
Best-in-Class Sequence Design Tools Centralized on One Platform

CENTRALIZED MANIPULATION

Run Virtual Digests and
Automate Primer Design

With Benchling's comprehensive analysis suite, point solutions for sequence design are no longer necessary. Run virtual digests and design primers powered by Primer3 or manual methods, with cut-site, overhang, and secondary structure visualization. Just as with custom annotation libraries, create custom primer libraries that can easily be shared across teams.

COMPLEX CONSTRUCTS

Cloning Features
Streamline
Assembly Design

Benchling is designed with real scientist workflows in mind, from the most cutting-edge techniques to the most reliable everyday ones. Our product supports automated Gibson, Type IIS, and Digestion and Ligation cloning, so scientists never have to switch between multiple unwieldy tools to manually piece together assemblies ever again.

REVOLUTIONIZING CRISPR

The New Industry
Standard for CRISPR

Existing CRISPR tools suffer from outdated scoring algorithms, slow speed, and privacy and security issues. Benchling works with scientists to implement the latest in CRISPR advances, resulting in a product powered by the latest scoring algorithms with speeds 100X faster than the leading competitor. Design guides and templates in one place, quickly and securely.

Sharing Features and Intuitive Interface Power Collaboration

LINK TO SEQUENCES

Centralized Sequences
Ensure Visibility

Beyond sharing the same tools, Benchling allows scientists to share links to the same sequence files. Oligos, assemblies, plasmids, protein sequences, and more can all be easily viewed and distributed. Scientists are no longer constrained to sharing only the results of disparate design tools; they can share the entire context of their experimental process. The unprecedented transparency that the Benchling platform offers means that no stakeholder (be they a scientist or a lawyer) has to spend time wondering where to get accurate information on a team's vectors.

FOR SCIENTISTS,

BY SCIENTISTS

User-Friendly
Functionality

Like all of Benchling's tools, the Molecular Biology Suite is designed for scientists, by scientists. This means that the Suite not only synthesizes and adds to the functions of scientists' existing disparate tools, but it does so in a way that's aesthetically pleasing and intuitively designed. Scientists can easily get up and running with the Molecular Biology Suite, and the read-only links that can be created for any sequence file means that even non-Benchling users can experience the benefits of Benchling's usability and sharability.

The screenshot displays the Molecular Bio Suite interface. On the left, the 'SEQUENCE MAP' tab is active, showing three DNA sequence segments with their corresponding 'U6 promoter' regions highlighted in orange. The top segment is labeled 'gRNA (363 bp)'. On the right, the 'LINEAR MAP' tab is active, showing a single DNA sequence with a 'U6 promoter' region in orange and a 'gRNA scaffold' region in blue. The interface includes various toolbars for editing and visualization, such as 'Create', 'Copy', 'Blast', 'Insert', 'B', 'I', 'U', and 'More'.

Powering Molecular Biology with Experimental Context

LAB NOTEBOOK

Integration with Benchling's Lab Notebook changes the Molecular Biology Suite from a standalone tool into a powerful driver of experimental context. With the Lab Notebook, sequence design and documentation can happen side-by-side, ensuring that every sequence is accompanied by its full experimental history. And since Benchling's tools all exist within the same platform, any updates to sequences will be automatically carried over into the Notebook entries in which they're mentioned or attached.

BIOREGISTRY

The Bioregistry appends a metadata tab to every molecular biology file, allowing for additional and more complex information tracking. Custom schemas allow scientists to track any piece of information about a sequence, as well as allow them to standardize information tracking across sequences. The Bioregistry also empowers scientists to view any other files that are relevant to a given sequence file. Lab Notebook entries, other sequence files, constructs, and biological entities relevant to a given sequence are easily viewable and searchable.

WORKFLOW AND RESULTS MANAGEMENT

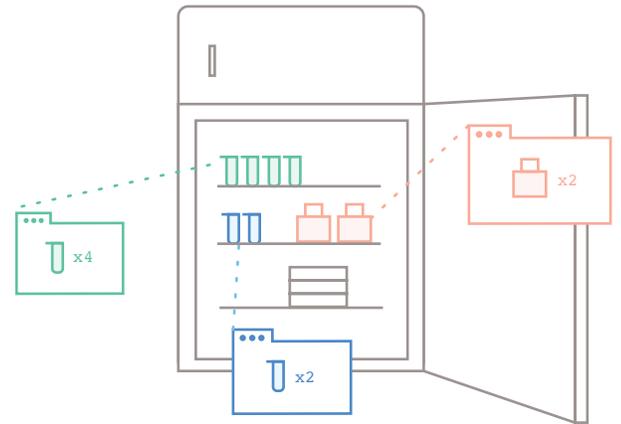
Everything on the Benchling platform happens with complete synchronicity. The Workflow and Results Management tool allows managers to assign specific tasks to scientists and teams with direct links to relevant files in the Molecular Biology Suite. This means that scientists can start building experimental context before they even begin carrying out their experiments, transforming the Molecular Biology Suite into a set of tools that drives research and experimental design, beyond just sequence visualization.



BIOREGISTRY

Intelligent Strain Management and Sample Tracking

Complex biologics workflows necessitate the tracking of biological entities across experiments and teams. Existing sample tracking solutions – from outdated, inflexible software to disparate homegrown approaches – are either too rigid to truly empower all labs, or too idiosyncratic to support consistent user adoption across teams, especially as an organization's structure changes. Benchling's Bioregistry is the next step in inventory management, flexible enough to adapt to any lab but powerful enough to accelerate research, all driven by the usability that Benchling's co-development practices ensure.



Create an Interconnected Web of Any Biological Entities

CUSTOM REGISTRATION

Register Any Biological Entity

A biological registration system should support all workflows with uncompromising functionality. With Benchling's custom data types, scientists can design and register any entity within the Bioregistry. Configurable schemas for each data type allow scientists to specify trackable metadata fields. From cell strains to mice, the Benchling Bioregistry is flexible enough to map to any life science R&D organization.

COMPLEX LINKING

Build Links Between Biological Entities

The Bioregistry's flexibility doesn't end with sample registration. A key element of effective inventory management is the ability to trace associations between biological entities. Benchling's powerful tagging and file linking features empower scientists to take configurable sample registration a step further. Build antibody complexes that link out to protein chains; link chains to expression plasmids; create connections between mice and their respective tissue samples. The possibilities are as varied as laboratories themselves.

AUTOMATED RESULTS

Tie Biological Entities to Results

The powerful linking features of the Bioregistry aren't limited to the tool itself. Benchling's Lab Notebook automatically associates recorded experimental results with the biological entity that the results correspond to. By combining experimental documentation with the Bioregistry's rich registration features, the Benchling platform empowers companies to increase organizational visibility and develop an institutional knowledge base so that every research decision is informed by past results.

VP OF GLOBAL BIOTECHNOLOGY COMPANY

" The Bioregistry is the master of all of the data and information systems at Agenus or any company... it's always essential to have something like this in a diverse data environment. It's an environment that's very difficult to integrate data across, but Benchling gives us access to it."

Accurately Track Biological Entities Across Experiments, Metadata, & Results

DATA CONSTRAINTS

Ensure Data Integrity with Centralized, Standardized Data

With existing inventory management solutions, individual teams or even scientists keep track of their own biomolecules in their own systems. Especially when data needs to be validated, this leads to frustration and wasted human hours spent searching through the various systems for the right data. Since the Benchling Bioregistry is flexible enough to meet any lab's needs, it can centralize data across organizations. And with its read-only registration environment, it combines unprecedented transparency with a high standard of data integrity. Data constraint features empower companies to conform registered entities to rules that are impossible to implement with existing solutions.

TRACE LOTS

Track Batches of Samples with Lot Management

For life science workflows where biological entities are fluid and can generate batches or derivative entities on a per-experiment basis, inventory management software has to be able to accommodate that fluidity. With Benchling's lot management features, batches of samples can be registered, tracked, and linked back to the sample that generated them. The Bioregistry's rich tracking features mean that the lineage of every sample and batch will always be transparent and reliable.

RICH SEARCHING

Search By Name, Tags, DNA Sequences, and More

Benchling's Bioregistry offers powerful search functions that make for easy navigation despite the complexity of inventory registration structures. Scientists can search for samples by name, tags, DNA sequences or sequence structures, and can even break down samples based on their metadata; the Bioregistry makes it simple to answer questions as complex as, "What are all my microbial strain batches that score an OD reading between 1.8 and 1.93?" And since samples are automatically linked to the Notebook entries they were used in, navigating results is just as easy.

