

Resource Summary Report

Generated by [RRID](#) on Aug 9, 2026

[pyLMM](#)

RRID:SCR_014525

Type: Tool

Proper Citation

pyLMM (RRID:SCR_014525)

Resource Information

URL: <https://github.com/nickFurlotte/pylmm>

Proper Citation: pyLMM (RRID:SCR_014525)

Description: A Python package for doing linear mixed model associations in genome wide association studies (GWAS). The software corrects for population structure using EMMA.

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

Defining Citation: [DOI:10.1534/genetics.107.080101](https://doi.org/10.1534/genetics.107.080101)

Keywords: python, data analysis software, linear mixed model, genome wide association studies, gwas, lmm, emma

Availability: Install using pip

Resource Name: pyLMM

Resource ID: SCR_014525

License: GNU Affero GPL

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260808T190032+0000

Ratings and Alerts

No rating or validation information has been found for pyLMM.

No alerts have been found for pyLMM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Ball RL, et al. (2024) GenomeMUSter mouse genetic variation service enables multitrait, multipopulation data integration and analysis. *Genome research*, 34(1), 145.

Singh A, et al. (2024) Genome-wide DNA methylation and their transgenerational pattern differ in *Arabidopsis thaliana* populations originated along the elevation of West Himalaya. *BMC plant biology*, 24(1), 936.

Zhang X, et al. (2023) The genomic and epigenetic footprint of local adaptation to variable climates in kiwifruit. *Horticulture research*, 10(4), uhad031.

Nadiger N, et al. (2021) Protocol for a prospective, observational, deep phenotyping study on adipose epigenetic and lipidomic determinants of metabolic homeostasis in South Asian Indians: the Indian Diabetes and Metabolic Health (InDiMeT) study. *BMJ open*, 11(5), e043644.

Rau CD, et al. (2020) Modeling epistasis in mice and yeast using the proportion of two or more distinct genetic backgrounds: Evidence for "polygenic epistasis". *PLoS genetics*, 16(10), e1009165.

Yao DW, et al. (2019) A linear mixed model approach to gene expression-tumor aneuploidy association studies. *Scientific reports*, 9(1), 11944.

Ashbrook DG, et al. (2018) Born to Cry: A Genetic Dissection of Infant Vocalization. *Frontiers in behavioral neuroscience*, 12, 250.

Thompson MJ, et al. (2018) A multi-tissue full lifespan epigenetic clock for mice. *Aging*, 10(10), 2832.

Kennedy EM, et al. (2018) An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. *BMC genomics*, 19(1), 476.

Gai L, et al. (2018) Finding associated variants in genome-wide association studies on multiple traits. *Bioinformatics (Oxford, England)*, 34(13), i467.

Ferland RJ, et al. (2017) Multidimensional Genetic Analysis of Repeated Seizures in the Hybrid Mouse Diversity Panel Reveals a Novel Epileptogenesis Susceptibility Locus. *G3 (Bethesda, Md.)*, 7(8), 2545.

Orozco LD, et al. (2015) Epigenome-wide association of liver methylation patterns and complex metabolic traits in mice. *Cell metabolism*, 21(6), 905.