

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

BLAT

RRID:SCR_011919

Type: Tool

Proper Citation

BLAT (RRID:SCR_011919)

Resource Information

URL: <http://genome.ucsc.edu/cgi-bin/hgBlat?command=start>

Proper Citation: BLAT (RRID:SCR_011919)

Description: Software designed to quickly find sequences of 95% and greater similarity of length 25 bases or more.

Abbreviations: BLAT

Resource Type: software resource

Keywords: bio.tools

Resource Name: BLAT

Resource ID: SCR_011919

Alternate IDs: biotools:blat, OMICS_01434

Alternate URLs: <https://bio.tools/blat>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T132716+0000

Ratings and Alerts

No rating or validation information has been found for BLAT.

No alerts have been found for BLAT.

Data and Source Information

Usage and Citation Metrics

We found 3808 mentions in open access literature.

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

Adami A, et al. (2026) Protocol for efficient CRISPRi-mediated silencing of retrotransposons in human pluripotent stem cells. STAR protocols, 7(1), 104398.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. Current biology : CB, 36(7), 1659.

Poulain F, et al. (2026) Clonal origin and early lineage divergence in adenosquamous carcinoma. Cell reports, 45(6), 117470.

Anwar M, et al. (2026) Human Left Ventricle circRNA-miRNA-mRNA Network Analyses Reveal a Novel Proangiogenic Role for circNPHP1 Under Ischemic Conditions. JACC. Basic to translational science, 11(2), 101468.

Robinson BR, et al. (2026) Acute testicular hyperthermia leads to rapid loss of global piRNA and a concurrent increase in LINE1 activity within heat sensitive male germ cells. Mobile DNA, 17(1), 7.

Mackey AI, et al. (2026) Temperature and genetic background drive mobilization of diverse transposable elements in a global human fungal pathogen. PLoS genetics, 22(1), e1011979.

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Huang AY, et al. (2026) Accurate detection of somatic single-nucleotide variants from bulk RNA-seq data using RNA-MosaicHunter. Nucleic acids research, 54(1).

Tulloch AJ, et al. (2026) Massively parallel reporter assay for mapping gene-specific regulatory regions at single-nucleotide resolution. eLife, 14.

Ren W, et al. (2026) A Murine Database of Structural Variants Identifies A Candidate Gene for a Spontaneous Murine Lymphoma Model. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e22890.

Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in Aceraceae family. Genome biology, 27(1).

Christinaki AC, et al. (2026) Cladobotryum rhodochroum sp. nov. (Hypocreales, Ascomycota): A New Fungicolous Species Revealed by Morphology, Phylogeny, and Comparative Genomics. Journal of fungi (Basel, Switzerland), 12(2).

Wang Z, et al. (2026) Low prevalence of GCK gene mutations in Chinese patients with gestational diabetes mellitus. Clinics (Sao Paulo, Brazil), 81, 100889.

Comerford M, et al. (2026) Mapping the gene regulatory landscape of archaic hominin introgression in modern Papuans. *PLoS genetics*, 22(3), e1012067.

Bird KA, et al. (2026) Structure and sequence evolution in the pennycress (*Thlaspi arvense*) pangenome. *The New phytologist*, 250(5), 2723.

Scimone ML, et al. (2026) Single-cell transcriptomics and RNAi screening define a hierarchical program of planarian eye regeneration. *Cell reports*, 45(4), 117245.

Dudragne L, et al. (2026) Diversity and Distribution of the Subtelomeric Y' Elements Across *Saccharomyces cerevisiae* Strains. *Genome biology and evolution*, 18(5).

Wu D, et al. (2026) Generative modeling for RNA splicing prediction and design. *eLife*, 14.

Hamilton BA, et al. (2026) *Mysm1* mutations in meander tail mice cause anterior-selective cerebellum malformation. *bioRxiv : the preprint server for biology*.

Hallast P, et al. (2026) Population-scale Y chromosome assemblies reveal recurrent remodeling within constrained architectures. *bioRxiv : the preprint server for biology*.