



Case Study

Going digital
to accelerate cell
and gene therapy
research and
development

ElevateBio



elevatebio[®]



Tackle infrastructure inefficiencies to accelerate viral vector, RNA, and cell therapy production

Cell and gene therapies (CGTs) are transforming the landscape of disease treatment and personalized medicines. Several have been approved by the US FDA. Having the right infrastructure is critical to optimizing CGT development processes. However, CGT companies often face significant infrastructure inefficiencies that represent a bottleneck to therapeutic development.

Experiencing these inefficiencies first-hand, ElevateBio's founders built their company to eliminate them and power CGT development. ElevateBio has built a first-of-its-kind solution to accelerate the design, manufacturing, and development of a broad array of genetic medicines. The company's integrated technologies model offers turnkey scale and biotechnological capabilities to power cell and gene therapy processes, programs, and companies to their full potential.

ElevateBio is enabling a growing number of CGT innovators, ranging from startups to large biopharmas by providing them with next-generation technology platforms, manufacturing capabilities, and industry-leading expertise. ElevateBio's R&D organization, including its next-generation sequencing (NGS) team, develops innovative therapeutics as well as novel technologies that can be applied to internal and partner programs. The R&D team works with Benchling to create an infrastructure to power the development of these key capabilities and expertise.

Company Profile

Number of Employees

400+

Industry

Biotech

Corporate HQ

**Waltham,
Massachusetts**

↑ Sample throughput

NGS core team went from processing 100s to 1000s of samples per week

↑ Scientist efficiency

Freed up scientists' time to focus on lab work and data analysis, increasing efficiency

↑ Probability of success

Can identify process bottlenecks earlier, achieving breakthroughs faster

Challenges

Establish a high-throughput CGT research pipeline

To increase throughput requires a data management ecosystem capable of ingesting, storing, and contextualizing growing amounts of metadata, viral titer parameters, and sequencing data.

Often, research organizations are offered one-off tools built for specific steps of the pipeline, leading to, at best, a piecemeal solution. Usually these tools can't scale to match infrastructure growth leading to increased data output.

To ensure scale and throughput, ElevateBio wanted a central platform like Benchling, consisting of an ELN integrated with a database, an inventory system, and sequence analysis capabilities.

Increase scientist efficiency by eliminating time consuming, manual data management tasks

ElevateBio initially relied on segmented systems and processes to track experiments and data. This led to siloed, unsearchable, and uncontextualized data and scientists lost precious time searching, correcting, and manually aggregating data sets.

Use of disparate files also meant a lack of standardization within and across experiments and groups. Tracing parent-child sample relationships was a challenge, and it was difficult to know which experiments were performed on which entities, particularly during material transfers across groups.

Increase the probability of success by identifying and addressing inefficiencies sooner

One of the best ways to increase the probability of a successful CGT is to identify and resolve problems and inefficiencies much earlier in the research and development timeline. Using spreadsheets, emails, and slide decks to track, present, and analyze data is slow and error-prone, often leading to lost data and making it difficult to identify operational bottlenecks.

ElevateBio's scientists found it difficult to trace samples and experiments from original donor to final product using disparate record-keeping methods, which could increase the risk of errors, lead to inconsistencies across experiments, and challenge the identification and correction of process inefficiencies.

“Benchling simplifies a lot of our more onerous record keeping, and it also greatly enables cross-functional collaboration and transfer of materials on experiments. Benchling makes our work easier and faster.”



Cherylene Plewa
Sr. Vice President
Cellular Engineering

Outcomes

ElevateBio's core NGS team increased throughput from processing 100s of sequences to 1000s each month after implementing Benchling and integrating it with modern lab instruments.

Acquisition of a new suite of instruments enabled ElevateBio's NGS core team to process thousands of sequences each week — at least in principle. Achieving that level of throughput in practice required full integration into Benchling. After adopting Benchling, the team went from processing hundreds of sequences each week to thousands, reaching a maximum output of 7000 per week after implementing Benchling.

Benchling facilitates tracking of exact sequences rather than nonspecific names. The structured storage of information possible in Benchling enables a rapid execution of sequencer runs in only 10 minutes. Data from Benchling Workflows are automatically extracted over the Benchling API and compiled into upload-ready spreadsheets for sequencing. This process readily scales to 384 samples commonly encountered in Amplicon Workflows.

Scientist efficiency increased with standardized data capture and elimination of paper notebooks

With Benchling, ElevateBio scientists can drag and drop raw data files as they move through their physical processes, creating a digital trail rather than cutting and pasting into paper lab notebooks.

Standardized ontologies and protocols enable all stakeholders to understand what has been done and when, while process control and user permissions can be used to manage data handoffs across multiple roles and organizations.

Benchling facilitates seamless transfer between teams, so they can work together on experiments in real-time. Scientists spend more time working together to make decisions and optimize the pipeline, instead of wasting time on manual, error-prone data management tasks.

Success rates were increased by faster identification of inefficiencies and full sample traceability

Using Benchling, ElevateBio scientists can track viral vector titers over time, enabling them to catch suboptimal parameters and course correct far earlier in the research and development pipeline. This saves a significant amount of time, material, and financial resources and increases the probability of success.

With Benchling as a central source of truth, they have full sample traceability from original donor to final product. The standardized vocabulary, inventory, and database ensure that all experimental details and metadata are findable, searchable, and traceable, increasing the probability of successful product development.