# **Resource Summary Report**

Generated by NIF on May 2, 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:** 20250420T014602+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 NIF.

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 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).

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.

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).

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

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.