# **Resource Summary Report**

Generated by <u>dkNET</u> on May 23, 2025

# 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

Funding:

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: 20250523T054517+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 5 mentions in open access literature.

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

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

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.

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

Amin V, et al. (2015) Epigenomic footprints across 111 reference epigenomes reveal tissuespecific 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.