

Resource Summary Report

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Human Epigenome Atlas

RRID:SCR_006153

Type: Tool

Proper Citation

Human Epigenome Atlas (RRID:SCR_006153)

Resource Information

URL: <http://www.genboree.org/epigenomeatlas/index.rhtml>

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Description: Collection of human reference epigenomes and results of their integrative and comparative analyses. Successive releases of the Atlas will provide progressively more detailed insights into locus-specific epigenomic states, including histone marks and DNA methylation marks across specific tissues and cell types, developmental stages, physiological conditions, genotypes, and disease states. The Human Epigenome Atlas is produced by the NIH Epigenomics Roadmap Consortium.

Abbreviations: Human Epigenome Atlas

Resource Type: atlas, data or information resource, reference atlas

Defining Citation: [PMID:20944597](#)

Keywords: locus, epigenomic state, histone, dna methylation, tissue, cell, developmental stage, physiological condition, genotype, disease state, exon, epigenome, epigenomics

Availability: Public; must adhere to the Data Access Policy

Resource Name: Human Epigenome Atlas

Resource ID: SCR_006153

Alternate IDs: nlx_151645

Alternate URLs: <http://www.genboree.org/site/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260808T190305+0000

Ratings and Alerts

No rating or validation information has been found for Human Epigenome Atlas.

No alerts have been found for Human Epigenome Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Chiu Y, et al. (2025) Time-resolved miRNA-mRNA integrated analysis reveals the miRNA-mRNA networks underlying plasma membrane damage-dependent senescence and DNA damage response-dependent senescence in WI-38 normal human fibroblasts. RNA biology, 22(1), 1.

Srinivasan S, et al. (2020) Discovery and Verification of Extracellular miRNA Biomarkers for Non-invasive Prediction of Pre-eclampsia in Asymptomatic Women. Cell reports. Medicine, 1(2).

Sun W, et al. (2016) Histone Acetylome-wide Association Study of Autism Spectrum Disorder. Cell, 167(5), 1385.

Pennington KL, et al. (2015) Epigenetic Mechanisms of the Aging Human Retina. Journal of experimental neuroscience, 9(Suppl 2), 51.

Roman TS, et al. (2015) Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American journal of human genetics, 97(6), 801.

Amin V, et al. (2015) Epigenomic footprints across 111 reference epigenomes reveal tissue-specific epigenetic regulation of lincRNAs. Nature communications, 6, 6370.

Hangauer MJ, et al. (2013) Pervasive transcription of the human genome produces thousands of previously unidentified long intergenic noncoding RNAs. PLoS genetics, 9(6), e1003569.