

Resource Summary Report

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TASSEL

RRID:SCR_012837

Type: Tool

Proper Citation

TASSEL (RRID:SCR_012837)

Resource Information

URL: <http://www.maizegenetics.net/tassel>

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Description: Software package which performs a variety of genetic analyses including association mapping, diversity estimation and calculating linkage disequilibrium. The association analysis between genotypes and phenotypes can be performed by either a general linear model or a mixed linear model. The general linear model now allows users to analyze complex field designs, environmental interactions, and epistatic interactions. The mixed model is specially designed to handle polygenic effects at multiple levels of relatedness including pedigree information. These new analyses should permit association analysis in a wide range plant and animal species. (entry from Genetic Analysis Software)

Abbreviations: TASSEL

Synonyms: and Linkage, Trait Analysis by aSSociation, Evolution

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java, web-based, bio.tools

Resource Name: TASSEL

Resource ID: SCR_012837

Alternate IDs: nlx_154674, biotools:tassel

Alternate URLs: <http://sourceforge.net/projects/tassel/>, <https://bio.tools/tassel>

Record Creation Time: 20220129T080312+0000

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Ratings and Alerts

No rating or validation information has been found for TASSEL.

No alerts have been found for TASSEL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2335 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bila L, et al. (2026) Genome-Wide Association Study (GWAS) for Linear Body Measurements of Sussex Cattle (*Bos taurus*) at Weaning and Yearling Age in South Africa. *Veterinary medicine and science*, 12(1), e70717.

Parker K, et al. (2026) Diverse reference genomes detect variants in the US winter wheat. *The plant genome*, 19(1), e70160.

Singh G, et al. (2026) Genetic analysis of a quantitative trait locus associated with resistance to the root-lesion nematode *Pratylenchus neglectus* in triticale. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(1), 24.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Gill HS, et al. (2025) Association mapping and genomic prediction for processing and end-use quality traits in wheat (*Triticum aestivum* L.). *The plant genome*, 18(1), e20529.

Hein K, et al. (2025) Genetic diversity and environmental adaptation in Ethiopian tef. *G3 (Bethesda, Md.)*, 15(3).

Bian R, et al. (2025) A novel quantitative trait locus for barley yellow dwarf virus resistance and kernel traits on chromosome 2D of a wheat cultivar Jagger. *The plant genome*, 18(1), e20548.

Wang G, et al. (2025) Molecular and Biochemical Mechanisms of Scutellum Color Variation in *Bactrocera dorsalis* Adults (Diptera: Tephritidae). *Insects*, 16(1).

Luo Y, et al. (2025) Characterization and functional analysis of conserved non-coding sequences among poaceae: insights into gene regulation and phenotypic variation in maize. *BMC genomics*, 26(1), 46.

Bazzer SK, et al. (2025) Genomic strategies to facilitate breeding for increased β -Glucan content in oat (*Avena sativa* L.). *BMC genomics*, 26(1), 35.

McBreen J, et al. (2025) Enhancing prediction accuracy of grain yield in wheat lines adapted to the southeastern United States through multivariate and multi-environment

genomic prediction models incorporating spectral and thermal information. The plant genome, 18(1), e20532.

Simko I, et al. (2025) Integrative path modeling and QTL mapping identify maturity, stem strength, and cell wall composition driving lettuce resistance to *Sclerotinia minor*. Scientific reports, 15(1), 19824.

Morinha F, et al. (2025) ?Molecular and morphological data support the synonymy of *Muricanthusradix* Gmelin, 1791 and *Muricanthusambiguus* Reeve, 1845 (Gastropoda, Muricidae). ZooKeys, 1239, 281.

Bagwell JW, et al. (2025) Discovering leaf and stripe rust resistance in soft red winter wheat through genome-wide association studies. The plant genome, 18(2), e70055.

Huang G, et al. (2025) Genomic Variation Underpins Genetic Divergence and Differing Salt Resilience in *Sesbania bispinosa*. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(32), e02600.

Hu M, et al. (2025) Accurate, Scalable Structural Variant Genotyping in Complex Genomes at Population Scales. Molecular biology and evolution, 42(8).

Torres I, et al. (2025) MINE: maximally informative next experiment-toward a new GWAS experimental design and methodology. G3 (Bethesda, Md.), 15(9).

Veerendrakumar HV, et al. (2025) Dissecting the genomic regions, candidate genes and pathways using multi-locus genome-wide association study for stem rot disease resistance in groundnut. The plant genome, 18(3), e70089.

Sonu , et al. (2025) Genome-wide association analysis of grain iron and zinc in rice grown under agroclimatic sites with contrasting soil iron status. Frontiers in plant science, 16, 1501878.

Syed S, et al. (2025) GWAS analysis of *Fusarium* head blight resistance in a Nordic-Baltic spring wheat panel. Frontiers in plant science, 16, 1604296.