When looking for the right software for molecular biology, scientists shouldn't have to settle for a tool without sufficient functions, easy usability, or support for sharing and collaboration. Existing molecular biology solutions offer just one, if any, of these features, forcing scientists to invest in point solutions for specific molecular biology tasks and hindering their ability to work together. Benchling Molecular Biology gives scientists a complete set of tools that support the bleeding-edge of life science research in a user-friendly interface. And with Molecular Biology's collaboration features, scientists no longer have to settle for software that they know doesn't offer everything they need.

Collaboration Begins with Rich Sequence Visualization Features

**UNIFORM VISUALIZATION**
- Custom Annotation Libraries
- Standardize Sequences

With Benchling, teams share not only their sequences, but their tools, so everyone can be on the same page from the start of an experiment. Custom annotation libraries empower scientists to visualize sequences in the same way across teams and larger organizations. And powerful import features from industry-standard external databases, as well as from 100+ genomes already stored on the Benchling platform, allow scientists to standardize the sources of their information.

**PROTEIN ANALYSIS**
- Protein Tools Support
- Biochemical Analysis

Benchling Molecular Biology isn't limited to just DNA sequences. Import protein files or create new protein sequences by translating from DNA sequences. Benchling Molecular Biology provides the same visualization and collaboration functionality for protein sequences as it does for DNA sequences. Additionally, protein sequences in Benchling feature live updating of biochemical properties, so your tools never lag behind your analysis.

**CUTTING-EDGE ALIGNMENTS**
- The Leading Tool for Multi-Sequence Alignment

Most existing tools only support consensus alignment between two or a small number of sequences, forcing scientists who want to compare alignments across many sequences to manually compare sequences one by one. With Benchling's multi-sequence alignment feature, scientists can compare more than one hundred sequences at once, with remarkable speed and simplicity. Scientists can view alignments that their colleagues have already done so work is never duplicated.
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.

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.

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.

Benchling allows scientists to easily share links to their 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 has to spend time wondering where to get the most accurate, up-to-date information on a team's constructs.

Like all of Benchling's tools, Molecular Biology is designed for scientists, by scientists. This means that it 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 intuitive. Scientists can easily get up and running with Molecular Biology and share sequence links even with teams that don't design their sequences in Benchling.
Powering Molecular Biology with Experimental Context

**NOTEBOOK**
Integration with Benchling’s Notebook changes Molecular Biology from a standalone tool into a powerful driver of experimental context. With 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 applications 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.

**REGISTRY**
The Registry 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 or construct, as well as allow them to standardize information tracking across sequences. The Registry also empowers scientists to view any other files that are relevant to a given sequence file; Notebook entries, other sequence files, constructs, and biological entities relevant to a given sequence are easily viewable and searchable.

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