

Resource Summary Report

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WashU Epigenome Browser

RRID:SCR_006208

Type: Tool

Proper Citation

WashU Epigenome Browser (RRID:SCR_006208)

Resource Information

URL: <http://epigenomegateway.wustl.edu/>

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Description: Software tool for visualizing and interacting with whole-genome datasets. Browser hosts Human Epigenome Atlas data produced by Roadmap Epigenomics project, but its use of advanced, multi-resolution data formats and its user-friendly interface make it possible for investigators to upload and visualize their own data as custom tracks. Developed and maintained by Epigenome Informatics Group at Washington University in St. Louis.

Abbreviations: Human Epigenome Browser

Synonyms: WashU Epigenome Browser, WashU Genome Browser, Human Epigenome Browser at Washington University

Resource Type: data analysis software, data or information resource, data processing software, data set, software application, software resource, source code

Defining Citation: [PMID:22127213](#)

Keywords: epigenomics, genome browser, visualization, clustering, genome, sequencing, next-generation sequencing, virus

Availability: Free, Freely available

Resource Name: WashU Epigenome Browser

Resource ID: SCR_006208

Alternate IDs: OMICS_00629, nlx_151754

Alternate URLs: <http://epigenomegateway.wustl.edu/browser/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260821T193800+0000

Ratings and Alerts

No rating or validation information has been found for WashU Epigenome Browser.

No alerts have been found for WashU Epigenome Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 184 mentions in open access literature.

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

Ma C, et al. (2026) Super enhancer-driven LINC01013 mediates hypoxia-induced mitochondrial dysfunction by HSPA9 to determine pulmonary arterial smooth muscle cell fate. Cellular and molecular life sciences : CMLS, 83(1), 57.

Zhang H, et al. (2026) The conserved noncoding sequence CNS11 is a master control region for Rorc transcription in type 17 immune cells. Science advances, 12(9), eadz6964.

Miao B, et al. (2026) Expression spectrum of TE-driven transcripts in human adult tissues. Genome biology, 27(1).

Zhou J, et al. (2026) MECP2 mutations disrupt pluripotent stem cell fate through remodeling of the three-dimensional genome. Cell death & disease, 17(1).

Hu H, et al. (2026) CD8+ T cells are primed by cDC1 and exacerbate tau-mediated neurodegeneration. bioRxiv : the preprint server for biology.

Liu Y, et al. (2026) Functional variants at 1p36.23 confer risk of schizophrenia through modulating RERE. Nature communications, 17(1), 1742.

Ye JY, et al. (2026) BRAHMA represses STOP1-NRT1.1 module to control plant rhizosphere alkalization and acid stress adaptation. Nature communications, 17(1).

Yang LP, et al. (2026) Targeted methylation of cg24067911 suppresses colorectal cancer metastasis through BCL6-ATXN1-CDH1 axis. Oncogene, 45(2), 295.

Zhang R, et al. (2026) Phase-Separation of YAP Mediates AJUBA Super Enhancer Activation to Promote Aberrant Mitosis in Breast Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(8), e09341.

Teixeira SK, et al. (2026) Ancestry-informative regulatory variants at KCNB1 modulate adipogenesis and body mass index. *Frontiers in endocrinology*, 17, 1805824.

Chen Q, et al. (2026) An integrated multi-omics and network analysis of neutrophil differentiation from initial- to late-stage. *Genome biology*, 27(1).

Wen R, et al. (2026) Dynamic changes in Lamin B1 and heterochromatin coincide with chromatin condensation during human erythropoiesis. *Genome biology*, 27(1).

Bhattacharyya S, et al. (2026) EpiExpr: Predicting gene expression using epigenetic data and chromatin interactions. *bioRxiv : the preprint server for biology*.

Williams EC, et al. (2026) Expression of endogenous retroviral elements is associated with extracellular matrix remodeling in prostate cancer. *Mobile DNA*, 17(1), 1.

Sun Z, et al. (2026) Multi-omics profiling of chromatin accessibility and H3K27ac reveals super-enhancer-mediated regulatory networks governing endometrial receptivity in goats. *Journal of animal science and biotechnology*, 17(1), 4.

Yang Y, et al. (2026) Tumor-specific lncRNA IGF1R-AS1 trans-regulates chromatin interactions associated with oncogenic MYC signaling. *Nature communications*, 17(1).

Zimmerman AJ, et al. (2026) Cell-specific variant-to-gene mapping identifies conserved neural and glial regulators of sleep. *bioRxiv : the preprint server for biology*.

Pereira-Martins DA, et al. (2026) ??Np73 isoform defines a TP53-mutant-like poor-risk subgroup of acute myeloid leukemia. *Cell reports. Medicine*, 102540.

Tang R, et al. (2025) Unfolded protein response kinase PERK supports survival and metastasis of circulating tumor cell clusters via SAM synthesis and H3K4me3-dependent PDGFB signaling. *Cancer communications (London, England)*, 45(12), 1706.

Bernardi S, et al. (2025) CircCDYL Association With hnRNPL Modulates CDYL Isoform Switching in Breast Cancer Cells. *Cancer science*, 116(10), 2750.