

 Benchling

Integration Snapshots



Introduction

Life science R&D is producing data of a greater quantity and complexity than ever before. At the same time, there's been a corresponding increase in the number of data sources and repositories that scientists work with on a daily basis. With robotics, analytical instruments, databases, and software all generating or interacting with data, it becomes a challenge for scientists to tie data together into meaningful conclusions.

Benchling's developer platform is designed for the complexity of modern life science R&D. By integrating Benchling's natively unified applications with other data sources and repositories, you can not only cut down on scientist busywork and manual errors, but build completely novel functions to help your organization reach breakthrough discoveries faster.



Benchling's developer platform supports a wide variety of **integration and ETL use cases**, from automatically syncing Benchling with other informatics tools and databases, to pushing and pulling data from instruments like liquid handlers and freezers. We designed Benchling's integration capabilities so that you can easily unify Benchling with your existing informatics ecosystem and build completely novel functionality specific to your business needs.

The developer platform offers REST APIs that provide CRUD access to most data in Benchling, a SQL warehouse to run database queries, and an events framework to notify your integrations about changes that have occurred. The APIs represent all data as JSON, and accepts JSON input to create and update data in Benchling. Customers have written integrations that can convert data from all kinds of formats, including CSV, TSV, and ADF (Allotrope Data Format), to JSON so that data can be uploaded into Benchling.

Our events framework allows you to configure a Webhook to receive messages every time an applicable event occurs on Benchling, or to receive events through AWS EventBridge. To learn more about our developer platform, check the docs here: <https://docs.benchling.com/docs/developer-platform-overview>

EXAMPLES OF SYSTEMS WE'VE INTEGRATED WITH

Software

- Informatics systems (ex. IDBS, Core LIMS, Genedata, Biovia, Sapio, CDDVault, Chromeleon, custom registries, custom LIMS)
- Molecular biology tools (ex. Snapgene, Geneious, Vector NTI)
- Analytics tools (ex. FlowJo, Prism, Spotfire, Tableau)

Databases

Amazon S3 buckets, Egnyte databases, NCBI gene database, custom network file systems.

Instruments

- Freezers (ex. Askion)
- Fermenters and bioreactors (ex. Eppendorf)
- Liquid handlers (ex. Tecan, PAA, Hamilton, Echo, and Biomek)
- Printers (ex. Zebra)
- Barcode scanners
- Materials testing machines (ex. DMA machines, Zwick machines, and light microscopes)
- qPCR machines and DNA sequencing machines (ex. Eppendorf)
- Plate readers and FACS machines (ex. Molecular Devices)

Connecting Benchling with third-party databases

THE CHALLENGE

The potential reasons to connect Benchling with a third-party database are manifold. Having a single database or data lake to standardize data across numerous systems is a business goal for many of our clients. In addition, archiving certain data from Benchling — chiefly, Notebook entries that have gone through a witness and review process — is oftentimes a regulatory necessity.

The screenshot displays the Benchling web interface. On the left, a sidebar shows a list of entities under the 'Registries / Benchling' section, including various 'ab' prefixed identifiers and their last modified dates. The main area shows a detailed view of a notebook entry titled 'pDusk - DsRed2 Cloning'. The entry includes a date 'SUNDAY, 12/6/2015', a description 'Today I'm going to insert the DsRed2 protein into the pDusk backbone.', and a list of steps: 'Find appropriate restriction enzyme sites.', 'Create primers for amplification.', and 'Insert DsRed2 protein into pDusk vector via copy paste.'. Below the steps is a circular diagram of the 'pDsRed2' plasmid, labeled '3311 bp'. A right-hand panel shows a metadata table with columns for Name, Folder, and Tags, and buttons for 'Delete entry' and 'Export entry'.

Benchling's Solution

Whether you're using an Amazon S3 bucket, an Egnyte database, a custom network file system, or an entirely different system, you can back up your Benchling data. Clients use event-based integrations to push PDFs of Benchling Notebook entries to their database of choice whenever an entry is signed off on. Alternatively, you can sync your Benchling data – Notebook entries, sequences, samples, and other data – into an external system at regular intervals of time or based on other triggers.

Event-based synchronization between Benchling and a third-party LIMS

THE CHALLENGE

The cell line development core of one of our largest antibody discovery clients receives dozens of requests via Benchling everyday. These requests contain a link to a plasmid in Benchling and a description of the desired output. The cell line development team then fulfills the request and creates samples in Benchling for the outputs. However, there's another team that needs to access these output samples, but they use a third-party LIMS.

The screenshot displays the Benchling interface with a modal form titled 'Assay' open. The background shows a project page for 'STUDIES / BIOT 0919' with a goal of 'Antibody discovery for C...'. A sidebar on the left lists a 'Screen Library' with steps: SCRE001 (Status Complete), SEQU001 (Status Complete), CREA001 (Status Completed and reviewed), CREA001 (Status Not started), EXPR001 (Status Complete), and SCRS001 (Status In progress). The modal form contains the following fields: 'Assay Type' (dropdown menu set to 'ELISA'), 'Sample' (dropdown menu set to 'BIOT0129'), 'Container' (dropdown menu set to '96W128'), 'DATA SOURCE' (radio buttons for 'Request assay' (selected) and 'Read from instrument'), 'Assign to' (dropdown menu set to 'Sequencing Support'), and 'Need by' (calendar icon and date '02/18/2017'). A blue 'Create' button is at the bottom right of the modal.

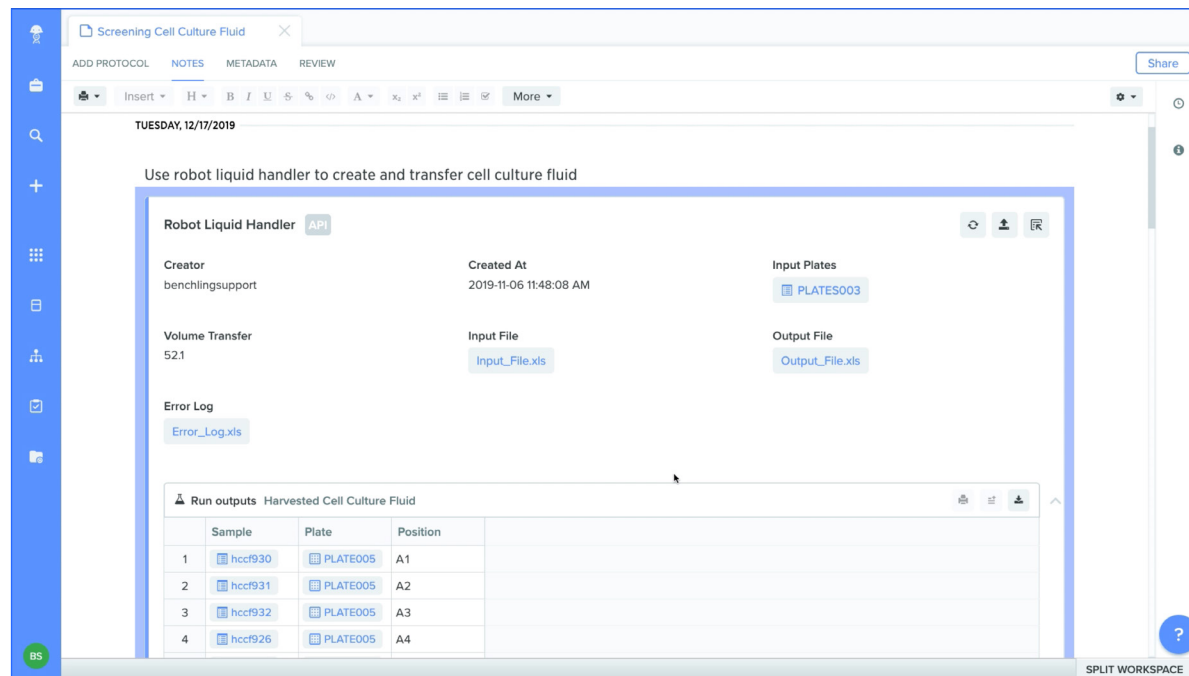
Benchling's Solution

Through an events-based integration, Benchling sends a message to the client's server whenever a cell line development request is created or updated. Subsequently, Benchling pushes the output samples and related data into the third-party LIMS. Among this data are the sequence and annotations of the input plasmid, the location of the output cell line, and user information. Certain Benchling clients leverage a version of this integration where the third-party LIMS conducts an automated analysis of the output sample and automatically pushes the results back to the sample record in Benchling.

Benchling for Lab Automation: Optimizing plate-based workflows with fully unified informatics

THE CHALLENGE

Lab automation has become a critical part of life science R&D, but companies are still unable to maximize the benefits from their automation investments. Lab informatics remain disconnected from high-throughput instruments and automation hardware, creating bottlenecks for data aggregation and sample traceability that impede the pace of research.



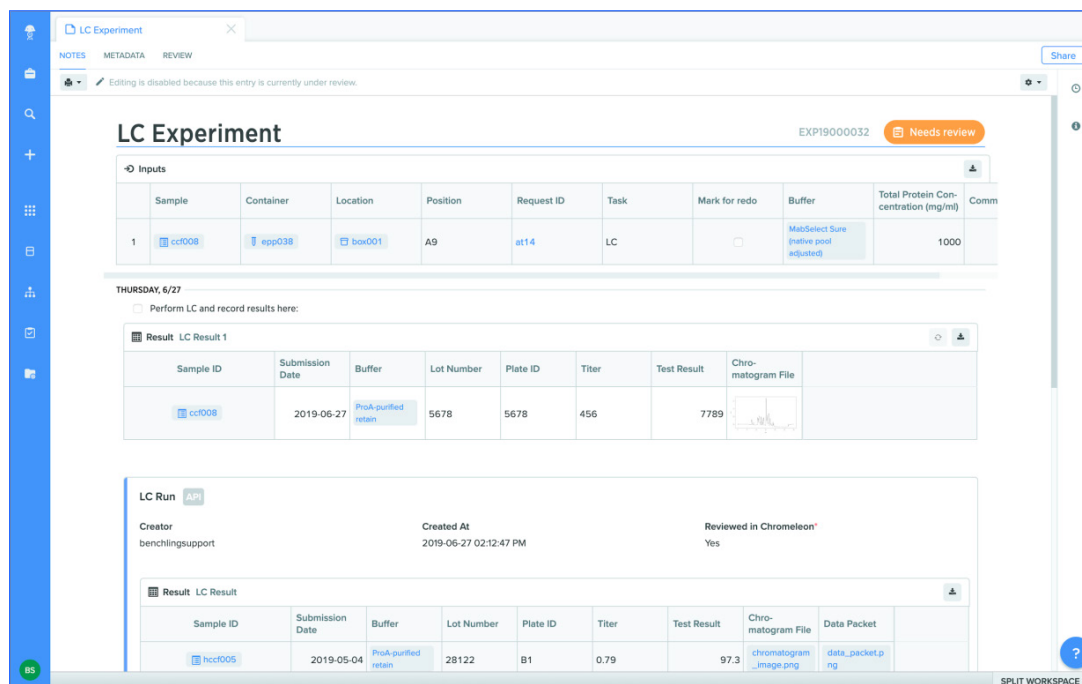
Benchling's Solution

Benchling for Lab Automation gives R&D teams a centralized environment to design, document, and run 100s-1000s of samples in their entire workflow with complete traceability. It makes possible a direct connection between Benchling and liquid handlers and analytical instruments, such that scientists can generate run instructions and capture results without ever leaving Benchling. Benchling automatically interlinks these instructions and results with the samples used and the experiment to which they are relevant. Beyond increasing scientist productivity and experimental throughput, this means that R&D teams can unlock new, data-driven insights from their high-throughput programs. *Learn more about Benchling for Lab Automation.*

Connecting high-performance liquid chromatography analysis with Benchling

THE CHALLENGE

One of our clients' biologics teams relies heavily on chromatography instruments. Their scientists would run a chromatography instrument, analyze the data in a third-party software, email another scientist requesting them to review the data, and then, upon passing the review, manually upload the analyzed data to a standalone lab notebook and a spreadsheet. Sending this data for review was cumbersome and didn't establish a reliable audit trail. And the manual step of uploading the output of the analyses to the lab notebook and spreadsheets was error-prone and tedious, leading to lost and disconnected data.



The screenshot displays the Benchling 'LC Experiment' interface. It features a top navigation bar with 'NOTES', 'METADATA', and 'REVIEW' tabs. Below this is a table titled 'Inputs' with columns: Sample, Container, Location, Position, Request ID, Task, Mark for redo, Buffer, Total Protein Concentration (mg/ml), and Comm. A single row is visible with sample 'ccf008'. Below the inputs table, there's a section for 'THURSDAY, 6/27' with a checkbox to 'Perform LC and record results here:'. This is followed by a 'Result LC Result 1' table with columns: Sample ID, Submission Date, Buffer, Lot Number, Plate ID, Titer, Test Result, and Chromatogram File. A row shows sample 'ccf008' with a submission date of 2019-06-27. Below this is an 'LC Run' section with a table for 'Result LC Result' with columns: Sample ID, Submission Date, Buffer, Lot Number, Plate ID, Titer, Test Result, Chromatogram File, and Data Packet. A row shows sample 'hccf005' with a submission date of 2019-05-04. The interface also includes a sidebar on the left with various icons and a 'Share' button in the top right.

Sample	Container	Location	Position	Request ID	Task	Mark for redo	Buffer	Total Protein Concentration (mg/ml)	Comm
ccf008	app038	box001	A9	at14	LC	<input type="checkbox"/>	MatSelect Sure (native pool adjusted)	1000	

Sample ID	Submission Date	Buffer	Lot Number	Plate ID	Titer	Test Result	Chromatogram File
ccf008	2019-06-27	ProA-purified retain	5678	5678	456	7789	

Sample ID	Submission Date	Buffer	Lot Number	Plate ID	Titer	Test Result	Chromatogram File	Data Packet
hccf005	2019-05-04	ProA-purified retain	28122	B1	0.79	97.3	chromatogram_image.png	data_packet.png

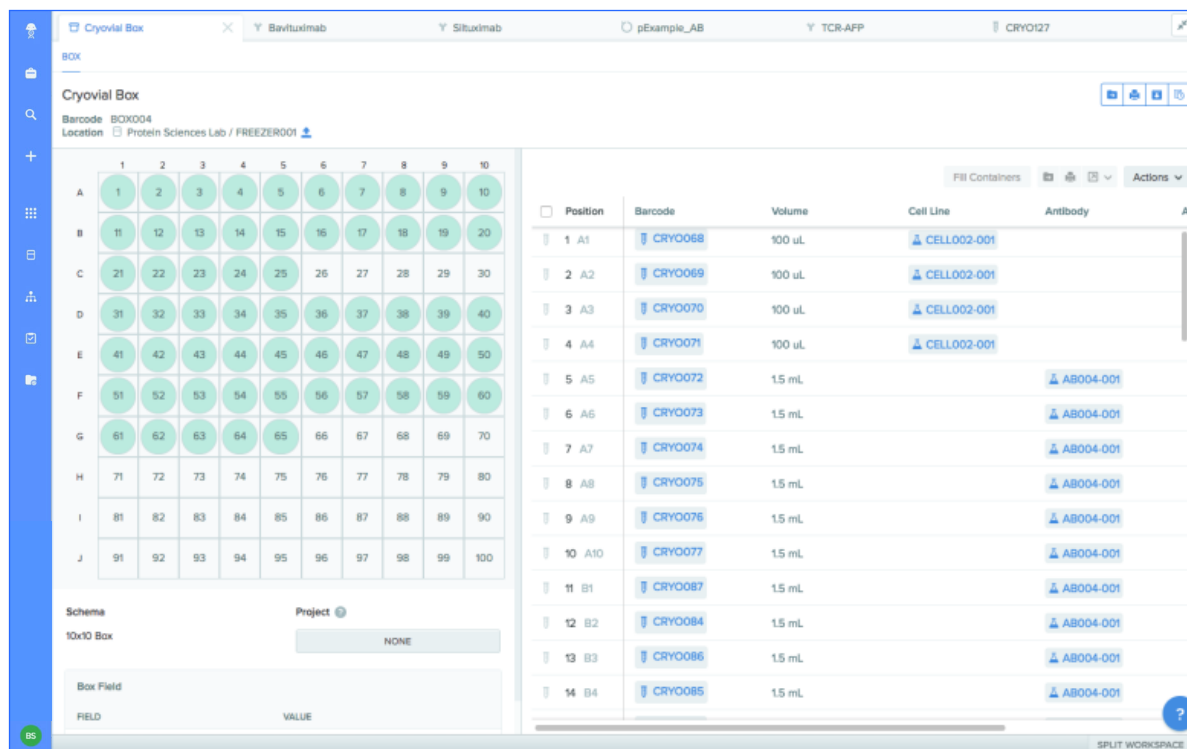
Benchling's Solution

Benchling integrates directly with our client's data analysis software so that upon completing their analysis, the scientist can directly send the results to Benchling, at which point it's automatically associated with the appropriate Notebook entry and linked to the appropriate samples and bio-entities. It's also submitted for review to the relevant parties via the Benchling Notebook's review functionality. With this integration, our client's scientists no longer need to send review requests via email, manually upload data to a standalone notebook and a disconnected spreadsheet, or spend subsequent hours searching for their data across disparate systems. It's all automatically centralized and interlinked within Benchling.

Automating check-in / check-out for smart freezers

THE CHALLENGE

Many of our clients use smart freezers and fridges to simplify inventory tracking. But keeping them in-sync with other inventory and sample tracking software – as well as connecting sample chain of custody with experimental results – is often a manual process. This routinely leads to incomplete or inaccurate data.



The screenshot displays the Benchling interface for a Cryovial Box. On the left, a 10x10 grid shows the layout of the box with vials numbered 1 to 100. On the right, a table lists the contents of the box, including position, barcode, volume, cell line, and antibody.

Position	Barcode	Volume	Cell Line	Antibody
1 A1	CRYO068	100 uL	CELL002-001	
2 A2	CRYO069	100 uL	CELL002-001	
3 A3	CRYO070	100 uL	CELL002-001	
4 A4	CRYO071	100 uL	CELL002-001	
5 A5	CRYO072	1.5 mL		AB004-001
6 A6	CRYO073	1.5 mL		AB004-001
7 A7	CRYO074	1.5 mL		AB004-001
8 A8	CRYO075	1.5 mL		AB004-001
9 A9	CRYO076	1.5 mL		AB004-001
10 A10	CRYO077	1.5 mL		AB004-001
11 B1	CRYO087	1.5 mL		AB004-001
12 B2	CRYO084	1.5 mL		AB004-001
13 B3	CRYO086	1.5 mL		AB004-001
14 B4	CRYO085	1.5 mL		AB004-001

Benchling's Solution

Our clients have connected Benchling to a wide variety of smart/robotic freezers and fridges. When a scientist wants to retrieve, for example, a vial of a particular cell line, they search for the cell line in Benchling Inventory. Then, they identify a particular vial of it and submit a request in Benchling to tell the freezer to retrieve the vial. This request is tied to a specific experiment that the scientist is working on. After the scientist picks up the vial from the freezer, Benchling denotes that vial as "checked out". Once the scientist is finished with the vial, they either mark it as expended or return it to the freezer so it can be automatically "checked back in" on Benchling.

Streamlining primer ordering for sequencing cores

THE CHALLENGE

For sequencing cores, keeping track of existing primers and knowing what to order is a fundamental but complex process. Determining the primers needed for a particular plasmid, comparing that against existing inventory (and keeping that inventory up-to-date), and compiling order forms while associating all of these activities back to a particular sequencing run is a tall order when operating with siloed legacy systems.



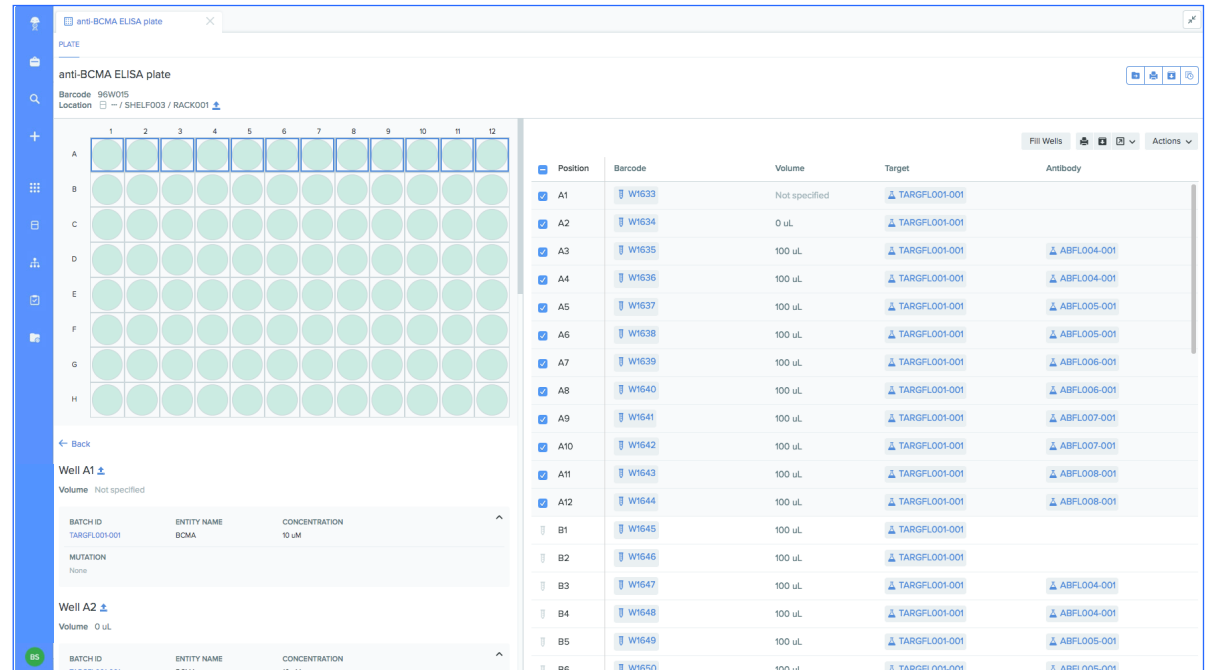
Benchling's Solution

The Benchling platform comprises fully unified applications for molecular biology design and inventory tracking. For our client's sequencing core, a scientist can specify, in a table in a Benchling Notebook entry, the plasmids that they plan to sequence. This triggers an event that runs a custom function on those plasmids to identify which primers are needed and are not already somewhere in the Benchling inventory. This custom function then creates an order form and returns it in the Notebook entry, complete with links to the primers in Benchling. The scientist can then upload that form to a third-party reagent provider.

Linking plate readers with Inventory and Workflow tracking

THE CHALLENGE

Many Benchling clients rely heavily on plate readers to run a wide variety of assays. However, these plate readers rarely synchronized with their storage or record keeping systems. As a result, experimental results weren't automatically linked to samples, necessitating frequent and manual data entry. Beyond requiring scientist time to be spent on data entry, records were frequently inaccurate. This limited our client's ability to maintain accurate institutional knowledge and prolonged time to IND filing.



Position	Barcode	Volume	Target	Antibody
A1	W1633	Not specified	TARGFL001-001	
A2	W1634	0 uL	TARGFL001-001	
A3	W1635	100 uL	TARGFL001-001	ABFL004-001
A4	W1636	100 uL	TARGFL001-001	ABFL004-001
A5	W1637	100 uL	TARGFL001-001	ABFL005-001
A6	W1638	100 uL	TARGFL001-001	ABFL005-001
A7	W1639	100 uL	TARGFL001-001	ABFL006-001
A8	W1640	100 uL	TARGFL001-001	ABFL006-001
A9	W1641	100 uL	TARGFL001-001	ABFL007-001
A10	W1642	100 uL	TARGFL001-001	ABFL007-001
A11	W1643	100 uL	TARGFL001-001	ABFL008-001
A12	W1644	100 uL	TARGFL001-001	ABFL008-001
B1	W1645	100 uL	TARGFL001-001	
B2	W1646	100 uL	TARGFL001-001	
B3	W1647	100 uL	TARGFL001-001	ABFL004-001
B4	W1648	100 uL	TARGFL001-001	ABFL004-001
B5	W1649	100 uL	TARGFL001-001	ABFL005-001
B6	W1650	100 uL	TARGFL001-001	ABFL005-001

Benchling's Solution

By integrating with plate readers, Benchling automatically connects assay results and changes in container locations and concentrations with sample records. Benchling also connects these results and changes with the Workflow task associated with the assay run. As a result, not only are samples automatically up-to-date, but assay runs are contextualized within a larger project. This allows our clients to save significant time and answer business questions with full experimental histories.

Running complex queries on data from a manufacturing data warehouse

THE CHALLENGE

A clinical-stage immunotherapy company frequently transfers clinical samples from a manufacturing facility (where data is tracked in a manufacturing database) to a laboratory facility (where data is tracked in an R&D database). When conducting the transfer, data must be pulled in from the manufacturing database, and new data (ex. location) must be appended to the samples. The APIs of their existing LIMS were incapable of transferring information between the two databases. In addition, groups at the laboratory facility needed to run complex queries on these samples, which the LIMS also couldn't support. As a result, the onus was on users to manually transfer relevant data between the databases, leading to lost time and unreliable data.

The screenshot shows the Benchling interface with a sample record for 'Viral Cells' (Batch JeLWORK003-001) and a terminal window displaying a complex SQL query. The query is a SELECT statement with multiple joins and filters, including a subquery in the WHERE clause. The terminal output shows the results of the query, including columns like 'id', 'source_id', 'name', 'creator', 'created_at', 'modified_at', 'schema_id', 'schema_name', 'concentration_sl', and 'concentration_display_units'.

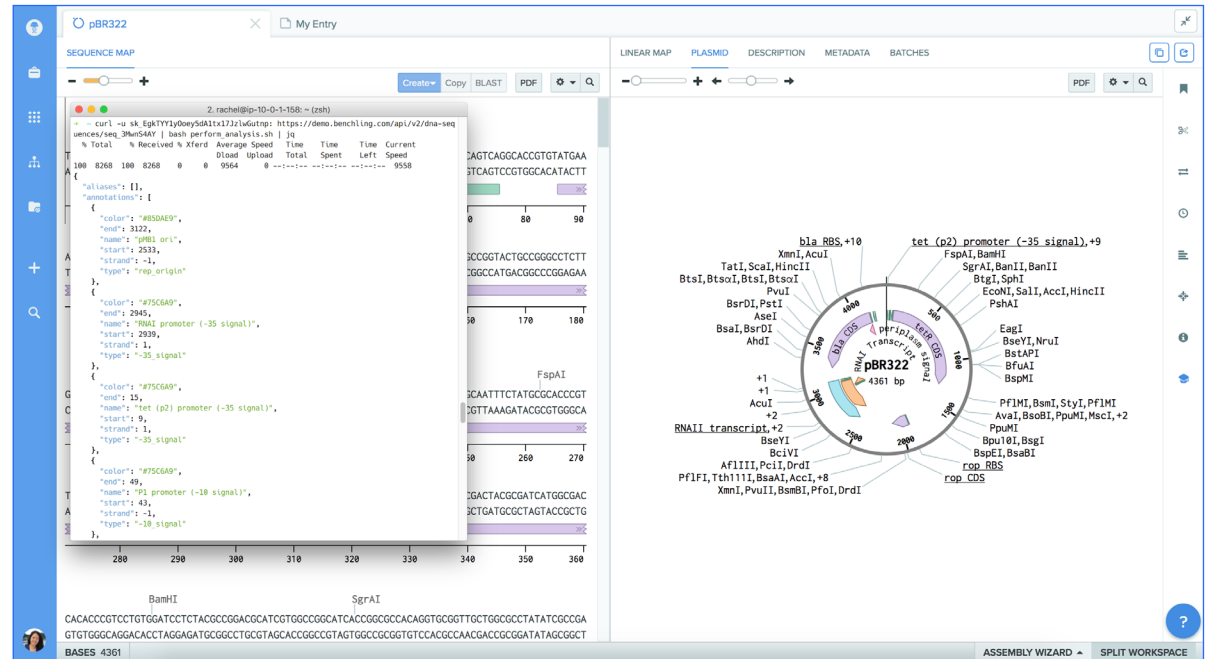
Benchling's Solution

Benchling automated data transfer between the client's databases, as well as running complex queries, saving scientists time and ensuring real-time data reliability. Upon arrival at the lab, samples are scanned into Benchling, pulling in relevant data from the manufacturing database, generating registered samples in Benchling, and associating them with locations in the lab. Additional information, such as when the sample was received at the lab, is also automatically appended. Instead of manually keeping track of the samples, everything is automated. And instead of having to export data and then run a manual search on it for samples ready for assays, assay groups simply run this query through the Benchling API.

Implementing proprietary algorithms within Benchling

THE CHALLENGE

A client in the gene therapy space runs high-volume proprietary analyses on sequence files. Previously, scientists would manually download, zip, and send these sequences over email to another team to run the analysis. Then, the sequences would be sent back over email and re-uploaded into a standalone molecular biology tool, creating duplicates of the newly analyzed sequences. Results from this analysis would also have to be manually added to other systems of record. These steps were time consuming, compounded the chances of errors, and negatively impacted accurate record-keeping.



Benchling's Solution

Since moving to the Benchling platform, this client now handles sequence analyses through Benchling's Requests application. A scientist selects the sequences they want to analyze, and the team responsible for the analysis is notified. Using Benchling's API, they then run a script on the sequences without extracting them from Benchling. The sequences are automatically updated in Benchling with the results of the analysis. Our client no longer has to manage complicated chains of exporting, zipping, running, re-uploading, scanning for duplicates, and updating links.