

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

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: 20260728T043431+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 1235 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Juanpere-Borras M, et al. (2026) Genome-wide Identification of conditionally essential genes supporting *Streptococcus suis* growth in serum and cerebrospinal fluid. *Virulence*, 17(1), 2600145.

An Y, et al. (2026) Activation and Spatial Redistribution of RNA Splicing Factors Trigger Hepatic Regeneration. *Cellular and molecular gastroenterology and hepatology*, 20(2), 101654.

Kama Y, et al. (2026) Notch interaction with RUNX factors regulates initiation of the T-lineage program. *The Journal of experimental medicine*, 223(2).

Galindo G, et al. (2026) AI-assisted protein design to rapidly convert antibody sequences to intrabodies targeting diverse peptides and histone modifications. *Science advances*, 12(1), eadx8352.

Keskinen T, et al. (2026) Genetic Correction of the Most Common Mutation Causing Primary Hyperoxaluria Restores Enzyme Localization and Oxalate Metabolism. *Journal of inherited metabolic disease*, 49(1), e70122.

Monteiro MP, et al. (2026) Deciphering strain differences in *codY* regulation of *Clostridioides difficile* sporulation. *Microbiology spectrum*, 14(1), e0170625.

Riley SE, et al. (2026) In vivo screen reveals specific roles of Hippo pathway components in development and regeneration. *Life science alliance*, 9(3).

Lloyd EG, et al. (2025) SMAD4 and KRAS Status Shapes Cancer Cell-Stromal Cross-Talk and Therapeutic Response in Pancreatic Cancer. *Cancer research*, 85(8), 1368.

Mehri S, et al. (2025) Identification of viral protease-dependent cleavage sites within the human astrovirus polyprotein. *Journal of virology*, 99(1), e0132124.

Pinilla-Macua I, et al. (2025) Cell migration signaling through the EGFR-VAV2-Rac1 pathway is sustained in endosomes. *Journal of cell science*, 138(2).

Lubrano P, et al. (2025) Metabolic mutations reduce antibiotic susceptibility of *E. coli* by pathway-specific bottlenecks. *Molecular systems biology*, 21(3), 274.

Rhea L, et al. (2025) ARHGAP29 promotes keratinocyte proliferation and migration in vitro and is dispensable for in vivo wound healing. *Developmental dynamics : an official publication of the American Association of Anatomists*, 254(4), 310.

Zetterdahl OG, et al. (2025) Generation of iPSC Lines with Tagged α -Synuclein for Visualization of Endogenous Protein in Human Cellular Models of Neurodegenerative Disorders. *eNeuro*, 12(6).

Gühmann M, et al. (2025) Diffdigester.uni-jena.de: a tool for optimized selection of restriction enzymes for plasmid identification in cloning procedures. *Nucleic acids research*, 53(W1), W238.

Liu L, et al. (2025) CXCR4-LASP1-G9a-SNAIL axis drives NEPC transdifferentiation via induction of EMT and downregulation of REST. *Cell genomics*, 5(8), 100916.

Xiang W, et al. (2025) Senescent macrophages induce ferroptosis in skeletal muscle and accelerate osteoarthritis-related muscle atrophy. *Nature aging*, 5(7), 1295.

Das S, et al. (2025) Constitutive expression of Cas9 and rapamycin-inducible Cre recombinase facilitates conditional genome editing in *Plasmodium berghei*. *Scientific reports*, 15(1), 2949.

Gridina M, et al. (2025) Targeted correction of megabase-scale CNTN6 duplication in induced pluripotent stem cells and impacts on gene expression. *PeerJ*, 13, e18567.

Milligan C, et al. (2025) Enhanced Interleukin 6 Trans-Signaling Modulates Disease Process in Amyotrophic Lateral Sclerosis Mouse Models. *Brain sciences*, 15(1).

Karpova Y, et al. (2025) PARG Mutation Uncovers Critical Structural Determinant for Poly(ADP-Ribose) Hydrolysis and Chromatin Regulation in Embryonic Stem Cells. *Cells*, 14(14).