Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Roadmap Epigenomics Project

RRID:SCR_008924
Type: Tool

Proper Citation

Roadmap Epigenomics Project (RRID:SCR_008924)

Resource Information

URL: http://roadmapepigenomics.org/

Proper Citation: Roadmap Epigenomics Project (RRID:SCR_008924)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 11, 2022. Project for human epigenomic data from experimental pipelines built around next-generation sequencing technologies to map DNA methylation, histone modifications, chromatin accessibility and small RNA transcripts in stem cells and primary ex vivo tissues selected to represent normal counterparts of tissues and organ systems frequently involved in human disease. Consortium expects to deliver collection of normal epigenomes that will provide framework or reference for comparison and integration within broad array of future studies. Consortium is also committed to development, standardization and dissemination of protocols, reagents and analytical tools to enable research community to utilize, integrate and expand upon this body of data.

Abbreviations: Roadmap Epigenomics Project

Synonyms: Epigenomics Program, Common Fund Epigenomics, NIH Roadmap Epigenomics Program, NIH Roadmap Epigenomics Project, Common Fund Epigenomics Program, NIH Common Fund Epigenomics, NIH Common Fund Epigenomics Program, Common Fund Roadmap Epigenomics Program

Resource Type: consortium, data or information resource, organization portal, portal, project portal

Defining Citation: PMID:22690667, PMID:20944595, PMID:20944597

Keywords: epigenomics, genome, genetic variation, gene regulation, genomics, stem cell, primary cell, tissue, blood, lung, heart, gastrointestinal tract, brain, embryonic stem cell, fetus, adult, cell, epigenome, methylome, chip-seq, rna, breast, muscle, connective, gastrointestinal, genitourinary, fat, hematopoietic stem cell, thymus, spleen, placenta, kidney, adrenal, induced pluripotent stem cell, skin, angular gyrus, anterior caudate, cingulate gyrus, hippocampus, inferior temporal lobe, mid frontal lobe, substantia nigra,

dna methylation, histone modification, chromatin, rna transcript, dna, methylation, histone, data set

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Roadmap Epigenomics Project

Resource ID: SCR_008924

Alternate IDs: nlx_151644, OMICS_01564

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260905T132630+0000

Ratings and Alerts

No rating or validation information has been found for Roadmap Epigenomics Project.

No alerts have been found for Roadmap Epigenomics Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 323 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Kuksa PP, et al. (2025) BTS: scalable Bayesian Tissue Score for prioritizing GWAS variants and their functional contexts across omics data. bioRxiv : the preprint server for biology.

Kosugi S, et al. (2025) TRsv: simultaneous detection of tandem repeat variations, structural variations, and short indels using long read sequencing data. Genome biology, 26(1), 246.

Razzaq A, et al. (2025) Exploring Differentially Methylated Genes among Preterm Birth and Full-Term Birth. Lifestyle genomics, 18(1), 76.

Yang F, et al. (2025) Cancer-specific bivalent promoters featuring low-level H3K27me3 signals favor active transcription and govern the cancer cell state transition. Acta biochimica et biophysica Sinica, 58(5), 989.

Tomooka R, et al. (2025) Phase separated condensates of ATRX regulate neural progenitor identity. Nature communications, 16(1), 6489.

Vasseur L, et al. (2025) Derepression of the epithelial transcription factor GRHL2 promotes direct hepatocyte-to-cholangiocyte transdifferentiation. PLoS biology, 23(12),

e3003547.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Chen Z, et al. (2025) Integrative genomics characterizes HCC eRNAs for prognosis and targeted therapy. Scientific reports, 15(1), 41913.

Shin T, et al. (2024) Rare variation in non-coding regions with evolutionary signatures contributes to autism spectrum disorder risk. Cell genomics, 4(8), 100609.

Feitosa MF, et al. (2024) Discovery of genomic and transcriptomic pleiotropy between kidney function and soluble receptor for advanced glycation end products using correlated meta-analyses: The Long Life Family Study. Aging cell, 23(10), e14261.

Law PJ, et al. (2024) Systematic prioritization of functional variants and effector genes underlying colorectal cancer risk. Nature genetics, 56(10), 2104.

Sudalagunta PR, et al. (2024) The Functional Transcriptomic Landscape Informs Therapeutic Strategies in Multiple Myeloma. Cancer research.

Nakamura T, et al. (2024) Topologically associating domains define the impact of de novo promoter variants on autism spectrum disorder risk. Cell genomics, 4(2), 100488.

Qiao X, et al. (2024) Diversifying the anthracycline class of anti-cancer drugs identifies aclarubicin for superior survival of acute myeloid leukemia patients. Molecular cancer, 23(1), 120.

Ounadjela JR, et al. (2024) Spatial multiomic landscape of the human placenta at molecular resolution. Nature medicine, 30(12), 3495.

Hillary RF, et al. (2024) Systematic discovery of gene-environment interactions underlying the human plasma proteome in UK Biobank. Nature communications, 15(1), 7346.

Caporale AL, et al. (2024) The Human Accelerated Region HAR202 Controls NPAS3 Expression in the Developing Forebrain Displaying Differential Enhancer Activity Between Modern and Archaic Human Sequences. Molecular biology and evolution, 41(10).

Michelatti D, et al. (2024) Oncogenic enhancers prime quiescent metastatic cells to escape NK immune surveillance by eliciting transcriptional memory. Nature communications, 15(1), 2198.

Sokolov AV, et al. (2023) Methylation in MAD1L1 is associated with the severity of suicide attempt and phenotypes of depression. Clinical epigenetics, 15(1), 1.

Mohammadi A, et al. (2023) Viral and host mediators of non-suppressible HIV-1 viremia. Nature medicine, 29(12), 3212.