

# Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

## EMMAX

RRID:SCR\_024012

Type: Tool

### Proper Citation

EMMAX (RRID:SCR\_024012)

### Resource Information

**URL:** <https://genome.sph.umich.edu/wiki/EMMAX>

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**Description:** Software statistical test for large scale human or model organism association mapping accounting for the sample structure. In addition to the computational efficiency obtained by EMMA algorithm, EMMAX takes advantage of the fact that each loci explains only a small fraction of complex traits, which allows us to avoid repetitive variance component estimation procedure, resulting in a significant amount of increase in computational time of association mapping using mixed model.

**Synonyms:** Efficient Mixed-Model Association eXpedited, emmax

**Resource Type:** software application

**Keywords:** statistical test, human or model organism association mapping, sample structure, association mapping

**Availability:** Free, Available for download, Freely available

**Resource Name:** EMMAX

**Resource ID:** SCR\_024012

**Alternate IDs:** OMICS\_08871

**Alternate URLs:** <https://sources.debian.org/src/emmax/>

**Record Creation Time:** 20230824T050211+0000

**Record Last Update:** 20260815T182739+0000

### Ratings and Alerts

No rating or validation information has been found for EMMAX.

No alerts have been found for EMMAX.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Liu W, et al. (2026) Genome-Wide Association Study Reveals the Genetic Architecture and Key Drought and Yield Related Genes in Common Vetch (*Vicia sativa* L.). *Plant biotechnology journal*, 24(3), 1082.

Parween S, et al. (2026) Host genome and bacterial taxa shape the Arabidopsis seed microbiome. *EMBO reports*, 27(1), 122.

Chen M, et al. (2026) Genome-wide association study identifies key loci and candidate genes for maize grain yield-related traits. *BMC plant biology*, 26(1).

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. *GigaScience*, 14.

Mugo JW, et al. (2025) Data simulation to optimize frameworks for genome-wide association studies in diverse populations. *Frontiers in genetics*, 16, 1559496.

Yang J, et al. (2022) Genome-wide association study of eigenvectors provides genetic insights into selective breeding for tomato metabolites. *BMC biology*, 20(1), 120.