

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

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: 20260729T044622+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 [SPARC SAWG](#) .

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.

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

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.

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.

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

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

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.

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*.

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