# **Resource Summary Report**

Generated by NIF on May 20, 2025

# **UCSC Genome Browser**

RRID:SCR 005780

Type: Tool

## **Proper Citation**

UCSC Genome Browser (RRID:SCR\_005780)

### Resource Information

URL: http://genome.ucsc.edu/

Proper Citation: UCSC Genome Browser (RRID:SCR\_005780)

**Description:** Portal to interactively visualize genomic data. Provides reference sequences and working draft assemblies for collection of genomes and access to ENCODE and Neanderthal projects. Includes collection of vertebrate and model organism assemblies and annotations, along with suite of tools for viewing, analyzing and downloading data.

**Synonyms:** The Human Genome Browser at UCSC, UCSC Genome Browser Group, University of California at Santa Cruz Genome Browser, UCSC Genome Bioinformatics

**Resource Type:** project portal, service resource, database, data or information resource, portal

Defining Citation: PMID:12045153, PMID:22908213, PMID:23155063

**Keywords:** Reference, sequence, assembly, collection, genome, visualize, genomic, data, ENCODE, Neanderthal, project, sequencing

Funding: UC BIOTEuropean UnionH;
Alfred P. Sloan Foundation;
David and Lucille Packard Foundation;
NIH;
HHMI;
CISI;
NHGRI;
DOE;
NSF DBI 9809007;

#### NIGMS GM52848

Availability: Restricted

Resource Name: UCSC Genome Browser

Resource ID: SCR\_005780

Alternate IDs: OMICS\_00926, SCR\_017502, nif-0000-03603, SciEx\_217, SCR\_012479

Alternate URLs: http://genome.cse.ucsc.edu

License URLs: http://genome.cse.ucsc.edu/conditions.html

**Record Creation Time:** 20220129T080232+0000

Record Last Update: 20250519T203418+0000

## Ratings and Alerts

 Used for genome assembly by the Human Islet Research Network community.
 Contact(s): Golnaz Vahedi, Klaus Kaestner - Human Islets Research Network https://hirnetwork.org/

No alerts have been found for UCSC Genome Browser.

### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 9604 mentions in open access literature.

**Listed below are recent publications.** The full list is available at <u>NIF</u>.

Zhou T, et al. (2025) Dog10K: an integrated Dog10K database summarizing canine multiomics. Nucleic acids research, 53(D1), D939.

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.

Smith JR, et al. (2025) Standardized pipelines support and facilitate integration of diverse datasets at the Rat Genome Database. Database: the journal of biological databases and curation, 2025.

Ogawa Y, et al. (2025) GATA4 binding to the Sox9 enhancer mXYSRa/Enh13 is critical for testis differentiation in mouse. Communications biology, 8(1), 81.

McGinty RJ, et al. (2025) Inherent instability of simple DNA repeats shapes an evolutionarily stable distribution of repeat lengths. bioRxiv: the preprint server for biology.

Lv J, et al. (2025) Pifithrin-? sensitizes mTOR-activated liver cancer to sorafenib treatment. Cell death & disease, 16(1), 42.

Estrada MD, et al. (2025) Transcriptional regulation of the non-homologous end joining gene Ligase IV by an intronic regulatory element directs thymocyte development. Research square.

Zhang S, et al. (2025) Exploratory analysis of a Novel RACK1 mutation and its potential role in epileptic seizures via Microglia activation. Journal of neuroinflammation, 22(1), 27.

De Paolis V, et al. (2025) An antisense-long-noncoding-RNA modulates p75NTR expression levels during neuronal polarization. iScience, 28(1), 111566.

Afshari MK, et al. (2025) The Transcriptomic and Gene Fusion Landscape of Pleomorphic Salivary Gland Adenomas. Genes, chromosomes & cancer, 64(1), e70023.

Cui Z, et al. (2025) Effect of SNORD113-3/ADAR2 on glycolipid metabolism in glioblastoma via A-to-I editing of PHKA2. Cellular & molecular biology letters, 30(1), 5.

Perez G, et al. (2025) The UCSC Genome Browser database: 2025 update. Nucleic acids research, 53(D1), D1243.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Tan I, et al. (2025) Alu-Sc-mediated exonization generated a mitochondrial LKB1 gene variant found only in higher order primates. Scientific reports, 15(1), 3360.

Skystad Kvernebo M, et al. (2025) Genetic Variants in the SCN9A Gene are Detected in a Minority of Erythromelalgia Patients. Acta dermato-venereologica, 105, adv42022.

Seth P, et al. (2025) Interaction of N-methylmesoporphyrin IX with a hybrid left-/right-handed G-quadruplex motif from the promoter of the SLC2A1 gene. Nucleic acids research, 53(2).

Macwan RS, et al. (2025) TPM4 overexpression drives colon epithelial cell tumorigenesis by suppressing differentiation and promoting proliferation. Neoplasia (New York, N.Y.), 59, 101093.

Moon Y, et al. (2025) PolyASite v3.0: a multi-species atlas of polyadenylation sites inferred from single-cell RNA-sequencing data. Nucleic acids research, 53(D1), D197.

He Y, et al. (2025) RPS 2.0: an updated database of RNAs involved in liquid-liquid phase

separation. Nucleic acids research, 53(D1), D299.

Truong AD, et al. (2025) Identification of immune-associated genes with altered expression in the spleen of mice enriched with probiotic Lactobacillus species using RNA-seq profiling. Animal bioscience, 38(2), 336.