# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 25, 2025

## Efficient Mixed-Model Association

RRID:SCR_008217
Type: Tool

## Proper Citation

Efficient Mixed-Model Association (RRID:SCR_008217)

## Resource Information

**URL:** http://mouse.cs.ucla.edu/emma/

**Proper Citation:** Efficient Mixed-Model Association (RRID:SCR_008217)

**Description:** Statistical test for model organisms association mapping correcting for the confounding from population structure and genetic relatedness. EMMA takes advantage of the specific nature of the optimization problem in applying mixed models for association mapping, which substantially increases the computational speed and the reliability of the results. The current implementation of EMMA is available in an R package. The documentation is included in the installation package.

**Abbreviations:** EMMA

**Synonyms:** Efficient Mixed-Model Association (EMMA), Efficient Mixed Model Association

**Resource Type:** software resource, algorithm resource

**Defining Citation:** PMID:18385116

**Keywords:** algorithm, organism statistical model, association mapping, r package

**Funding:**

**Availability:** Available for download

**Resource Name:** Efficient Mixed-Model Association

**Resource ID:** SCR_008217

**Alternate IDs:** nif-0000-21753

**Record Creation Time:** 20220129T080246+0000

**Record Last Update:** 20250525T032505+0000

## Ratings and Alerts

No rating or validation information has been found for Efficient Mixed-Model Association.

No alerts have been found for Efficient Mixed-Model Association.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 59 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

Durán A, et al. (2021) Identification of genetic modifiers of murine hepatic ?-glucocerebrosidase activity. Biochemistry and biophysics reports, 28, 101105.

Zhang J, et al. (2021) A Fast Multi-Locus Ridge Regression Algorithm for High-Dimensional Genome-Wide Association Studies. Frontiers in genetics, 12, 649196.

Doolittle ML, et al. (2020) Genetic analysis of osteoblast activity identifies Zbtb40 as a regulator of osteoblast activity and bone mass. PLoS genetics, 16(6), e1008805.

Chang T, et al. (2019) A Fast and Powerful Empirical Bayes Method for Genome-Wide Association Studies. Animals : an open access journal from MDPI, 9(6).

Fradgley N, et al. (2019) A large-scale pedigree resource of wheat reveals evidence for adaptation and selection by breeders. PLoS biology, 17(2), e3000071.

Mesner LD, et al. (2019) Mouse genome-wide association and systems genetics identifies Lhfp as a regulator of bone mass. PLoS genetics, 15(5), e1008123.

Chen JA, et al. (2018) Neurodegenerative disease biomarkers A?1-40, A?1-42, tau, and p-tau181 in the vervet monkey cerebrospinal fluid: Relation to normal aging, genetic influences, and cerebral amyloid angiopathy. Brain and behavior, 8(2), e00903.

Wen YJ, et al. (2018) Methodological implementation of mixed linear models in multi-locus genome-wide association studies. Briefings in bioinformatics, 19(4), 700.

Bumgardner SA, et al. (2018) Genetic influence on splenic natural killer cell frequencies and maturation among aged mice. Experimental gerontology, 104, 9.

Robledo M, et al. (2018) An sRNA and Cold Shock Protein Homolog-Based Feedforward Loop Post-transcriptionally Controls Cell Cycle Master Regulator CtrA. Frontiers in microbiology, 9, 763.

Urrea L, et al. (2018) Involvement of Cellular Prion Protein in ?-Synuclein Transport in Neurons. Molecular neurobiology, 55(3), 1847.

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.

Zorzi V, et al. (2017) Mouse Panx1 Is Dispensable for Hearing Acquisition and Auditory Function. Frontiers in molecular neuroscience, 10, 379.

Tamba CL, et al. (2017) Iterative sure independence screening EM-Bayesian LASSO algorithm for multi-locus genome-wide association studies. PLoS computational biology, 13(1), e1005357.

Henke NA, et al. (2017) Isoprenoid Pyrophosphate-Dependent Transcriptional Regulation of Carotenogenesis in Corynebacterium glutamicum. Frontiers in microbiology, 8, 633.

Ingham NJ, et al. (2016) S1PR2 variants associated with auditory function in humans and endocochlear potential decline in mouse. Scientific reports, 6, 28964.

Mataloni F, et al. (2016) Morbidity and mortality of people who live close to municipal waste landfills: a multisite cohort study. International journal of epidemiology, 45(3), 806.

Phelan J, et al. (2016) Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC medicine, 14, 31.

Fan B, et al. (2016) New SigD-regulated genes identified in the rhizobacterium Bacillus amyloliquefaciens FZB42. Biology open, 5(12), 1776.

Kucab JE, et al. (2016) TP53 and lacZ mutagenesis induced by 3-nitrobenzanthrone in Xpa-deficient human TP53 knock-in mouse embryo fibroblasts. DNA repair, 39, 21.