Benchling for CRISPR Screening

CRISPR screening is a revolutionary methodology to identify genes of interest underlying a specific phenotype. CRISPR can be scaled up for screening applications because of the versatility of CRISPR/Cas9 in disrupting target DNA and the ease of gRNA/plasmid generation. However, the large-scale use of this technology requires scientists to track the viability of edited cells, maximize editing efficiency, minimize off-target effects, optimize vector design, and improve transformation efficiency. A data platform that can assimilate the results from all the steps and provides actionable insights is required to overcome these challenges.

Benchling provides a modern, fully configurable, and user-friendly platform to power CRISPR screening. Benchling helps you manage the entire screening workflow from guide library design to phenotypic selection with the latest in silico sequence design tools, configurable data models, collaborative experiment management, integrated sample tracking, automation integration, and advanced data analytics.



Generate a CRISPR guide library with smart in silico design tools, custom library management, and structured data capture.

- Perform CRISPR guide design with builtin on-target and off-target scoring for both knock outs and knock ins
- Manage a library of gRNAs, Cas9 enzymes, and target genes with rich sequence and attribute metadata
- Streamline record keeping of gRNA synthesis with Notebook's built-in Results tables for standardized data capture



Transduce cells efficiently with collaborative study design, integrated inventory management, and actionable insights.

- Centralize and automatically link
 experiments and results from
 characterization of parent cell lines
- Manage inventory of edited cells and clones with container locations, sample positions, and quantity information
- Monitor editing efficiency, transfection efficiency, yield, and other metrics with custom schema fields and visual dashboards



Design and package viral vectors by using a suite of molecular biology tools, flexible data modeling, and intelligent sample tracking.

- Design viral vectors with high transfection efficiency by using the latest in silico molecular biology tools
- Track relationships between genes of interest, gRNA, Cas9, and plasmids with fully configurable data models
- Map every step from in silico design to vector production and storage of viral lots in a single platform

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Select phenotypes of interest with automation integration, advanced analytics, and auto linking of analytics with sample metadata.

- Integrate with high throughput automation and analytical instruments for full traceability of phenotypic selection experiments
- Optimize clone enrichment, selection, and expansion methods with longitudinal data from Benchling Insights
- Link deep sequencing analysis output with metadata of validated hits in the Registry

