Resource Summary Report

Generated by nidm-terms on Jul 29, 2026

Database of Immune Cell Epigenomes

RRID:SCR_018259
Type: Tool

Proper Citation

Database of Immune Cell Epigenomes (RRID:SCR_018259)

Resource Information

URL: https://dice-database.org

Proper Citation: Database of Immune Cell Epigenomes (RRID:SCR_018259)

Description: Database of Immune Cell Expression, Expression quantitative trait loci (eQTLs) and Epigenomics. Collection of identified cis-eQTLs for 12,254 unique genes, which represent 61% of all protein-coding genes expressed in human cell types. Datasets to help reveal effects of disease risk associated genetic polymorphisms on specific immune cell types, providing mechanistic insights into how they might influence pathogenesis.

Abbreviations: DICE

Synonyms: Database of Immune Cell Expression, Expression quantitative trait loci (eQTLs) and Epigenomics

Resource Type: data or information resource, database, data access protocol, software resource, web service

Defining Citation: PMID:30449622

Keywords: Data set, immune cell expression, expression quantitative trait loci, epigenomics, data, cis-eQLC, gene, protein coding gene, human cell type, genetic polymorphism disease, immune cell, pathogenesis

Funding: William K. Bowes Jr Foundation ;
NIAID R24 AI108564;
NCRR S10 RR027366;
NIH Office of the Director S10 OD016262

Availability: Free, Freely available

Resource Name: Database of Immune Cell Epigenomes

Resource ID: SCR_018259

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260729T044439+0000

Ratings and Alerts

No rating or validation information has been found for Database of Immune Cell Epigenomes.

No alerts have been found for Database of Immune Cell Epigenomes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Zhang ZE, et al. (2025) Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping. medRxiv : the preprint server for health sciences.

Wang L, et al. (2025) An atlas of single-cell eQTLs dissects autoimmune disease genes and identifies novel drug classes for treatment. Cell genomics, 5(4), 100820.

Zhang Z, et al. (2025) Unveiling genetic signatures of immune response in immune-related diseases through single-cell eQTL analysis across diverse conditions. Nature communications, 16(1), 7134.

Merchant W, et al. (2025) The molecular components of the anti-inflammatory cholinergic pathway are extrasplenic. PloS one, 20(9), e0331707.

Chen J, et al. (2025) mastR: an R package for automated identification of tissue-specific gene signatures in multi-group differential expression analysis. Bioinformatics (Oxford, England), 41(3).

Beckhaus T, et al. (2025) Genome-Wide Association Analyses of HPV16 and HPV18 Seropositivity Identify Susceptibility Loci for Cervical Cancer. Journal of medical virology, 97(2), e70195.

Holling GA, et al. (2024) CD8+ T cell metabolic flexibility elicited by CD28-ARS2 axis-driven alternative splicing of PKM supports antitumor immunity. Cellular & molecular immunology, 21(3), 260.

Andrabi SBA, et al. (2024) Long noncoding RNA LIRIL2R modulates FOXP3 levels and suppressive function of human CD4+ regulatory T cells by regulating IL2RA. Proceedings

of the National Academy of Sciences of the United States of America, 121(23), e2315363121.

Trang KB, et al. (2024) 3D chromatin-based variant-to-gene maps across 57 human cell types reveal the cellular and genetic architecture of autoimmune disease susceptibility. medRxiv : the preprint server for health sciences.

Lagattuta KA, et al. (2024) The genetic basis of autoimmunity seen through the lens of T cell functional traits. Nature communications, 15(1), 1204.

Chong AY, et al. (2024) A common NFKB1 variant detected through antibody analysis in UK Biobank predicts risk of infection and allergy. American journal of human genetics, 111(2), 295.

Redmer T, et al. (2024) MET receptor serves as a promising target in melanoma brain metastases. Acta neuropathologica, 147(1), 44.

Bate T, et al. (2024) Investigating the association between genetically proxied circulating levels of immune checkpoint proteins and cancer survival: protocol for a Mendelian randomisation analysis. BMJ open, 14(2), e075981.

Avery CN, et al. (2024) Shared genomic segments analysis identifies MHC class I and class III molecules as genetic risk factors for juvenile idiopathic arthritis. HGG advances, 5(2), 100277.

Bhattacharyya S, et al. (2024) Identifying genetic variants associated with chromatin looping and genome function. Nature communications, 15(1), 8174.

Song S, et al. (2024) Partitioning and aggregating cross-tissue and tissue-specific genetic effects to identify gene-trait associations. Nature communications, 15(1), 5769.

Li J, et al. (2024) Integrative multi-omics analysis identifies genetically supported druggable targets and immune cell specificity for myasthenia gravis. Journal of translational medicine, 22(1), 302.

Boom G, et al. (2023) Spatially constrained gene regulation identifies key genetic contributions of preeclampsia, hypertension, and proteinuria???. Biology of reproduction, 108(4), 659.

Pagadala M, et al. (2023) Germline modifiers of the tumor immune microenvironment implicate drivers of cancer risk and immunotherapy response. Nature communications, 14(1), 2744.

Sookoian S, et al. (2023) Genetics in non-alcoholic fatty liver disease: The role of risk alleles through the lens of immune response. Clinical and molecular hepatology, 29(Suppl), S184.