

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

EpiExplorer

RRID:SCR_007301

Type: Tool

Proper Citation

EpiExplorer (RRID:SCR_007301)

Resource Information

URL: <http://epiexplorer.mpi-inf.mpg.de/>

Proper Citation: EpiExplorer (RRID:SCR_007301)

Description: A web tool that allows you to use large reference epigenome datasets for your own analysis without complex scripting or laborious preprocessing.

Abbreviations: EpiExplorer

Resource Type: data analysis service, service resource, production service resource, analysis service resource

Defining Citation: [PMID:23034089](#)

Availability: Acknowledgement requested

Resource Name: EpiExplorer

Resource ID: SCR_007301

Alternate IDs: OMICS_00632

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260801T190937+0000

Ratings and Alerts

No rating or validation information has been found for EpiExplorer.

No alerts have been found for EpiExplorer.

Data and Source Information

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Chiang IKN, et al. (2023) The blood vasculature instructs lymphatic patterning in a SOX7-dependent manner. The EMBO journal, 42(5), e109032.

Loh M, et al. (2022) Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications biology, 5(1), 329.

Bayat A, et al. (2021) Fast and accurate exhaustive higher-order epistasis search with BitEpi. Scientific reports, 11(1), 15923.

Broche J, et al. (2021) Genome-wide investigation of the dynamic changes of epigenome modifications after global DNA methylation editing. Nucleic acids research, 49(1), 158.

McCann AJ, et al. (2021) A dominant-negative SOX18 mutant disrupts multiple regulatory layers essential to transcription factor activity. Nucleic acids research, 49(19), 10931.

Ilijazi D, et al. (2020) Discovery of Molecular DNA Methylation-Based Biomarkers through Genome-Wide Analysis of Response Patterns to BCG for Bladder Cancer. Cells, 9(8).

Qin Y, et al. (2020) Alterations in promoter interaction landscape and transcriptional network underlying metabolic adaptation to diet. Nature communications, 11(1), 962.

Reina-Campos M, et al. (2019) Increased Serine and One-Carbon Pathway Metabolism by PKC γ Deficiency Promotes Neuroendocrine Prostate Cancer. Cancer cell, 35(3), 385.

Savini L, et al. (2019) EpiExploreR: A Shiny Web Application for the Analysis of Animal Disease Data. Microorganisms, 7(12).

Milenkovic D, et al. (2018) A systems biology network analysis of nutri(epi)genomic changes in endothelial cells exposed to epicatechin metabolites. Scientific reports, 8(1), 15487.

Chatterjee A, et al. (2017) Genome-wide methylation sequencing of paired primary and metastatic cell lines identifies common DNA methylation changes and a role for EBF3 as a candidate epigenetic driver of melanoma metastasis. Oncotarget, 8(4), 6085.

Mauser R, et al. (2017) Application of dual reading domains as novel reagents in chromatin biology reveals a new H3K9me3 and H3K36me2/3 bivalent chromatin state. Epigenetics & chromatin, 10(1), 45.

Alvizi L, et al. (2017) Differential methylation is associated with non-syndromic cleft lip and palate and contributes to penetrance effects. Scientific reports, 7(1), 2441.

Istas G, et al. (2017) Identification of differentially methylated BRCA1 and CRISP2 DNA regions as blood surrogate markers for cardiovascular disease. *Scientific reports*, 7(1), 5120.

Jurkowska RZ, et al. (2017) H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. *Nature communications*, 8(1), 2057.

Declerck K, et al. (2017) Interaction between prenatal pesticide exposure and a common polymorphism in the PON1 gene on DNA methylation in genes associated with cardio-metabolic disease risk-an exploratory study. *Clinical epigenetics*, 9, 35.

Kungulovski G, et al. (2016) Application of recombinant TAF3 PHD domain instead of anti-H3K4me3 antibody. *Epigenetics & chromatin*, 9, 11.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. *Bioinformatics and biology insights*, 10, 267.

Chatterjee A, et al. (2016) Placental Hypomethylation Is More Pronounced in Genomic Loci Devoid of Retroelements. *G3 (Bethesda, Md.)*, 6(7), 1911.

Bell CG, et al. (2016) Novel regional age-associated DNA methylation changes within human common disease-associated loci. *Genome biology*, 17(1), 193.