

Resource Summary Report

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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: softwre 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: 20260912T200044+0000

Ratings and Alerts

No rating or validation information has been found for EMMAX.

No alerts have been found for EMMAX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.

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).

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

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.