Accelerate RNA Therapeutics R&D with a Modern Informatics Platform

Software to realize the potential of RNA therapeutics R&D

Given the seminal role of RNA in nature, scientists continue to use oligonucleotides for a variety of research, diagnostic, and therapeutic applications. Because RNA therapeutics can target conditions that small molecules and proteins cannot address, researchers are now on the verge of treating previously 'undruggable' diseases. From the approval of the first antisense oligonucleotide, aptamer, and small interfering RNA, to the now famous launch of mRNA-based COVID-19 vaccines, the pipeline of RNA therapies and vaccines has expanded dramatically. By combining the powers of biology and chemistry, RNA molecules are fundamentally changing our understanding of biology and how we address disease.

RNA therapeutics require more advanced, dynamic software

As RNA therapeutics have gained traction scientifically and clinically, the software tools to engineer them have been frustratingly limited. The design of these oligos, study of functional properties, and analysis of results require an evolving solution that can adeptly handle both chemistry and biology workflows.

- **Syntax standardization:** Without a clear standard to represent chemical modifications, scientists and RNA vendors have come up with their own syntaxes. These teams spend a significant amount of time translating their bases into a shared language. Standardized nomenclature will make data sharing easier and accelerate oligo design.
- **Support for both chemistry and biology:** Scientists studying intracellular delivery mechanisms and RNA biology seek to improve the biophysical properties of RNA therapeutics with chemical modifications. Software tools must be able to design chemically modified oligos while connecting the biological assays with complete context.
- **Iterative oligo design:** Scientists continue to improve potency, specificity, stability, and tolerability of RNA molecules, which require research teams to design, test, and refine oligos quickly. Modern software should streamline iterative oligo design, collaboration, and institutional knowledge sharing.

Design, analyze, and develop RNA therapeutics on Benchling's unified informatics solution

Benchling is a modern, unified, fully configurable, and easy-to-use solution that adapts to the rapidly evolving needs of RNA therapeutics R&D. For the first time, scientists can design chemically modified oligonucleotides, standardize on syntax, centralize experimental results, and collaborate with teammates more effectively on a single platform. The platform is flexible, easy-to-use, and purpose-built to drive efficient experimentation. With Benchling, researchers creating cutting edge RNA therapeutics can bring these breakthrough therapies to market faster.

PRODUCTIVITY

66%

reduction in manual R&D tasks

INSIGHTS

2x

increase in confidence in data quality and completeness

COLLABORATION

95%

improvement in cross-team data transfer

INFORMATICS

4.5x

typical ROI realized by Benchling customers

The RNA Therapeutics R&D Solution

Notebook
Ensure documentation completeness and compliance

Molecular Biology
Accelerate DNA, amino acid, and oligo design, at scale

Registry
Standardize, connect, and contextualize sample data

Inventory
Track and manage every sample and reagent

Requests
Coordinate work across specialized teams

Workflows
Design, test, and optimize R&D processes

Insights
Translate R&D data into actionable insights

Benchling for Lab Automation
Automate instrument orchestration

Design chemically modified oligonucleotides with ease

Standardize oligo sequence design with HELM and IDT syntax

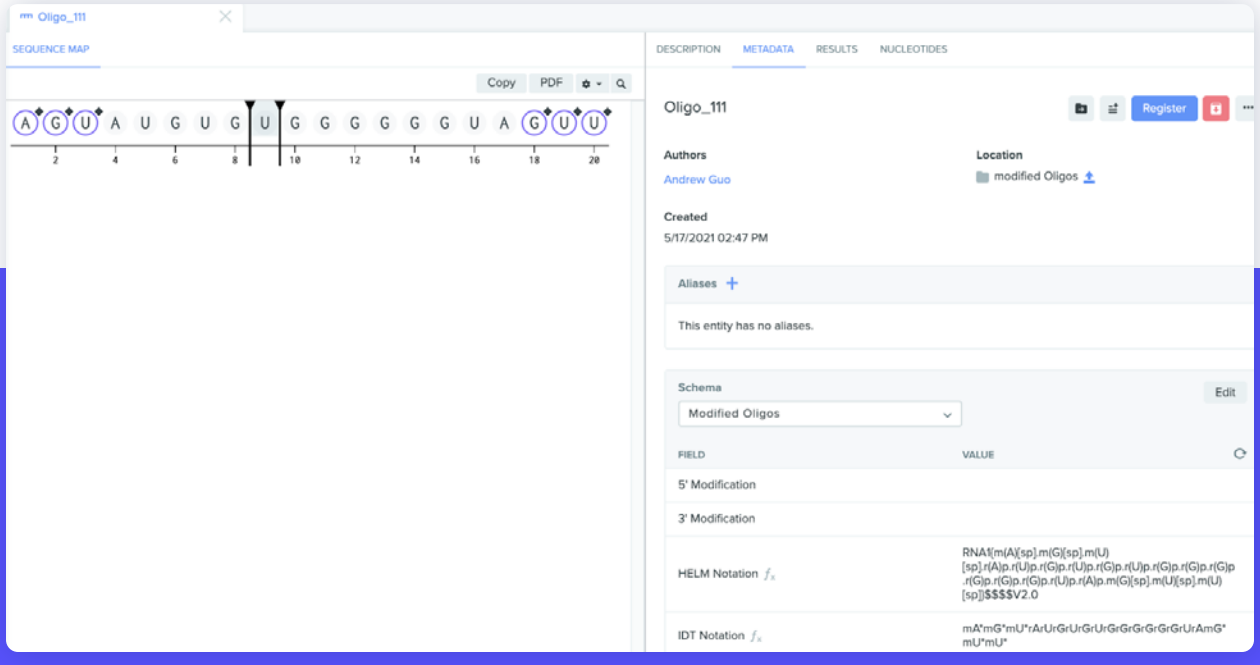
Model chemically modified oligos using HELM notation. This increasingly popular notation helps standardize sequence design and ensures sequence and naming uniqueness during registration. Also, interconvert HELM sequences to IDT syntax making it easy to order designed sequences from the vendor.

Visualize and modify sequences with an intuitive user interface

Create oligo sequences with ease using distinct modals for monomer, sequence, and entity-level information. This clearly displays contextual information in each modal and makes it easy to find relevant information quickly.

Automate creation and modification of oligo sequences with REST APIs

Design or modify oligo sequences with HELM syntax in a high-throughput manner by leveraging API endpoints to list out specific modified oligos, create modified oligos, or update modified oligos via HELM.



Centralize experimental data for faster, contextually-relevant insights

Standardize experimental data capture with results table

Keep consistent records across experiments and scientists with structured results tables. This ensures high data integrity and reduces the need for redundant or repeat work.

Centralize all sample-relevant results automatically

Automatically link all key data related to an oligo entity such as inventory location, pertinent experiments, sequence history, and associated analytical results. This improves data traceability and makes it easy to track the experimental history of an oligo sample.

Visualize analytical results with custom dashboards

Aggregate oligo characterization results from diverse assays and tests and visualize the results with in-platform visualization tools. This saves scientists time in aggregating data and helps them draw actionable insights quickly.

Collaborate with teammates focused on biology and chemistry effectively

Leverage institutional knowledge across teams with a custom monomer library

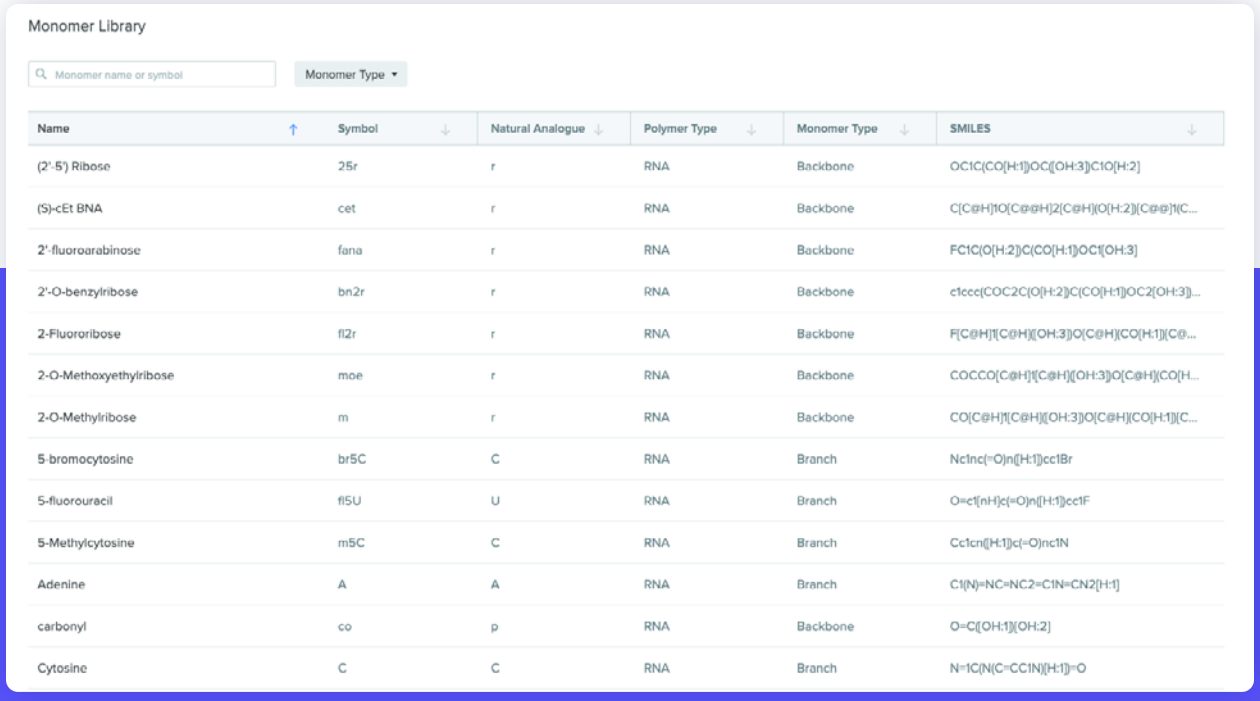
Start with a centralized pre-built monomer library that can be further customized to meet organizational needs and is accessible to all relevant users designing sequences. This helps not only secure institutional knowledge but also ensures the information is disseminated and used across the organization in a consistent manner.

Find both natural and chemically modified sequences with search features

Use advanced search functionality, including sorting and filtering options, to quickly find oligo sequences. This improves transparency across teams and provides ready access to all your team's sequences and related data with just a few clicks.

Share HELM and IDT notations of oligo sequences with vendors and collaborators

Automatically generate HELM and IDT notations while designing new sequences with computed fields. This provides instant access to both syntaxes of a sequence so that scientists can easily export relevant sequences to share with both internal and external collaborators or vendors.



Name	Symbol	Natural Analogue	Polymer Type	Monomer Type	SMILES
(2'-5') Ribose	25r	r	RNA	Backbone	OC1C(CO[H:1])OC([OH:3])C1O[H:2]
(S)-cEt BNA	cet	r	RNA	Backbone	C[C@H]1O[C@@H]2[C@H](O[H:2])[C@@]1(C...
2'-fluoroarabinose	fana	r	RNA	Backbone	FC1C(O[H:2])C(CO[H:1])OC1[OH:3]
2'-O-benzylribose	bn2r	r	RNA	Backbone	c1ccc(COC2C(O[H:2])C(CO[H:1])OC2[OH:3])...
2-Fluororibose	fl2r	r	RNA	Backbone	F[C@H]1[C@H]([OH:3])O(C@H)(CO[H:1])[C@...
2-O-Methoxyethylribose	moe	r	RNA	Backbone	COCCO[C@H]1[C@H]([OH:3])O(C@H)(CO[H...
2-O-Methylribose	m	r	RNA	Backbone	CO[C@H]1[C@H]([OH:3])O(C@H)(CO[H:1])[C...
5-bromocytosine	br5C	C	RNA	Branch	Nc1nc(=O)n([H:1])cc1Br
5-fluorouracil	fl5U	U	RNA	Branch	O=c1[nH]c(=O)n([H:1])cc1F
5-Methylcytosine	m5C	C	RNA	Branch	Cc1cn([H:1])c(=O)nc1N
Adenine	A	A	RNA	Branch	C1(N)=NC=NC2=C1N=CN2[H:1]
carbonyl	co	p	RNA	Backbone	O=C([OH:1])[OH:2]
Cytosine	C	C	RNA	Branch	N=1C(N(C=CC1N)[H:1])=O