

Resource Summary Report

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Benchling

RRID:SCR_013955

Type: Tool

Proper Citation

Benchling (RRID:SCR_013955)

Resource Information

URL: <https://benchling.com>

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Description: An online resource which helps researchers manage and organize labs and experimental results by supplying molecular biology software tools for experimental design and data analysis. Benchling provides tools for functions such as primer design and colony counting as well as CRISPR guide design and automated Gibson and Golden Gate cloning. Users can take notes in line with data, link data across entries, keep files and data in one place, and manage and keep track of team progress. An enterprise version of Benchling is available for scientists working within an organization with additional administrative, compliance, and security protocols.

Resource Type: web application, software resource, computational hosting, service resource

Keywords: web application, computational hosting, lab management, organization, collaboration, Crispr

Funding: Andreessen Horowitz

Availability: Free, Public

Resource Name: Benchling

Resource ID: SCR_013955

License URLs: <https://benchling.com/terms>

Record Creation Time: 20220129T080318+0000

Record Last Update: 20260808T190018+0000

Ratings and Alerts

No rating or validation information has been found for Benchling.

No alerts have been found for Benchling.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1579 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#).

Myers JA, et al. (2026) E-cadherin expression promotes tumor growth via KLRG1-dependent pathways. *Journal of immunology* (Baltimore, Md. : 1950), 215(4).

Eriksson J, et al. (2026) Single-Cell Lineage Tracing Uncovers Resistance Signatures and Sensitizing Strategies to FLT3 Inhibitors in Acute Myeloid Leukemia. *Cancer research*, 86(7), 1724.

Lee J, et al. (2026) Perturbation of genes linked to common schizophrenia risk variants identifies cilia programs. *bioRxiv : the preprint server for biology*.

Campbell AS, et al. (2026) Molecular insights into electroreceptor ribbon synapses from differential gene expression in sturgeon lateral line organs. *Journal of anatomy*, 248(5), 784.

Yu Q, et al. (2026) Promoting Autophagy Mitigates Stress-Induced Remodeling in Patient iPSC-CMs with the Phospholamban R9C Mutation. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(7), e11480.

Rosendal E, et al. (2026) Rapid drug resistance prediction in positive *Mycobacterium tuberculosis* clinical samples using an extensive targeted next-generation sequencing panel. *Emerging microbes & infections*, 15(1), 2627072.

Vihma H, et al. (2026) A dual-reporter mouse for therapeutic discovery in Angelman syndrome. *JCI insight*, 11(5).

Chung HK, et al. (2026) Atlas-guided discovery of transcription factors for T cell programming. *Nature*, 651(8107), 1077.

Nguyen T, et al. (2026) Systematic functional dissection of germline noncoding risk variants impacting clonal hematopoiesis. *bioRxiv : the preprint server for biology*.

Aharon-Hefetz N, et al. (2026) Essentiality and dynamic expression of the human tRNA pool during viral infection. *Molecular systems biology*, 22(4), 519.

Marzluf JP, et al. (2026) Towards a cleaner CHO chassis: systematic knockout of host cell proteins for efficient biopharmaceutical manufacturing. *Frontiers in bioengineering and*

biotechnology, 14, 1750646.

Romadhon PZ, et al. (2026) Clinical and Genetic Pattern of β -Thalassemia Major in East Java, Indonesia. *Journal of blood medicine*, 17, 573064.

Arroyo Villora S, et al. (2026) A Bioinformatics and Wet-Lab-Based Pipeline Identifies CLDN10 and GJB2 as Epigenetically Silenced Tumor Suppressor Genes in Cutaneous Melanoma. *International journal of molecular sciences*, 27(5).

Yu Z, et al. (2026) Elucidating the kinetics of CRISPR-SaCas9 action to obtain effective HIV DNA excision with two gRNAs. *Nucleic acids research*, 54(6).

Lee G, et al. (2026) Template nicking suppresses promoter-independent antisense transcription in IVT via R-loop-mediated strand displacement. *Nucleic acids research*, 54(2).

Wan J, et al. (2026) MAPK Pathway Mutations Emerge in Mutant IDH1 Inhibitor-Resistant Cholangiocarcinoma and Attenuate the IFN Response. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(5), 925.

Humer D, et al. (2026) NR2F6 deletion revives CAR-T cell function and induces antigen-agnostic immune memory in solid tumors. *Nature communications*, 17(1).

Berlureau J, et al. (2026) An atypical F-type ATPase is necessary for the function of the antibody cleavage system MIB-MIP in mycoplasmas. *PLoS pathogens*, 22(3), e1014043.

Baba S, et al. (2026) CRISPR-Cas based plasmid design for multidrug-resistant *Klebsiella pneumoniae* isolates. *FEMS microbiology letters*, 373.

Kováč B, et al. (2026) Genetic and environmental determinants of multicellular-like phenotypes in fission yeast. *Genetics*, 233(1).