

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

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: 20260805T044133+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 145 mentions in open access literature.

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

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

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

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.

Nguyen M, et al. (2025) MAPL regulates gasdermin-mediated release of mtDNA from lysosomes to drive pyroptotic cell death. *Nature cell biology*, 27(10), 1708.

Seng C, et al. (2025) WashU Epigenome Browser update 2025. *Nucleic acids research*, 53(W1), W554.

Xia T, et al. (2025) Empowering integrative and collaborative exploration of single-cell and spatial multimodal data with SGS genome browser. *Cell genomics*, 5(5), 100848.

Zhang B, et al. (2025) KLF6-mediated recruitment of the p300 complex enhances H3K23su and cooperatively upregulates SEMA3C with FOSL2 to drive 5-FU resistance in colon cancer cells. *Experimental & molecular medicine*, 57(3), 667.

Müller L, et al. (2025) Sex-specific role of epigenetic modification of a leptin upstream enhancer in adipose tissue. *Clinical epigenetics*, 17(1), 21.

Harada A, et al. (2025) Hypoxia-induced Wnt5a-secreting fibroblasts promote colon cancer progression. *Nature communications*, 16(1), 3653.

Ma J, et al. (2025) BACH1 recruits STAT3 to enhance leukemia inhibitory factor receptor activity and augments the self-renewal capacity of mouse embryonic stem cells. *Stem cell research & therapy*, 16(1), 483.

Li S, et al. (2025) Non-coding genetic variants underlying higher prostate cancer risk in men of African ancestry. *Nature communications*, 16(1), 10202.

Han Y, et al. (2025) Dissecting the Single-Cell Diversity and Heterogeneity Underlying Cervical Precancerous Lesions and Cancer Tissues. *Reproductive sciences (Thousand Oaks, Calif.)*, 32(5), 1502.

Yang Q, et al. (2025) The NEXT complex regulates H3K27me3 levels to affect cancer progression by degrading G4/U-rich lncRNAs. *Nucleic acids research*, 53(4).

Hardwick J, et al. (2025) The common murine retroviral integration site activating Hhex marks a distal regulatory enhancer co-opted in human early T-cell precursor leukemia. *The Journal of biological chemistry*, 301(3), 108233.

Carreño-Tarragona G, et al. (2025) The JAK2 46/1 haplotype influences PD-L1 expression. *Blood*, 145(19), 2196.

Tracey LJ, et al. (2025) Functional and molecular single-cell analyses implicate PRDM14 in the initiation of B cell leukemia in mice. *Scientific reports*, 15(1), 8827.

Zhang J, et al. (2025) Acetylation at lysine 27 on maternal H3.3 regulates minor zygotic genome activation. *Cell reports*, 44(1), 115148.

Deng J, et al. (2025) *Fusobacterium mortiferum* and its metabolite 5-aminovaleric acid promote the development of colorectal cancer in obese individuals through Wnt/ β -catenin pathway by DKK2. *Gut microbes*, 17(1), 2502138.

Ji K, et al. (2025) HIF1A facilitates hypoxia-induced changes in H3K27ac modification to promote myometrial contractility. *Communications biology*, 8(1), 475.