

Resource Summary Report

Generated by [RRID](#) on Apr 11, 2025

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

Funding:

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: 20250410T070222+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3575 mentions in open access literature.

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

Andersen K, et al. (2025) Complex Genetic Evolution and Treatment Challenges in Myeloid Neoplasms: A Case of Persistent t(2;3)(p15~23;q26)/MECOM Rearrangement, SF3B1 Mutation, and Transient TNIP1::PDGFRB Chimera. *Cancer genomics & proteomics*, 22(1), 24.

Olson J, et al. (2025) Mating system of *Biomphalaria sudanica*, a vector of *Schistosoma mansoni*. *Current research in parasitology & vector-borne diseases*, 7, 100241.

Gruys ML, et al. (2025) Gene model for the ortholog of Glys in *Drosophila simulans*. *microPublication biology*, 2025.

Wang J, et al. (2025) Comparing acute versus AIDS ART initiation on HIV-1 integration sites and clonal expansion. *Signal transduction and targeted therapy*, 10(1), 23.

Wang C, et al. (2025) Discovery of Novel Diagnostic Biomarkers for Common Pathogenic *Nocardia* Through Pan-Genome and Comparative Genome Analysis, with Preliminary Validation. *Pathogens (Basel, Switzerland)*, 14(1).

Xiong Y-R, et al. (2025) Patterns of spontaneous and induced genomic alterations in *Yarrowia lipolytica*. *Applied and environmental microbiology*, 91(1), e0167824.

Cerqueira de Araujo A, et al. (2025) Genome sequences of four Ixodes species expands understanding of tick evolution. *BMC biology*, 23(1), 17.

Medrano JF, et al. (2025) De novo whole-genome assembly and annotation of *Coffea arabica* var. Geisha, a high-quality coffee variety from the primary origin of coffee. *G3 (Bethesda, Md.)*, 15(1).

Grobecker P, et al. (2025) A dedicated caller for DUX4 rearrangements from whole-genome sequencing data. *BMC medical genomics*, 18(1), 24.

Zhou X, et al. (2025) Transethnic analysis identifies SORL1 variants and haplotypes protective against Alzheimer's disease. *Alzheimer's & dementia : the journal of the*

Alzheimer's Association, 21(1), e14214.

Zhou Y, et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes. *GigaScience*, 14.

Lu X, et al. (2025) Cellular Senescence in Hepatocellular Carcinoma: Immune Microenvironment Insights via Machine Learning and In Vitro Experiments. *International journal of molecular sciences*, 26(2).

Wang X, et al. (2024) Chromosome level genome assembly and transcriptome analysis of E11 cells infected by tilapia lake virus. *Fish & shellfish immunology*, 148, 109505.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.

Shen X, et al. (2024) Exploring the cobia (*Rachycentron canadum*) genome: unveiling putative male heterogametic regions and identification of sex-specific markers. *GigaScience*, 13.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. *GigaScience*, 13.

Christinaki AC, et al. (2024) Genomic insights into the evolution and adaptation of secondary metabolite gene clusters in fungicolous species *Cladobotryum mycophilum* ATHUM6906. *G3 (Bethesda, Md.)*, 14(4).

Gu X, et al. (2024) TE-TSS: an integrated data resource of human and mouse transposable element (TE)-derived transcription start site (TSS). *Nucleic acids research*, 52(D1), D322.

Santos LGC, et al. (2024) SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. *International journal of molecular sciences*, 25(2).

McEwan AR, et al. (2024) An ancient polymorphic regulatory region within the BDNF gene associated with obesity modulates anxiety-like behaviour in mice and humans. *Molecular psychiatry*, 29(3), 660.