

Resource Summary Report

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MatrixEQTL

RRID:SCR_025513

Type: Tool

Proper Citation

MatrixEQTL (RRID:SCR_025513)

Resource Information

URL: http://www.bios.unc.edu/research/genomic_software/Matrix_eQTL/

Proper Citation: MatrixEQTL (RRID:SCR_025513)

Description: Software tool for ultra fast eQTL analysis via large matrix operations.

Synonyms: Matrix Expression Quantitative Trait Loci

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: [PMID:22492648](#)

Keywords: expression Quantitative Trait Loci, fast eQTL analysis, large matrix operations,

Funding: NIMH R01 MH090936;
NIEHS R01 ES015241;
US Environmental Protection Agency ;
NCI R01 CA138255;
NSF ;
Gillings Innovation Laboratory in Statistical Genomics

Availability: Free, Freely available,

Resource Name: MatrixEQTL

Resource ID: SCR_025513

Record Creation Time: 20240720T053301+0000

Record Last Update: 20260731T043152+0000

Ratings and Alerts

No rating or validation information has been found for MatrixEQTL.

No alerts have been found for MatrixEQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 69 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zou J, et al. (2025) Genome-wide identification and analysis of recurring patterns of epigenetic variation across individuals. *Communications biology*, 8(1), 888.

Chen X, et al. (2025) Identification of the putative regulatory regions and candidate genes associated with backfat thickness and intramuscular fat content traits in Xiang pigs. *BMC genomics*, 26(1), 733.

Tanaka K, et al. (2025) The influence of genetics on the endocannabinoid system gene expression and relevance for targeting reproductive conditions. *Journal of cannabis research*, 7(1), 29.

Martínez-López J, et al. (2025) A Strong Dysregulated Myeloid Component in the Epigenetic Landscape of Systemic Sclerosis: An Integrated DNA Methylome and Transcriptome Analysis. *Arthritis & rheumatology (Hoboken, N.J.)*, 77(4), 439.

Botey-Bataller J, et al. (2025) Genetic and molecular landscape of comorbidities in people living with HIV. *Nature medicine*, 31(10), 3350.

Huber A, et al. (2025) Phenotypic and epigenetic profiles of circulating NK cells in spontaneous HIV-1 controllers. *EBioMedicine*, 120, 105948.

Valim JMBC, et al. (2025) Integrative Genomic and Metabolomic Analysis Identifies mQTLs Associated with Genetic Selection for Tenderness in Nellore Cattle. *Metabolites*, 15(12).

Cerván-Martín M, et al. (2025) Unraveling the molecular landscape of Erdheim-Chester disease: new insights from methylome and transcriptome integration. *Leukemia*, 39(11), 2758.

Li Y, et al. (2025) Multi-omics analysis identifies novels genes involved in glioma prognosis. *Scientific reports*, 15(1), 5806.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Haglund A, et al. (2025) Cell state-dependent allelic effects and contextual Mendelian randomization analysis for human brain phenotypes. *Nature genetics*, 57(2), 358.

Chen B, et al. (2025) A system genetics analysis uncovers the regulatory variants controlling drought response in wheat. *Plant biotechnology journal*, 23(5), 1565.

Leblanc FJA, et al. (2024) Atrial fibrillation variant-to-gene prioritization through cross-ancestry eQTL and single-nucleus multiomic analyses. *iScience*, 27(9), 110660.

Niciura SCM, et al. (2024) Multi-omics data elucidate parasite-host-microbiota interactions and resistance to *Haemonchus contortus* in sheep. *Parasites & vectors*, 17(1), 102.

Shore CJ, et al. (2024) Genetic effects on the skin methylome in healthy older twins. *American journal of human genetics*, 111(9), 1932.

Cote AC, et al. (2024) Critical reasoning on the co-expression module QTL in the dorsolateral prefrontal cortex. *HGG advances*, 5(3), 100311.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. *bioRxiv : the preprint server for biology*.

Bravo JI, et al. (2024) An eQTL-based approach reveals candidate regulators of LINE-1 RNA levels in lymphoblastoid cells. *PLoS genetics*, 20(6), e1011311.

Polakkattil BK, et al. (2024) Methylome-wide and meQTL analysis helps to distinguish treatment response from non-response and pathogenesis markers in schizophrenia. *Frontiers in psychiatry*, 15, 1297760.

Rompala G, et al. (2023) Profiling neuronal methylome and hydroxymethylome of opioid use disorder in the human orbitofrontal cortex. *Nature communications*, 14(1), 4544.