

Resource Summary Report

Generated by [NIF](#) on Sep 9, 2026

PEER

RRID:SCR_009326

Type: Tool

Proper Citation

PEER (RRID:SCR_009326)

Resource Information

URL: <http://www.sanger.ac.uk/resources/software/peer/>

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Description: Software collection of Bayesian approaches to infer hidden determinants and their effects from gene expression profiles using factor analysis methods. Applications of PEER have * detected batch effects and experimental confounders * increased the number of expression QTL findings by threefold * allowed inference of intermediate cellular traits, such as transcription factor or pathway activations This project offers an efficient and versatile C++ implementation of the underlying algorithms with user-friendly interfaces to R and python.

Abbreviations: PEER

Resource Type: software application, software resource

Defining Citation: [PMID:21283789](#), [PMID:20463871](#)

Keywords: gene, genetic, genomic, c++, r, python

Resource Name: PEER

Resource ID: SCR_009326

Alternate IDs: nlx_154532, OMICS_04597

Alternate URLs: <https://github.com/PMBio/peer/wiki>

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260905T133250+0000

Ratings and Alerts

No rating or validation information has been found for PEER.

No alerts have been found for PEER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 579 mentions in open access literature.

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

Zhang Q, et al. (2026) Long-term enhancement mechanisms of peer support on college students' mental health: testing a chain mediation model based on three-year longitudinal tracking. BMC psychology, 14(1), 179.

Marešová P, et al. (2026) A Systematic Review of the Cost-Effectiveness of Interventions for Chronic Wounds. International wound journal, 23(3), e70858.

Cayley J, et al. (2026) PEERing into the Future: Benchmarking the ANSTO Australian Synchrotron's Very-High-Energy Electron Linac for Ultra-High Dose-Rate, In Vivo FLASH Radiotherapy Research. Cancers, 18(4).

Hugo L, et al. (2026) Recommendations for the Support of Clinical Facilitators' Mental Well-Being in Undergraduate Health Professions Education: A Scoping Review. Journal of nursing scholarship : an official publication of Sigma Theta Tau International Honor Society of Nursing, 58(3), e70083.

Sampson J, et al. (2026) Paired DNA and RNA sequencing uncovers common and rare variation regulating human retinal gene expression. Nature communications, 17(1).

Krockenberger L, et al. (2026) FastGxC: Fast and powerful context-specific eQTL mapping in bulk and single-cell data. Cell genomics, 6(6), 101250.

Tardaguila M, et al. (2026) Integrating natural and engineered genetic variations to decode regulatory influence on blood traits. Cell reports, 45(2), 116937.

Tian W, et al. (2026) Genetic alternative splicing regulation mapping of cartilage and synovium reveals tissue-specific mechanisms of joint-related traits. Nature communications, 17(1).

Liu Q, et al. (2026) Cell-type-aware transcriptome-wide association studies identify 91 independent risk genes for Alzheimer's disease dementia. Communications biology, 9(1).

McClelland P, et al. (2026) A multi-ancestry genetic reference for the Quebec population. Nature communications, 17(1), 1319.

Esmaeili M, et al. (2026) Distinct regulatory elements of SLC6A14 expression contribute to modification of cystic fibrosis phenotypes. *Human genetics*, 145(1), 8.

Voigt AP, et al. (2026) Single-Cell Gene Expression and eQTL Analyses in the Human Retina, RPE, and Choroid in Macular Degeneration. *bioRxiv : the preprint server for biology*.

Nishiyama NC, et al. (2026) eQTL in diseased colon tissue identifies potential target genes associated with IBD. *Nature communications*, 17(1).

Sun Y, et al. (2026) Climate Action Impacts on Steelmaking Emissions of Persistent Organic Pollutants Highlight a Gap Between the Paris Agreement and the Stockholm Convention. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(29), e19769.

Dangana RS, et al. (2026) Gene Expression, Docking and Machine Learning in Malaria Drug Discovery: A Systematic Review. *Biochemistry research international*, 2026, 2724332.

Hu J, et al. (2026) Full-length transcriptome atlas of porcine skeletal muscle reveals isoform-resolved genetic regulatory mechanisms for muscle growth. *BMC genomics*, 27(1).

Popplestone S, et al. (2026) Home-Based Learning Opportunities, Responsive Caregiving and the Development of Preschool-Aged Children in Low- and Middle-Income Countries of the East Asia and Pacific Region: A Systematic Review. *Child: care, health and development*, 52(3), e70265.

Tierney J, et al. (2026) "It has tentacles into every single aspect of me" a qualitative evidence synthesis of the lived experiences and perceptions of ADHD youth. *European child & adolescent psychiatry*, 35(5), 1435.

Chen G, et al. (2026) Identification and Characterization of sQTLs and eQTLs Associated with Growth Traits in Yellow-Feathered Broilers. *Poultry science*, 105(5), 106659.

Cheruiyot EK, et al. (2026) Effects of testosterone on gene expression in males and females across 40 human tissues. *Scientific reports*, 16(1).