How to Upgrade from Vector NTI® to



benchling.com

Modern molecular biology deserves modern software

In the past decade, molecular biology has evolved tremendously, but sequence design software has stagnated. Most sequence design tools are point solutions that weren't built for modern scientific workflows or cross-team collaboration. While such tools might seem to "check the box" for certain functions, they ultimately can't meet the full needs of complex R&D workflows, since they don't meaningfully integrate with broader informatics infrastructures. As a result, R&D organizations struggle to tie downstream assay data back to sequences and can't fully leverage the data they're producing. This regularly slows down research and and introduces risks into process development and scale up.

Within today's life science R&D organizations, molecular biology is highthroughput, collaborative, and organizationally complex. To meet these needs, companies need much more than a desktop-based point solution. They need cloud-based software unified with a broader informatics platform, so they can transfer context across teams and trace from sequences down to the results of individuals candidates.

With Vector NTI[®] set to be officially discontinued by Thermo Fisher, now is the ideal time for life science R&D organizations to digitally transform their molecular biology with a modern, cloud-based platform.

Vector NTI[®] and Other Legacy Molecular Biology Tools

- Low throughput design
- Individual contributor
- Desktop-based
- Manual design and analysis
- Standalone tools

Benchling Molecular Biology

- High throughput design
- Large collaborative teams
- Web-based
- > Automated design and analysis
- Natively unified with the Benchling Life Sciences R&D Cloud

WHY BENCHLING

Benchling is built for modern science

Best in class high throughput capabilities

- Batch cloning, alignment, and translation tools were designed for modern, high-throughput workflows.
- Bulk CRISPR guide design with on-/off-target scoring is the industry-leading tool for highthroughput CRISPR workflows.

Features for the latest scientific workflows

- From CRISPR, to sequencing, to cloning, Benchling Molecular Biology is built to power the latest techniques.
- Share a gRNA repository with your organization, access more than 100 genomes, and create assemblies with cutting-edge cloning techniques.

A single comprehensive suite of tools

- Unify CRISPR, sequence design, and more with 10+ tools on one intuitive interface.
- Translate directly from DNA sequences to amino acid sequences, automatically compute biochemical properties for any sequence, and perform multi-sequence alignments all in the same cloud-based tool.

benchling.com 🙎 3

WHY BENCHLING

Benchling is purpose-built for collaboration

Web-based, simple, and intuitive user interface

- When replacing legacy systems such as Vector NTI[®], Benchling increases user adoption by over 90%.
- Benchling Molecular Biology was designed to be as usable as modern consumer software.

Seamless handoffs with full experimental context

- Use shareable links and annotation libraries to standardize analysis across your teams.
- Track all sequence edits through a complete version history.
- Trace from the assay data produced by physical samples to their upstream sequences.

Access controls and role-based permissions

- Grant Author-Only, Read, Edit, and Admin permissions for particular sequences to particular users.
- Share specific sequences with external collaborators to limit IP exposure.

WHY BENCHLING

Benchling is a unified data management platform, not a point solution

Native unification with other Benchling applications

- Benchling Molecular Biology enables workflows that standalone apps simply cannot support.
- Design and register sequences in the same interface. For example, in Requests and Workflows, specify registered sequences to be used in fulfillment. In Notebook, drag-anddrop sequences to link to them in the middle of Notebook entries.

Track complex relationships

- Model complex relationships between sequences and other biological entities.
- See the downstream samples and results that any sequence has led to. For example, see the binding affinity of all antibody lots with a given light chain variable fragment.

Cut down manual work with automation

- When registering a construct, Benchling automatically parses out, registers, and interlinks the construct's components.
- Automatically compute the biochemical properties of constructs based on parts detection.

Open Developer Platform for integration

- Through modern REST APIs, easily integrate Benchling with your existing IT infrastructure.
- Auto-sync with instruments, software, and databases.
- Automatically backup all entities and related analysis.



Professional services and training make for an effortless migration and ongoing success

Our team is made of experienced biotech consultants, Silicon Valley software engineers, and molecular and cellular biology PhDs. We have published industry standards for life science R&D data models and have 100% customer retention across our hundreds of Benchling Enterprise clients.





Workflow Discovery and Configuration

Your dedicated Benchling Customer Success team takes the time to understand your requirements, your research workflows, and your organizational structure. Based on these needs and on industry best practices, we then design ideal workflows for you and map your science and processes onto the Benchling platform.



Go-Live

The same Customer Success representatives that craft your Benchling instance will be the ones to train your scientists on it. We offer comprehensive go-live training to get all stakeholders up and running. Designated "super users" are given additional training so that they can serve as an ongoing resource to your team.



Migration and Integration

Benchling will coordinate all configuration, data import, and automation integration activities in close communication with you to ensure that the platform fits seamlessly into your existing research and IT infrastructure.



Ongoing Success

Following the initial roll-out, your Customer Success team will continue to engage with you to ensure long-term success, resolve any issues that arise, and develop new Benchling Molecular Biology features. In addition, live in-app support chat gives your scientists a direct line to Benchling Customer Success 24/7. **Case Study**

Benchling has a successful track record of transitioning customers from Vector NTI®

By migrating them off of Vector NTI[®], Benchling cut down busywork at a top-10 pharma by 96%

Before

.....O

- Customer had 100s of users with significant experience using Vector NTI[®].
- Some workflows took up to 80 hours due to the lack of molecular biology automation.
- Experimental results were not linked with sequence data making it difficult to apply predictive machine learning.
- Clunky and dated software had **poor uptake among users**.

The Transition Process

- 1. Workflow Discovery and Configuration
 - Requirements gathering
 - Organization structure mapping
 - Understanding research workflows
 - Designing ideal workflows and industry best practices
 - Transferring all existing molecular biology data (including 1000s of legacy Vector NTI® files)
 - Project management



Case Study

The Transition Process (continued)

- 2. Migration and Integration
 - Importing of data into Benchling
 - Integrating with Registry and other custom applications
 - Integrating with automation for request submission steps
 - Configuring Benchling platform
 - Versioning and audit log support

3. Go-Live and Ongoing Success

- Power user training and roll-out
- Phased roll-out to users across multiple sites
- Go-live training for all users
- Post-roll out support
- Regular updates and feature enhancements
- Extensive feedback and feature request system
- Robust roadmap of new functionality
- Ongoing training



After

.....

- Integrated Molecular Biology application with Benchling Registry and other internal systems - resulting in a more complete system of record.
- Synced Benchling platform with **custom automation to handle request submission tasks** freeing up scientists from redundant manual work (96% time savings).
- Flexible data models, sequence-level intelligence, and robust developer platform now power machine learning applications.
- Support for modern scientific workflows fostered higher uptake among scientists right from the start.

Benchling meets or exceeds Vector NTI® functionality in all core areas.

| Functionality | | Benchling | Vector NTI® |
|--|---|-----------|-------------|
| Cloud-based Platform | Use from any computer anywhere Wide OS support Import data from public databases | ~ | × |
| Native Integration with Other Apps | Link sequences directly to notebook entries Flexibly record results and properties of a variety of samples in a single software Track lineage of biological entities with parent-child relationships Manage inventory locations of DNA and AA constructs | ~ | × |
| Bio-intelligent Analysis | Auto-detect and fill parts based on sequence-level intelligence Smart compute biochemical properties of sequences Import, search, and reuse oligos | ~ | × |
| Collaboration | Share links and annotation libraries to standardize analysis across teams Set-up role-based permissions for clear accountability Manage information sharing with advanced access controls Share construct designs and parts with downstream teams | ~ | × |
| Automation | Automate laborious and time consuming analysis steps Auto sync with instruments, software, and databases Automatically backup all entities and related analysis | ~ | × |
| Support | Leverage professional services for effortless migration Keep up-to-date with the science with regular feature updates | ~ | × |
| High- throughput Tools | Bulk cloning / assembly Bulk auto-annotations Bulk auto-alignments Bulk primer attachment Bulk translations | ~ | × |

| Functionality | | Benchling | Vector NTI [®] |
|-----------------------------|---|--------------------|---|
| CRISPR | Guide RNA design On-target / off-target scoring HR templates Plasmid assembly | ~ | × |
| Construct Design | Restriction-based cloning wizard Gibson assembly Golden gate assembly | ~ | ~ |
| Primer Design | Primer creation wizard Pre-existing primer library import Gibson primer design Golden gate primer design Secondary structure checks | ~ | ~ |
| Cloning | Enzyme search Virtual digests Enzyme cut sites Ladders library Enzyme lists | ~ | ~ |
| Sequence Visualization | Plasmid map ORF customization Annotations Sequence search | ~ | ~ |
| Sequence Alignment | Alignment to templatesConsensus alignments | \checkmark | \checkmark |
| AA / Protein Analysis | AA alignments Translations Biochemical properties computation | ~ | ~ |
| Codon Optimization | | Coming in Q2, 2019 | ~ |
| RNA Design and Analysis | | 2020 Roadmap | Image: A set of the set of the |
| Other Assembly Technologies | | 2020 Roadmap | \checkmark |
| Circuit Visualization | | × | \checkmark |

Benchling has modernized molecular biology at hundreds of companies.



Request a demo to learn more about how to upgrade from Vector NTI® to Benchling www.benchling.com/request-demo/