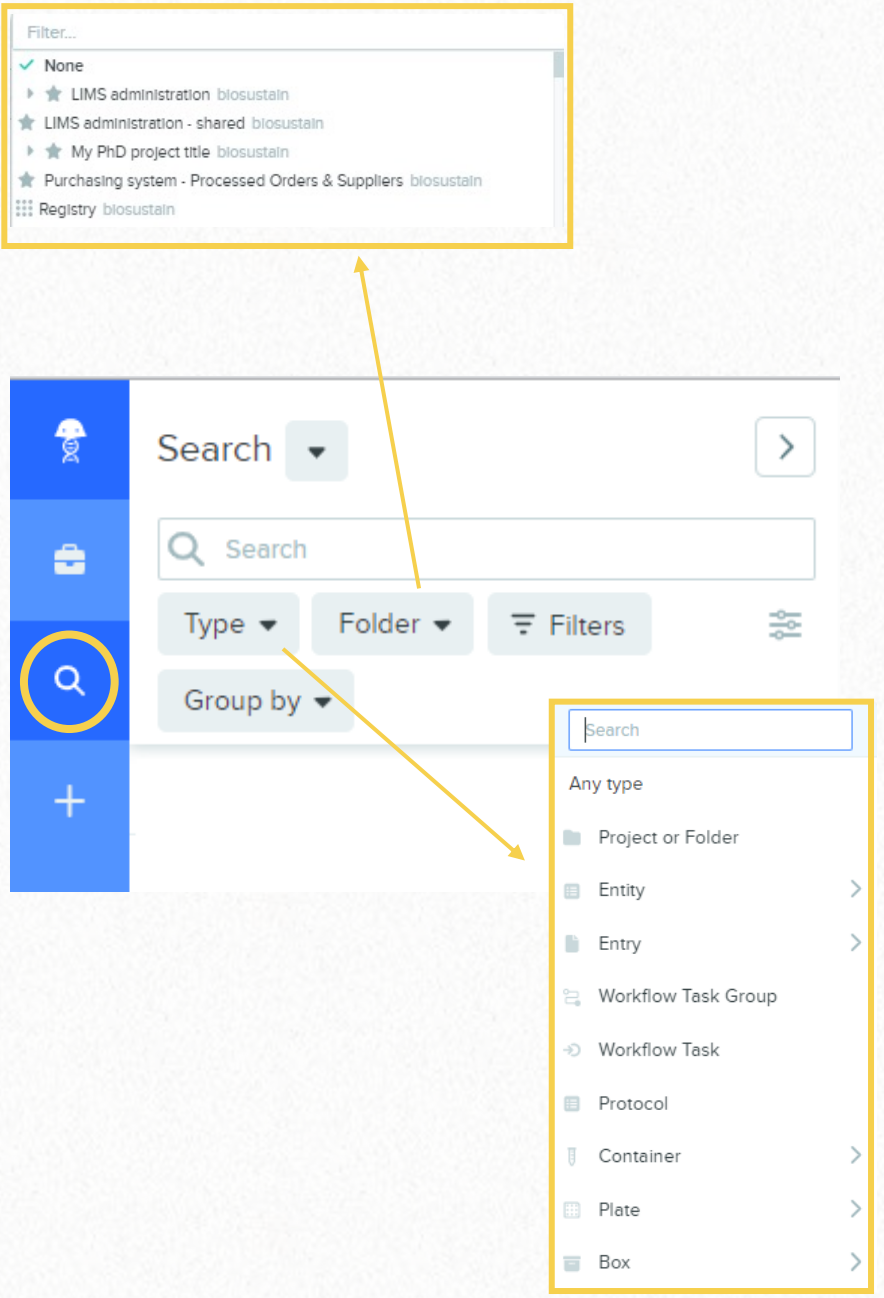
Navigate through your data



Global search

It allows to search through all your data and filter by:

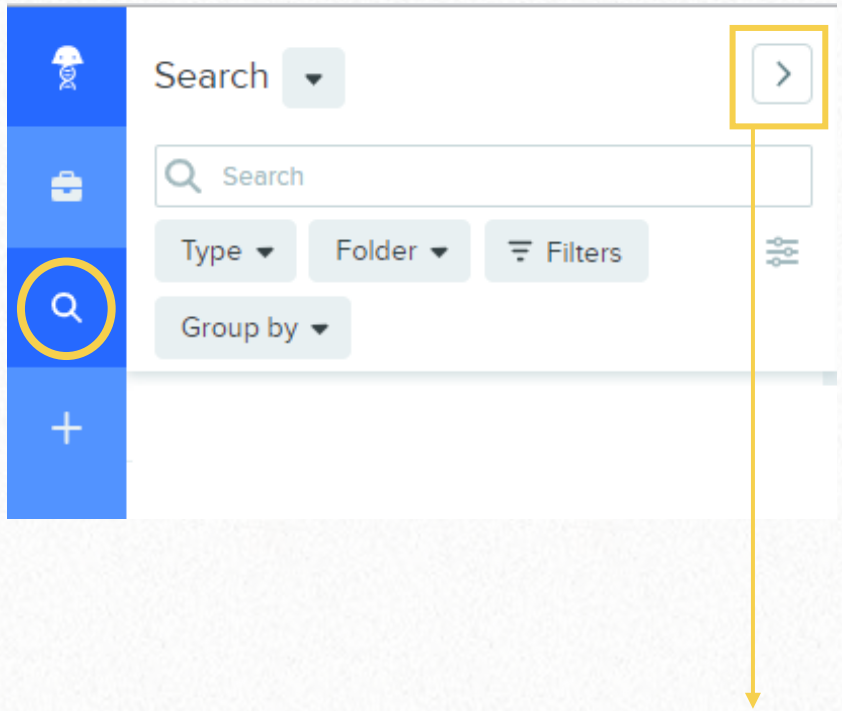
- Data type (samples, boxes…)
- Folder
- Metadata field



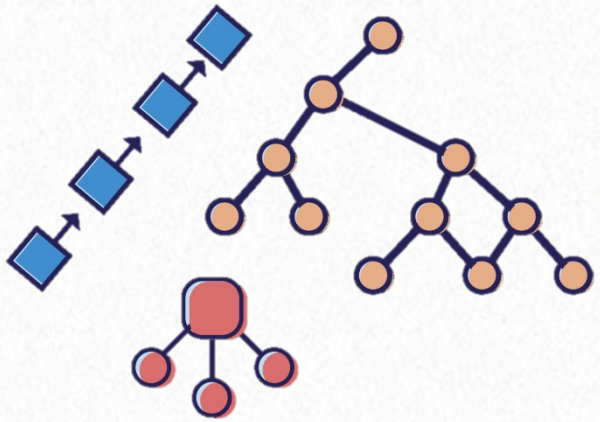
Global search

Expand view to do bulk actions on your data:

- Bulk **edit** of metadata fields
- Bulk **registration** of imported sequences
- Bulk **transfer** to a different folder
- Bulk **archive**



Benchling entities:
what you need to know



1. Entities can store different information

Entity types that can store:

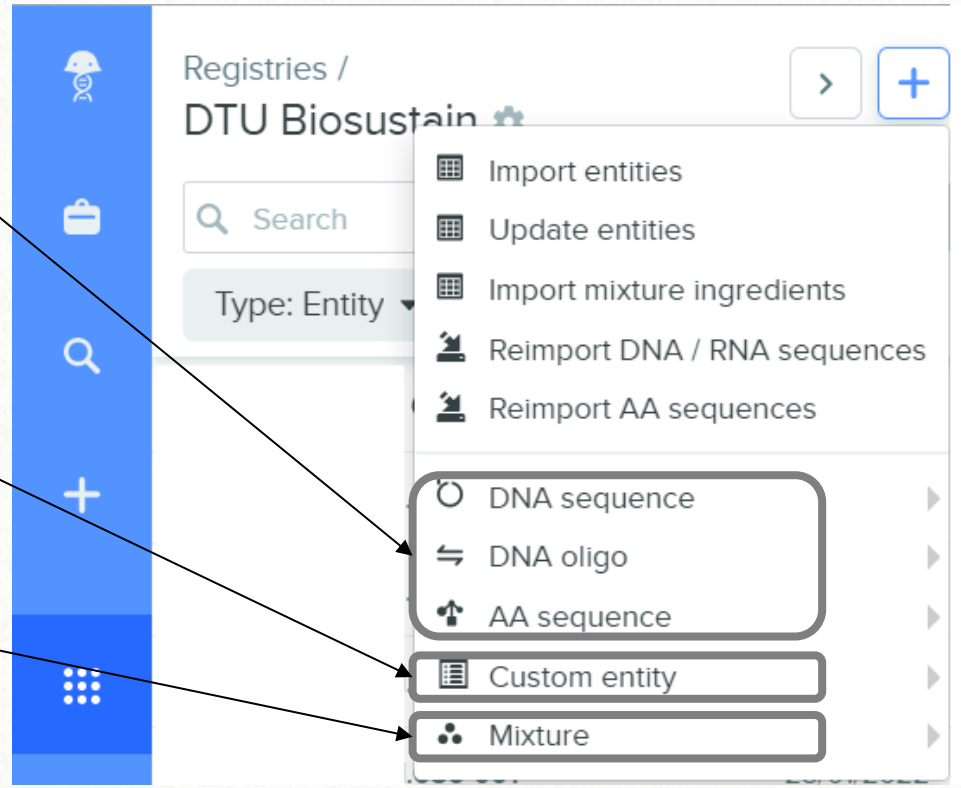
- metadata
- a sequence

Entity type that can store:

- metadata

Entity type that can store:

- metadata
- media ingredients and recipe

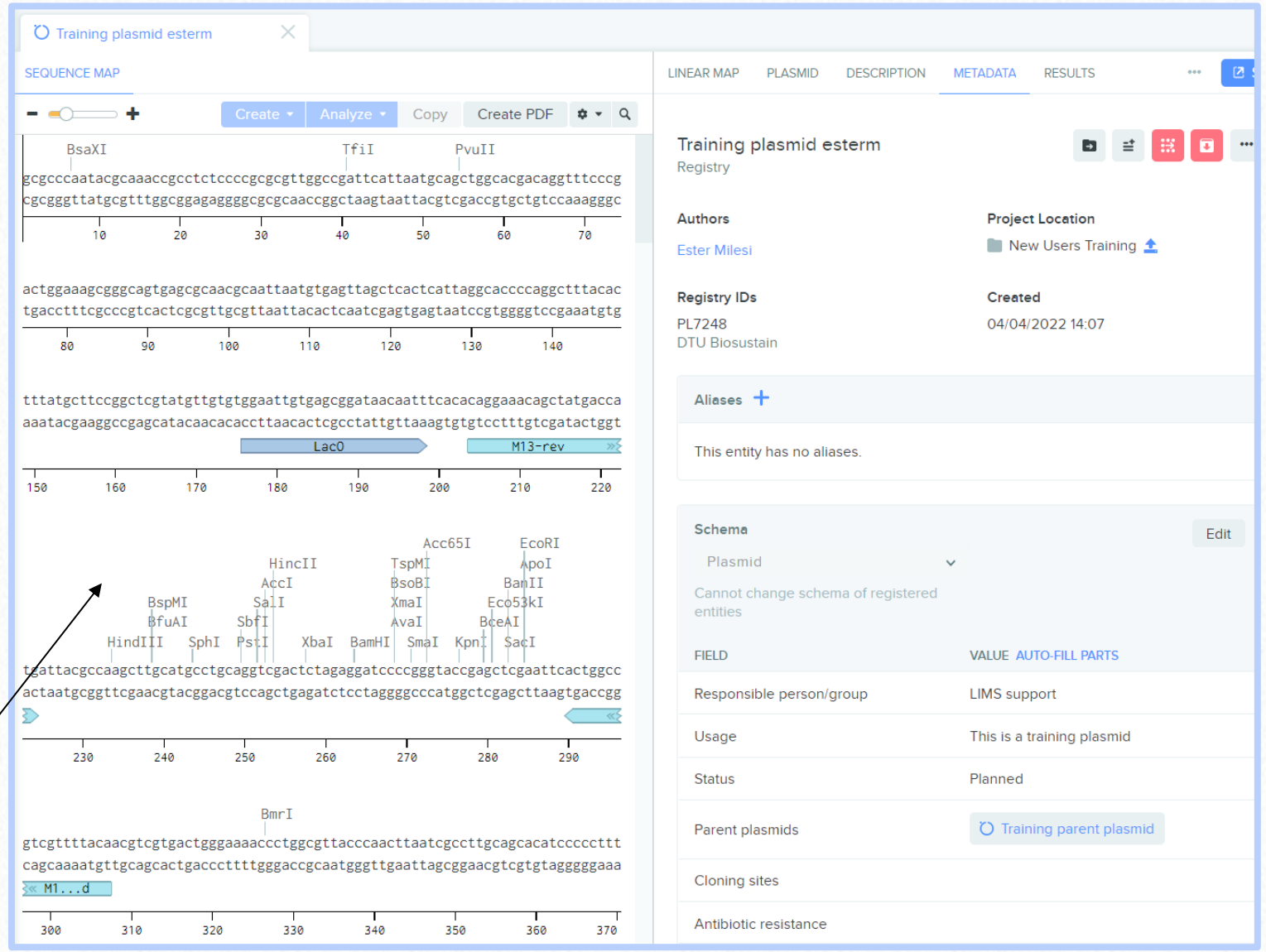


Entity types that can store:

- metadata
- a sequence

DNA sequence
DNA oligo
AA sequence

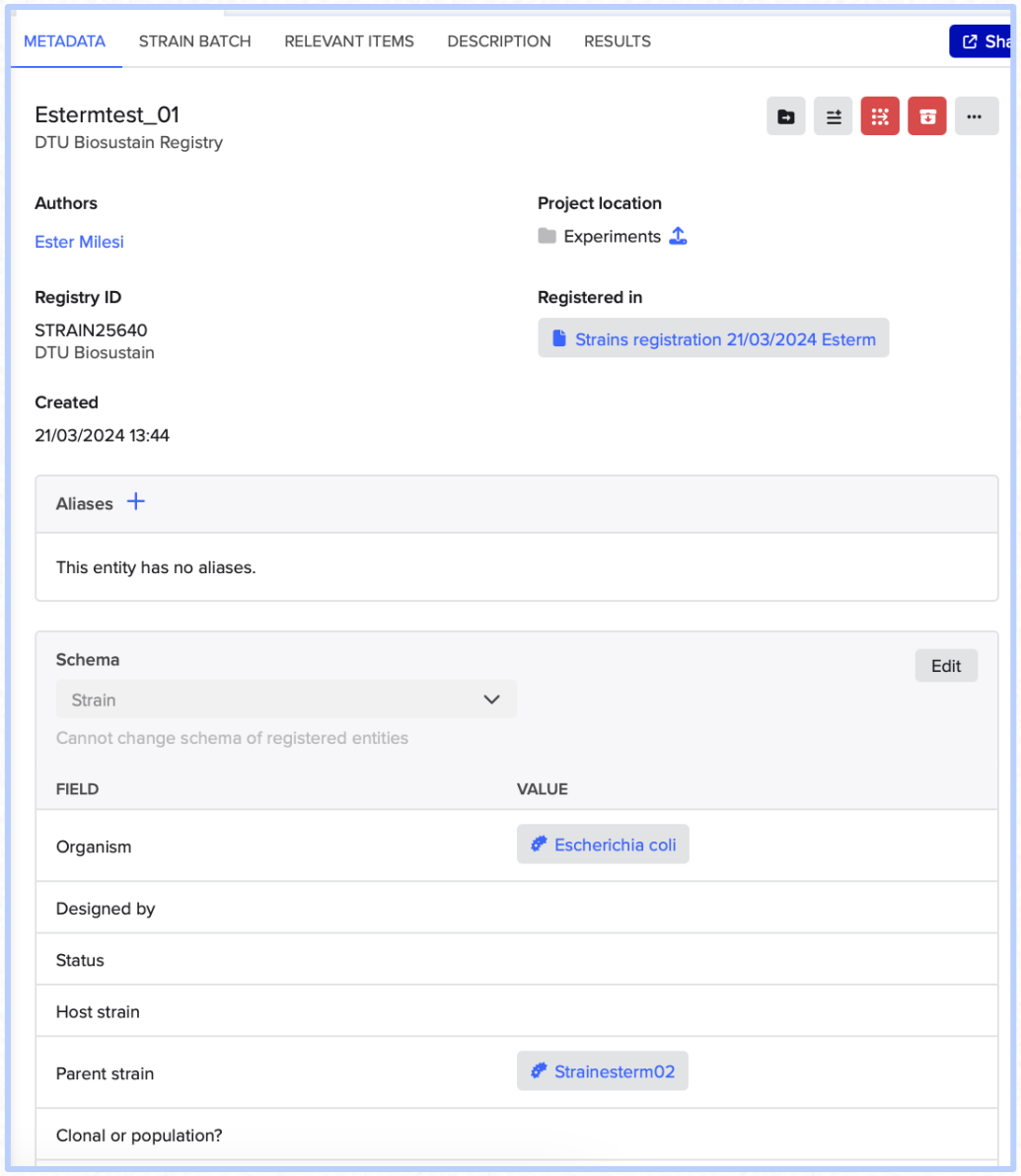
Sequence



Entity types that can store:

- metadata

Custom entity

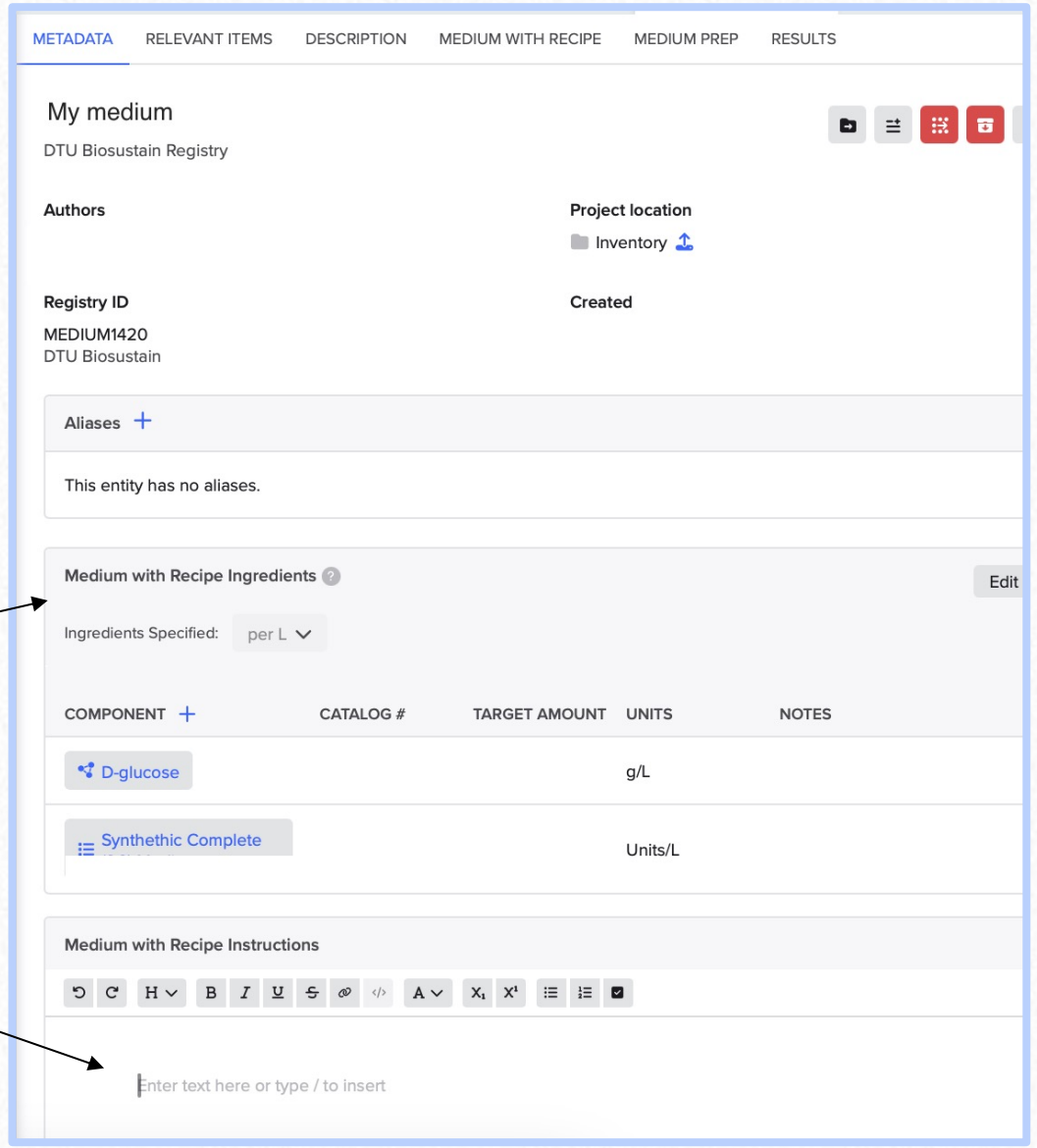


Entity types that can store:

- metadata
- media ingredients and recipe

Mixture

Metadata



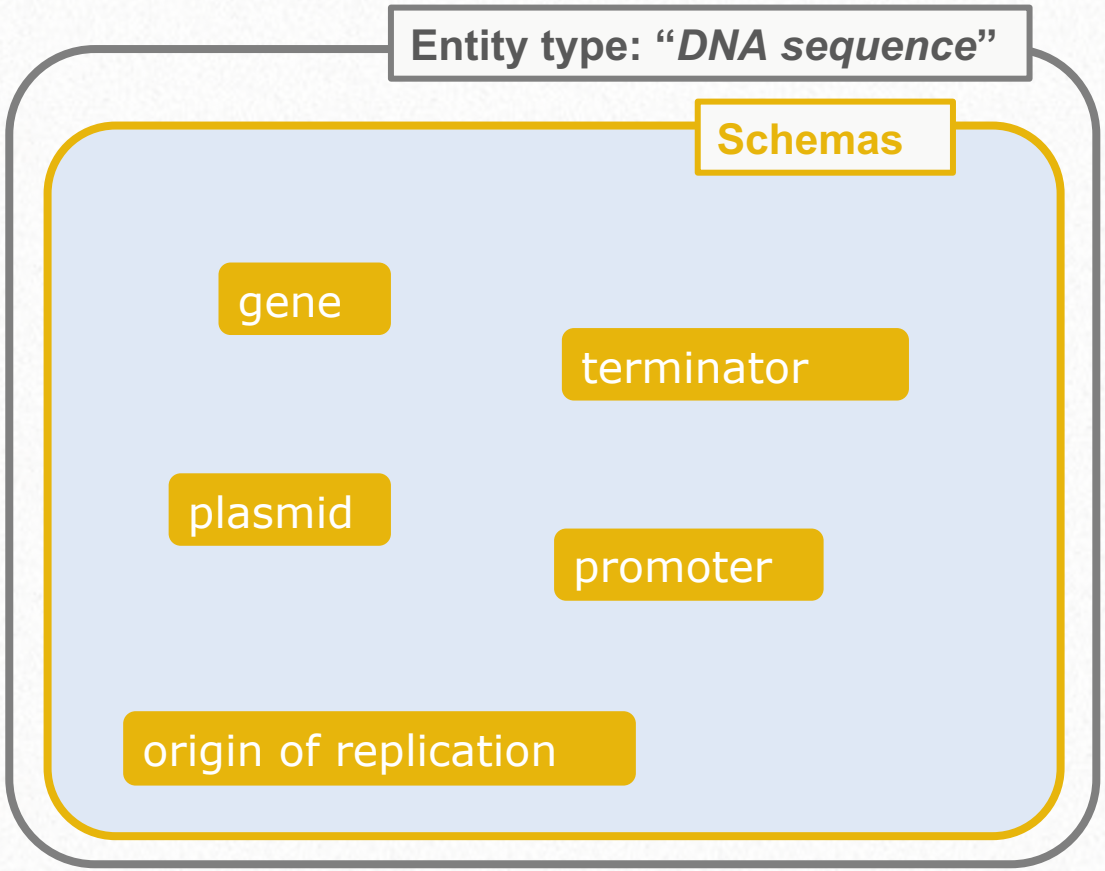
Component list
(with amount)

Recipe

2. Entities are assigned a “schema”

→ The “**type**” only tells you which information the entity stores

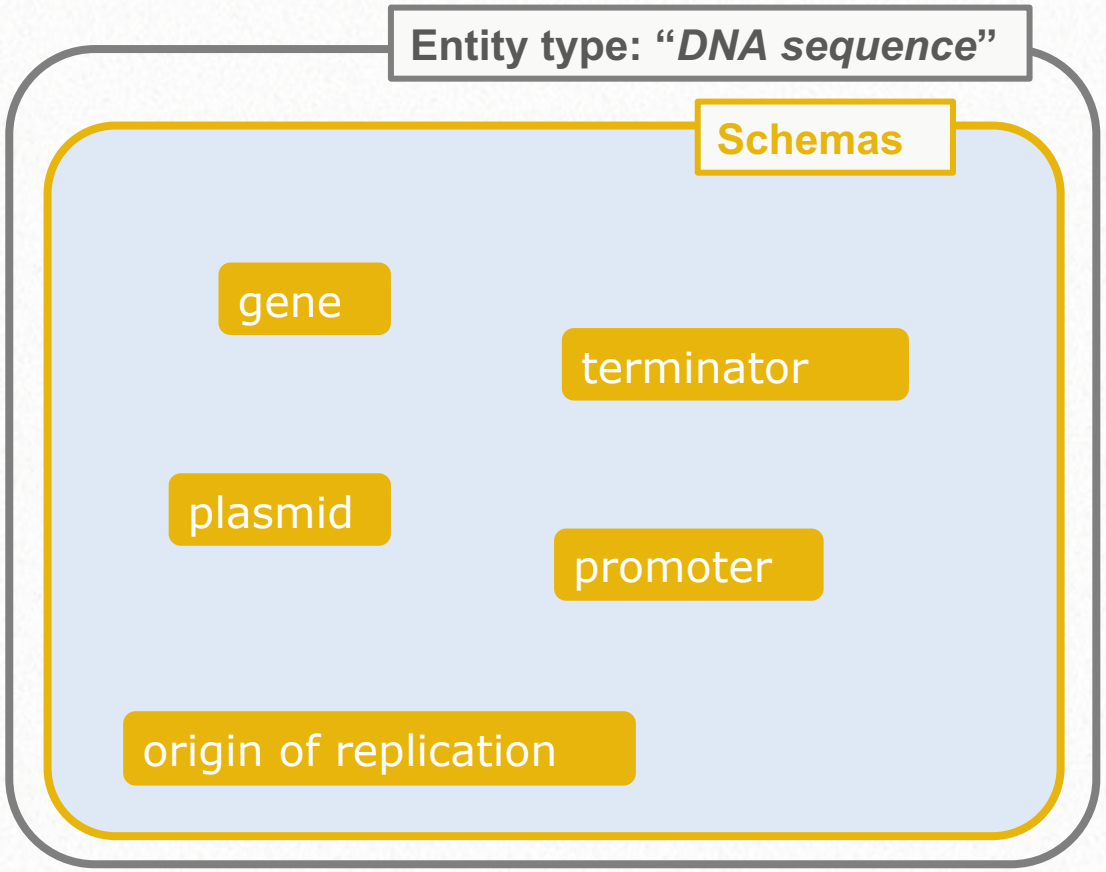
The various sample types are described by “**schemas**”



2. Entities are assigned a “schema”

A schema specifies:

- sample type
- required information to fill-in
- **links** to other schemas



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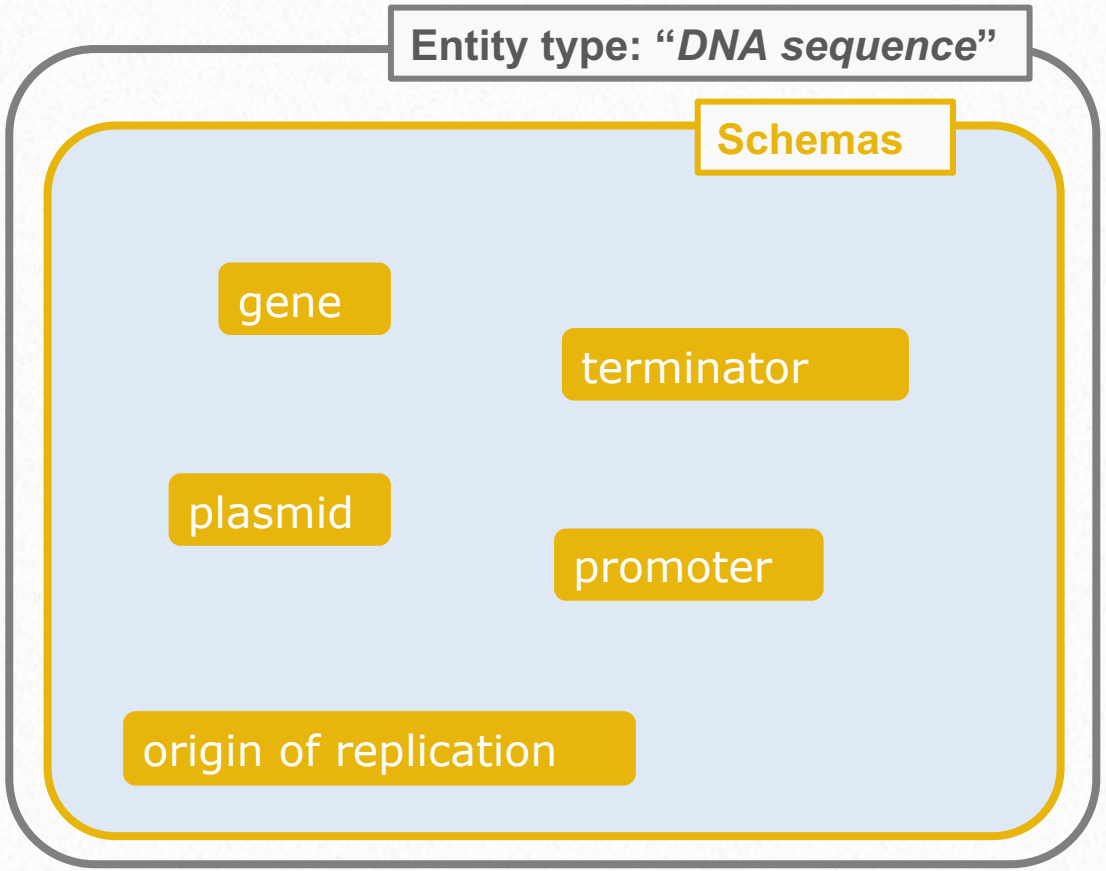
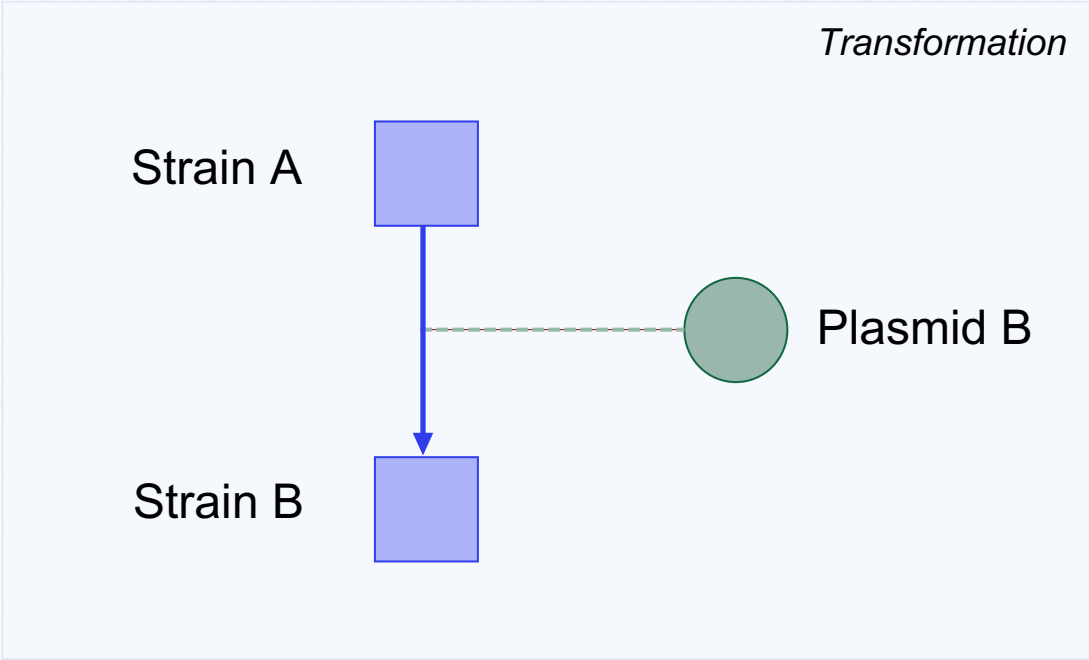


2. Entities are assigned a “schema”

For example, the schema “**Strain**” can link to another strain (parent) and to a plasmid

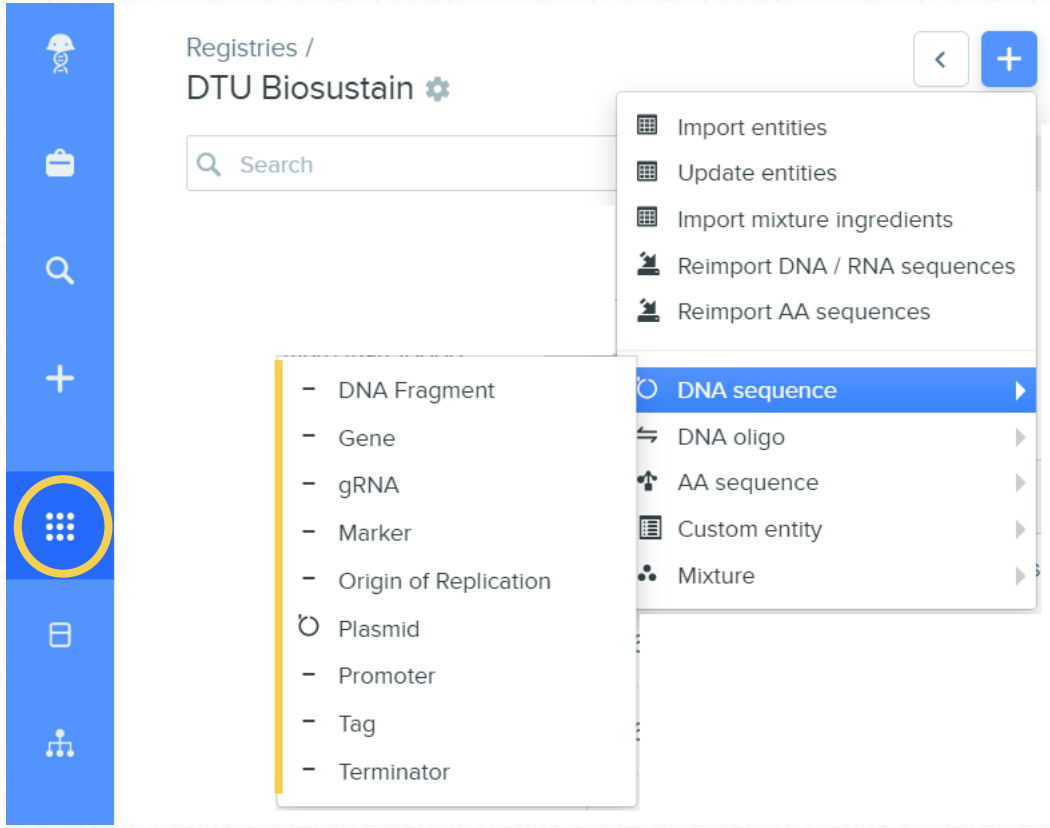


Links 🔗 allow to track the sample “history”

3. You can create entities 1-by-1 or in bulk

To create entities 1-by-1:

- Go to Registry > Click on the “+” icon
- Select the **entity type** e.g., “DNA sequence”
- Select the **schema** e.g., “Plasmid”

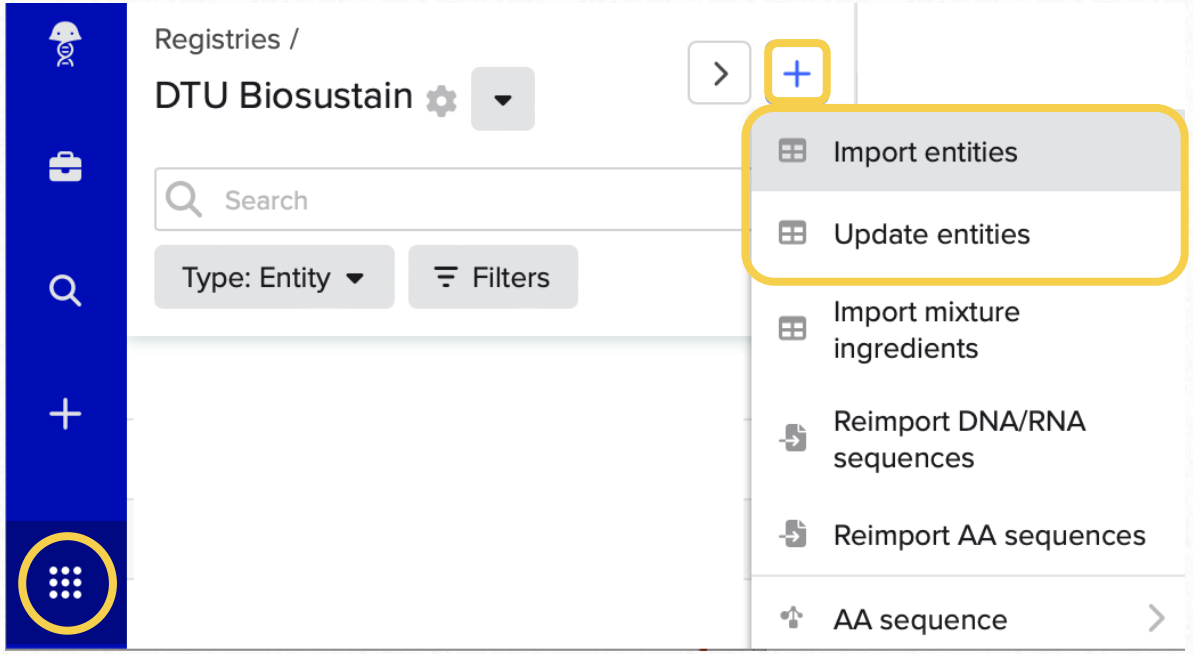


3. You can create entities 1-by-1 or in bulk

To create entities in bulk:

- Upload a **spreadsheet**
  Select *import* or *update entities*

(make sure that the values in the cells are the one that Benchling expects)

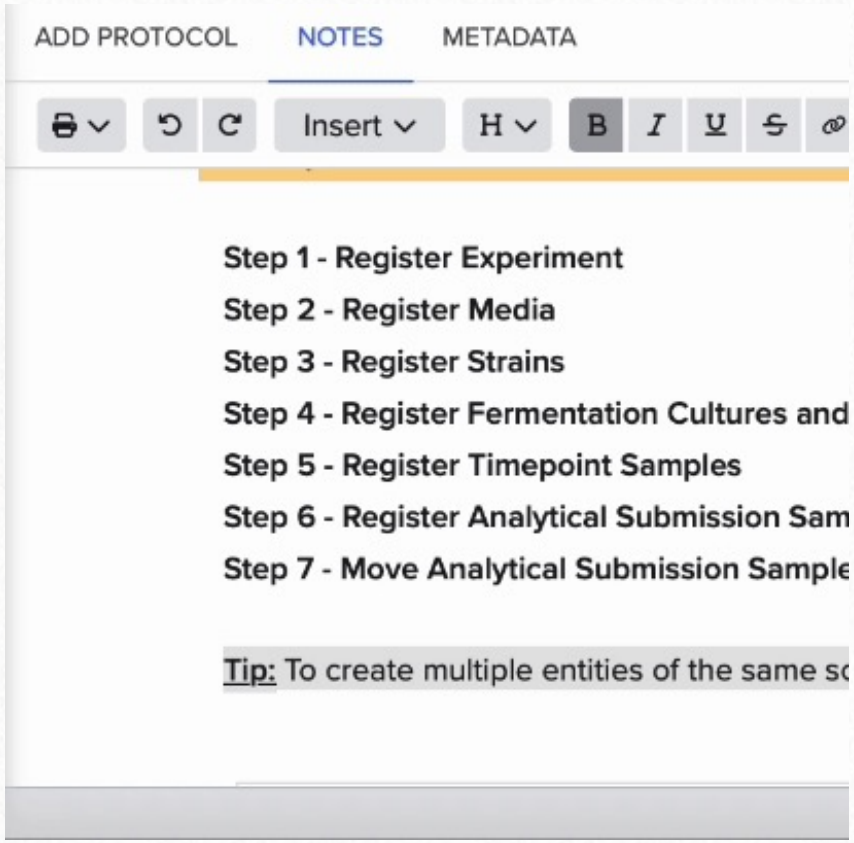


3. You can create entities 1-by-1 or in bulk

To create entities in bulk:

- Use a registration table directly in the **Electronic Notebook**

Click “**Insert**” > ”Registration table” > Select Schema



4. Some entities have “batches” schemas

Batches = physical samples

- When storing your sample long-term, create **batches in Benchling**
- This helps your team to track where samples are stored

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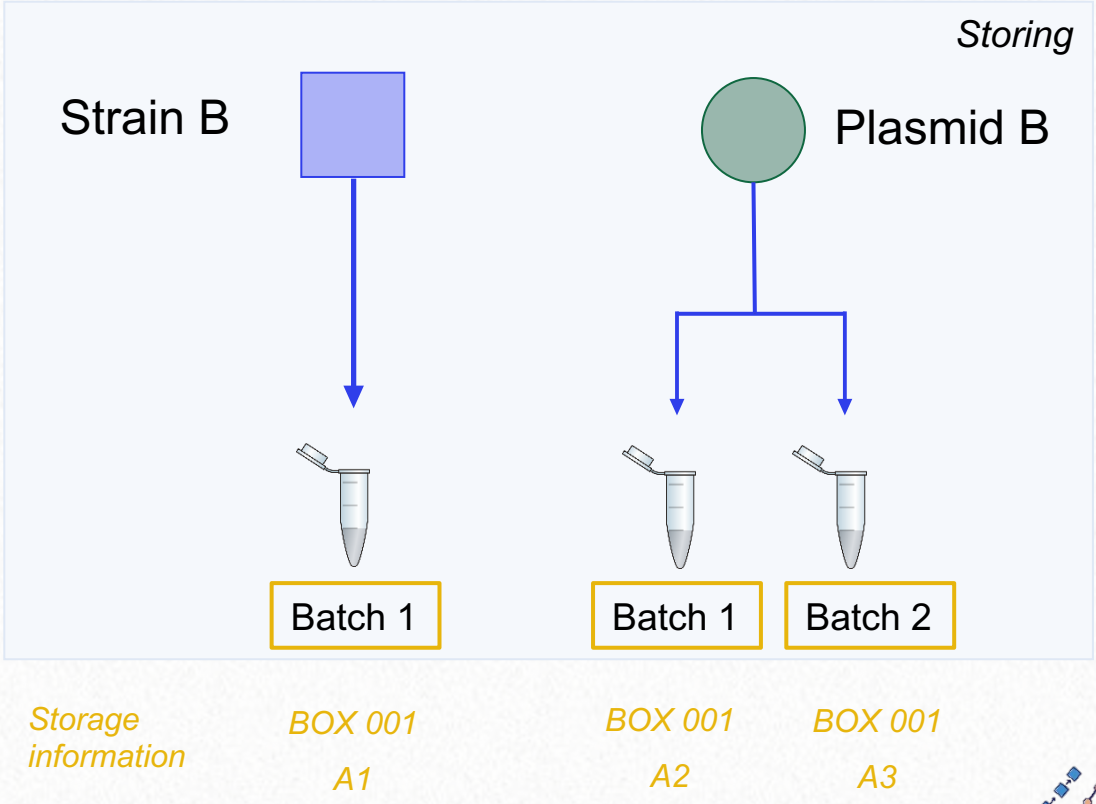
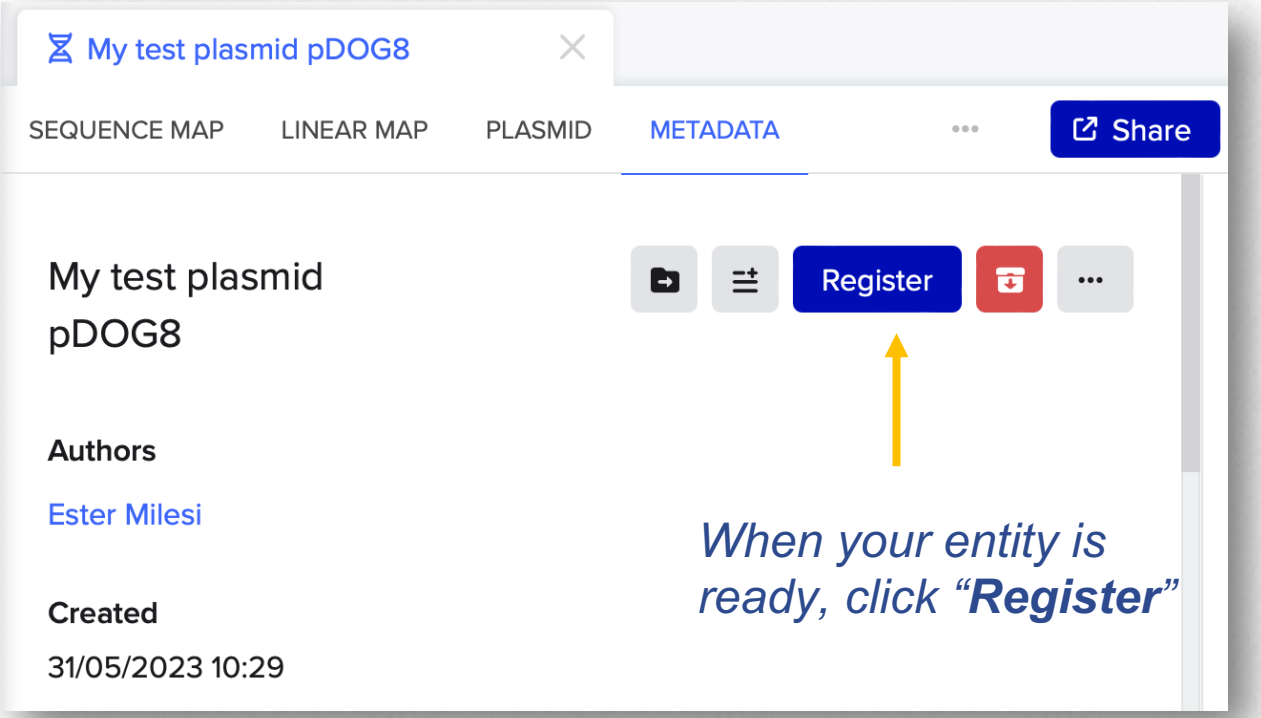


5. Entities can exist outside of the Registry

Sometime, entities are not automatically registered

- In order to register an entity, you need to **select the Schema** (entity type)
- Registering the entity will add a **unique identifier** to your sample



Good practices

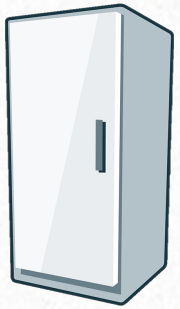
(If you haven't done this consistently during your project)

At the end of your project:

- ✓ **Re-organize** your registered samples and entries and **give access** to your team
- ✓ Register **important strains/other samples** and their **location**, and print the label for the Box before moving it in the freezer

Storage:

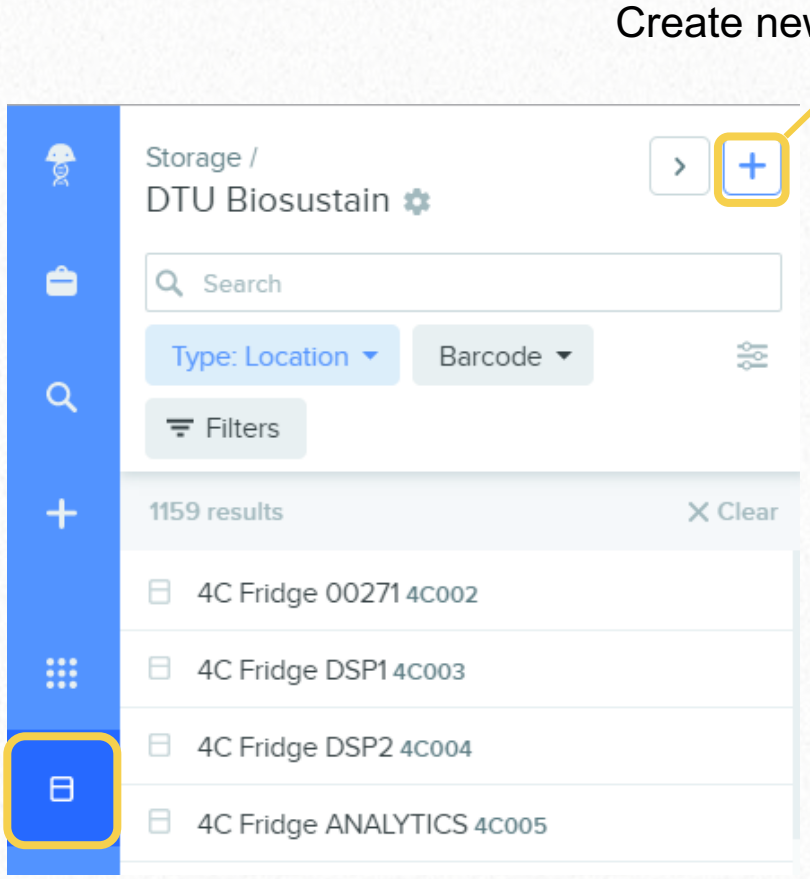
track your samples



The Inventory

Benchling allows you to track the location of your samples

Room > Fridge > Box > Vial

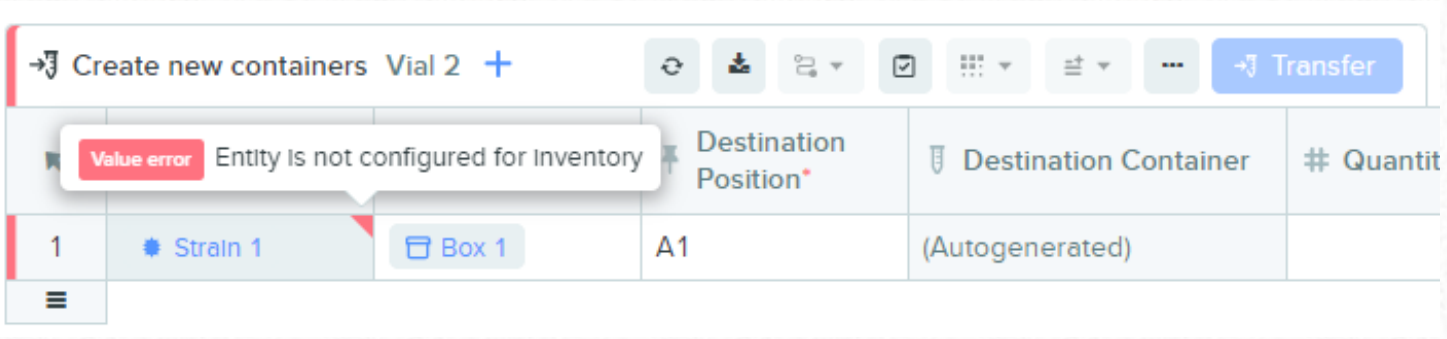


If your fridge/location is not registered, let RDM support know

The Inventory

Storable samples include:

- Batches
  (e.g., “Strain batch”)
- Fermentation cultures
- Submission samples
  (e.g., for analysis)

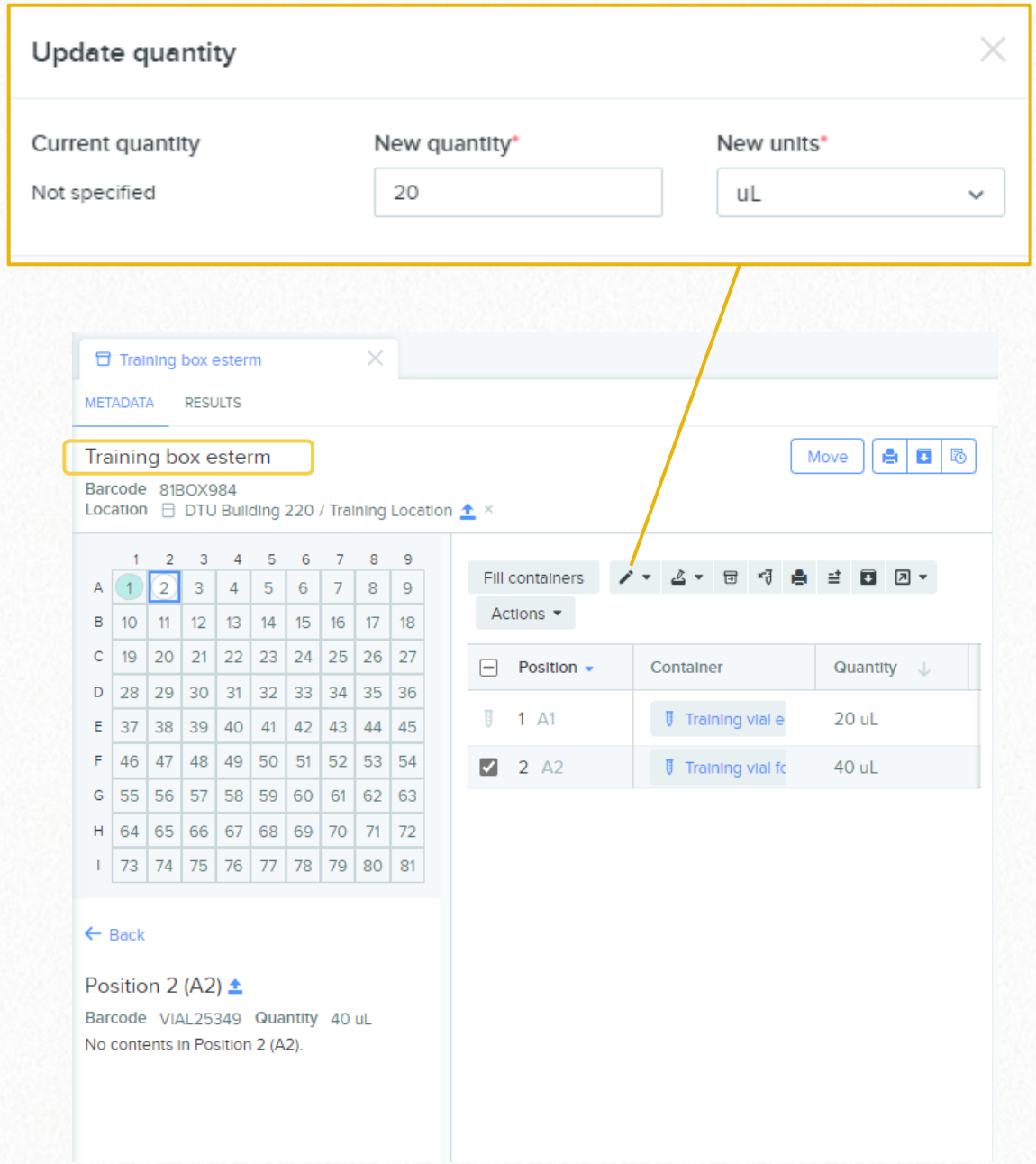


Error showed in an Inventory table **in the Notebook** when trying to move a “Strain” in a Vial instead of a “Strain batch”

The Inventory

Benchling allows you to track the volume or concentration in of each vial

- Example of a **Box** in Benchling



Lastly:

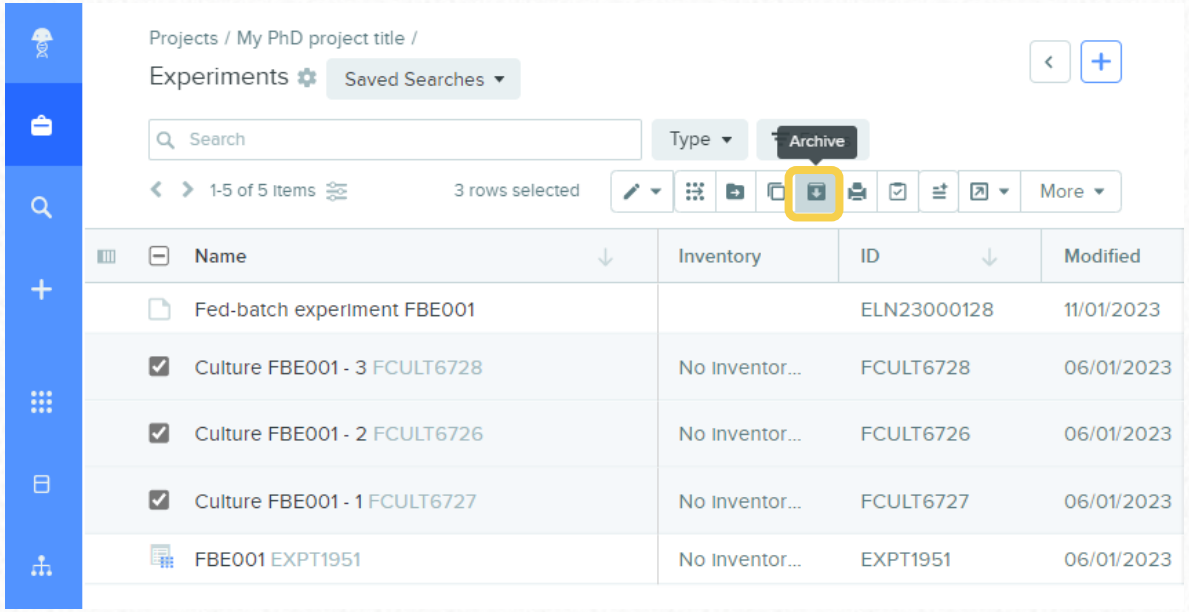
Archiving

Archiving entities

Nothing can be deleted but only archived

- You can archive
  - ✓ Project folders
  - ✓ ELN entries
  - ✓ Entities

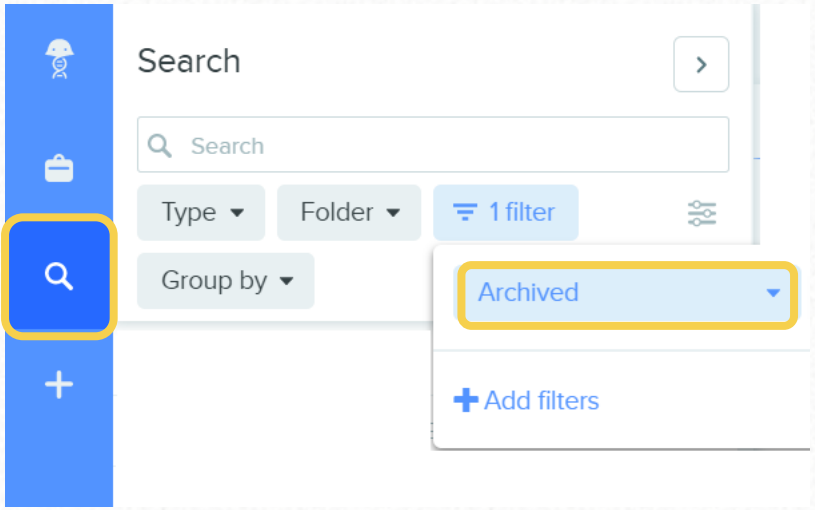
If you created them **by mistake** or if they are not relevant



Archiving entities

It is still possible to go trough archived items and unarchive them

- In the search tab, filter by “Archive” status



Questions?

Agenda

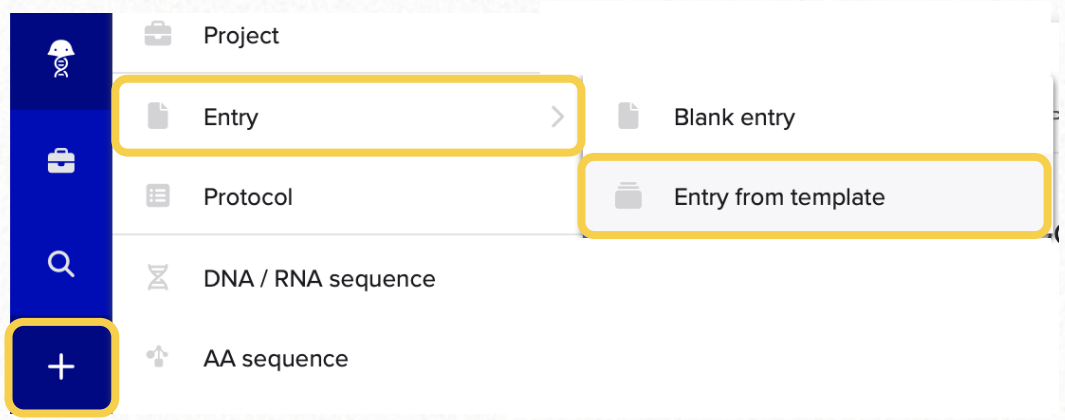
- Introduction to Benchling and best practices — ~ 30 min
- Hands-on — ~ 15 min

Agenda

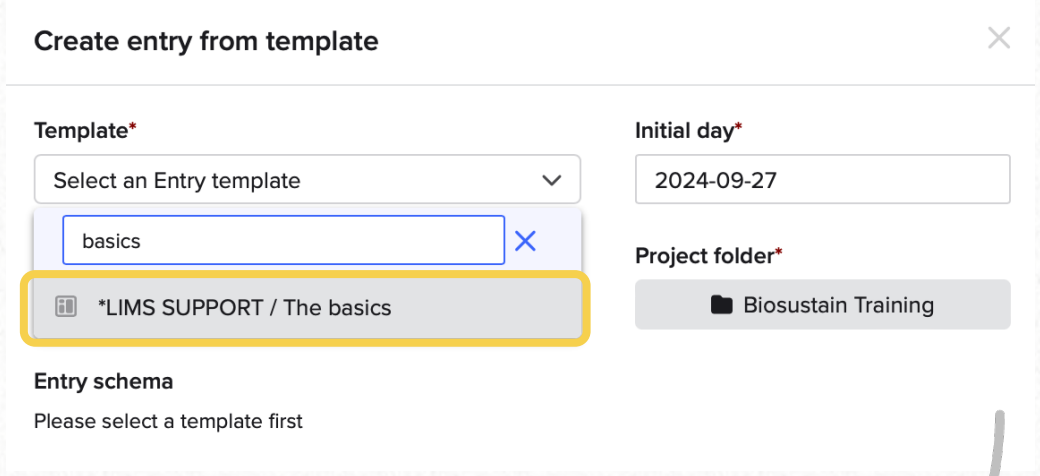
Introduction to Benchling and best practices	~ 30 min
Hands-on	~ 15 min

Explore the Notebook functionalities

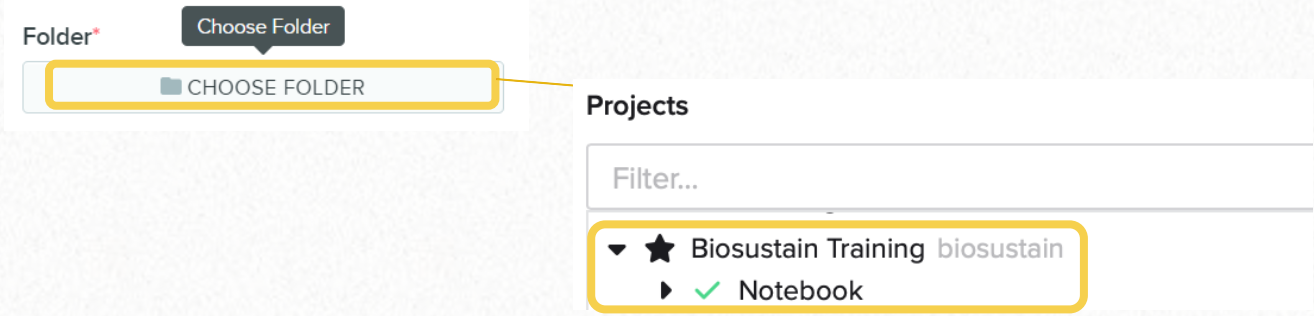
1 CREATE ENTRY FROM TEMPLATE



2 CHOSE “THE BASICS” TEMPLATE



3 SAVE IT IN THE *BIOSUSTAIN TRAINING* FOLDER



Questions?