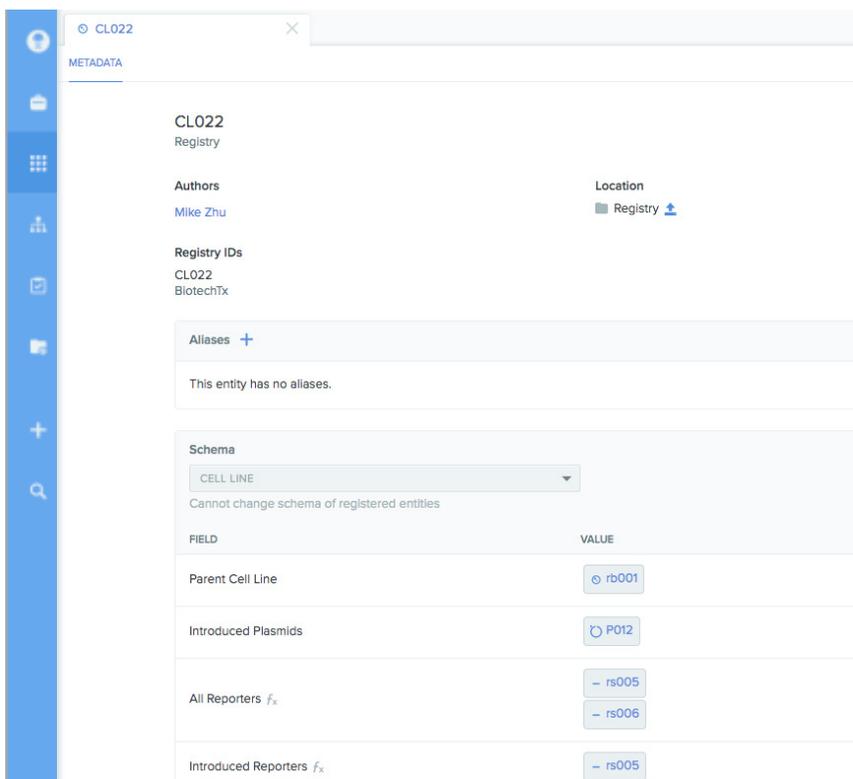


Model the Complexity of Large Molecules

Legacy registration software and spreadsheets weren't built to manage the complex structures and interlinkages of biological entities. To accelerate life sciences R&D, organizations need a simple system that can digitally model any large molecule, track all the data that's relevant to that molecule, and link it to every related molecule.

Benchling Registry is the first registration system built from the ground up for large molecule R&D. It's flexible enough to model the biological entities of any organization, while making it easy for scientists to enter and extract the data they need. And since it's all configured in a point-and-click interface, you can easily adjust the system as your needs evolve.



The screenshot displays the Benchling Registry interface for entity CL022. The interface includes a sidebar with navigation icons and a main content area with the following sections:

- CL022 Registry**
- Authors:** Mike Zhu
- Location:** Registry
- Registry IDs:** CL022, BiotechTx
- Aliases:** This entity has no aliases.
- Schema:** CELL LINE (dropdown menu)
- Table:** A table with columns 'FIELD' and 'VALUE' containing the following data:

FIELD	VALUE
Parent Cell Line	rb001
Introduced Plasmids	P012
All Reporters <i>f_x</i>	rs005, rs006
Introduced Reporters <i>f_x</i>	rs005



Configure entities without code

- Model any biological entity. Track any data (ex. molecular weight, assay data) and inter-link all related entities.
- Adjust the configurations of your entities directly in the user interface, without coding or vendor involvement.



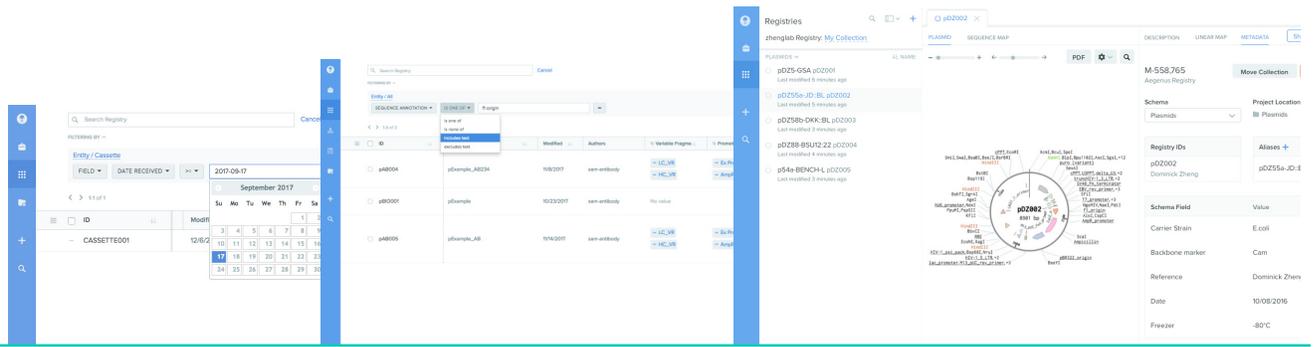
Build a knowledge base for biology

- See every experiment where a particular large molecule was used.
- Track the complete lineage of any large molecule.
- Find all the entities that link to one particular entity. For example, search for all cell lines that express a specific gene.



Trace from entities to physical samples

- From any large molecule, locate every sample of it that has ever been produced.
- View results across multiple samples of the same large molecule.
- Based on samples, compare the effectiveness of similar entities. For example, compare the effectiveness of multiple antibodies against a single target.



1 Configure any biological entity

- In a point-and-click interface, model any entity, data fields, and data types with built-in biological awareness.
- Assign specific units and data types to data fields; or, configure them as dropdowns, multi-select picklists, and other structures.
- Remove vendor dependence by granting permissions to specific end-users to adjust entity configuration.

2 Interlink any biological entities

- Require that an entity link to an entity of a specific type. For example, require that all antibodies link to a light chain.
- Automatically detect and link component entities. For example, when you register an expression plasmid, Benchling will automatically detect and link the light and heavy chain entities to your newly-registered plasmid.

3 Structure data constraints on entities

- Make particular fields required for an entity.
- Build business rules that enforce uniqueness. For example, require each antibody to link to a unique combination of light and heavy chains.
- To ensure data integrity, define acceptable data types for particular fields.

4 Run calculations on data across related entities

- Across interlinked entities, surface data from one entity onto an entity that it links to. For example, surface the resistance of a plasmid onto the cell lines that it links to.
- Embed calculations to automatically fill in entity data. For example, fill in an antibody's molecular weight by automatically computing the weight of the protein chains that comprise it.

5 Register and link to entities from any application

- Directly register new entities from Benchling Notebook and Molecular Biology.
- @-mention any registered entity within Notebook entries.
- Link registered entities to stages in Workflows and Requests as necessary.
- From any entity, see every place in Benchling where it is used or mentioned.

