Resource Summary Report

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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 FDI Lab - SciCrunch.org.

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).

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.

Tamang P, et al. (2024) Mining Biosynthetic Gene Clusters of Pseudomonas vancouverensis Utilizing Whole Genome Sequencing. Microorganisms, 12(3).

Bowman J, et al. (2024) Rapid evolution of genes with anti-cancer functions during the origins of large bodies and cancer resistance in elephants. bioRxiv : the preprint server for biology.

Liu ZT, et al. (2024) Organic fertilization co-selects genetically linked antibiotic and metal(loid) resistance genes in global soil microbiome. Nature communications, 15(1), 5168.

Wang Q, et al. (2024) A consensus genome of sika deer (Cervus nippon) and transcriptome analysis provided novel insights on the regulation mechanism of transcript factor in antler development. BMC genomics, 25(1), 617.