

Resource Summary Report

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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 access protocol, data or information resource, database, software resource, web service

Defining Citation: [PMID:30449622](#)

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

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NIAID R24 AI108564;
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William K. Bowes Jr Foundation

Availability: Free, Freely available

Resource Name: Database of Immune Cell Epigenomes

Resource ID: SCR_018259

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260829T182606+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 73 mentions in open access literature.

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

Jiang K, et al. (2026) Functional and computational interrogation of juvenile idiopathic arthritis risk loci in CD4+ T cells. HGG advances, 7(3), 100619.

Chatterjee T, et al. (2026) Macrophage ferritin heavy chain/??-synuclein regulatory axis modulates ferroptosis during kidney injury. JCI insight, 11(8).

Leviatan Ben-Arye S, et al. (2026) An atlas of human siglecs integrates expression, affinity, and cis/trans sialoglycan recognition profiles. Nature communications, 17(1).

Li N, et al. (2026) Integrative Multi-Omics Mendelian Randomization Reveals Oxidative Stress Mechanisms in Major Depressive Disorder, Bipolar Disorder, and Schizophrenia. Antioxidants (Basel, Switzerland), 15(2).

Zhang H, et al. (2026) Single-cell transcriptome-wide Mendelian randomization during CD4+ T cell activation reveals immune-mediated mechanisms and drug targets for neuropsychiatric disorders. Communications biology, 9(1).

Ristin S, et al. (2026) Asymmetry and redundancy of STAT5 paralogs across CD8+ T cell differentiation states. Communications biology, 9(1).

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 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.

Zheng J, et al. (2025) Integrating Single-Cell Transcriptome-Wide Mendelian Randomization and Differentially Expressed Gene Analyses to Prioritize Dynamic Immune-Related Drug Targets for Cancers. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(46), e07451.

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).

Mehta M, et al. (2025) Functional Role of Single-Nucleotide Polymorphisms on IFNG and IFNGR1 in Humans with Cardiovascular Disease. *International journal of molecular sciences*, 26(18).

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.

Trang KB, et al. (2025) 3D chromatin-based variant-to-gene maps across 57 human cell types reveal the cellular and genetic architecture of autoimmune disease susceptibility. *Genome biology*, 26(1), 414.

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*.

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

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