

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

FaST LMM

RRID:SCR_015506

Type: Tool

Proper Citation

FaST LMM (RRID:SCR_015506)

Resource Information

URL: <https://github.com/MicrosoftGenomics/FaST-LMM>

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Description: FaST-LMM (Factored Spectrally Transformed Linear Mixed Models) is a set of tools for efficiently performing genome-wide association studies (GWAS), prediction, and heritability estimation on large data sets.

Synonyms: Factored Spectrally Transformed Linear Mixed Models, fastlmm

Resource Type: software resource, software toolkit

Keywords: gwas, association study, heritability, single-snp, snp-set, genome

Availability: Free, Available for download

Resource Name: FaST LMM

Resource ID: SCR_015506

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260905T133300+0000

Ratings and Alerts

No rating or validation information has been found for FaST LMM.

No alerts have been found for FaST LMM.

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 [dkNET](#) .

Cirulli ET, et al. (2019) Profound Perturbation of the Metabolome in Obesity Is Associated with Health Risk. *Cell metabolism*, 29(2), 488.

Fournier T, et al. (2019) Extensive impact of low-frequency variants on the phenotypic landscape at population-scale. *eLife*, 8.

Gurdasani D, et al. (2019) Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, 179(4), 984.

Zhu G, et al. (2018) Rewiring of the Fruit Metabolome in Tomato Breeding. *Cell*, 172(1-2), 249.

Elliott LT, et al. (2018) Genome-wide association studies of brain imaging phenotypes in UK Biobank. *Nature*, 562(7726), 210.

Lees JA, et al. (2017) Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. *eLife*, 6.