

Resource Summary Report

Generated by [NIF](#) on Oct 21, 2026

PEER

RRID:SCR_009326

Type: Tool

Proper Citation

PEER (RRID:SCR_009326)

Resource Information

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

Proper Citation: PEER (RRID:SCR_009326)

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: 20261017T203404+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 have not found any literature mentions for this resource.