

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 application, software resource

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

Record Last Update: 20260912T200248+0000

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 2476 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Mourad AMI, et al. (2026) Unlocking the genetic control of early seedling resistance to wheat powdery mildew through microphenomics. *Pest management science*, 82(2), 1668.

Wang X, et al. (2026) Genome-wide association analysis of wheat quality traits in Qinghai Province. *BMC plant biology*, 26(1), 218.

Wei L, et al. (2026) Allelic Variation in Maize Malate Dehydrogenase 7 Shapes Promoter Methylation and Banded Leaf and Sheath Blight Resistance. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 13(7), e11356.

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.

Søndreli KL, et al. (2026) Transcriptomic and functional analyses uncover a conserved effector driving genotype-dependent virulence in the *Sphaerulina musiva*-*Populus trichocarpa* interaction. *mBio*, 17(5), e0312025.

Li K, et al. (2026) A 18 kb upstream deletion of H2AFY is associated with the feathered leg trait in Yanying chickens. *Poultry science*, 105(8), 107011.

Liang H, et al. (2026) Genome-Wide Association Study Identifies Candidate Genes for Salt Tolerance in Traditional Rice Landraces. *Rice* (New York, N.Y.), 19(1).

Behnken B, et al. (2026) Natural variation in expression of a plant immune receptor mediates elicitor sensitivity. *PloS one*, 21(4), e0343332.

Carmona A, et al. (2026) From gene discovery to breeding tools: functional KASP markers for flowering time selection in chickpea. *BMC plant biology*, 26(1).

Ramirez-Gil JG, et al. (2026) GermVersity: A free and user-friendly interface to enhance the visualization and analysis of genebank data. *PloS one*, 21(1), e0340826.

Wang A, et al. (2026) Cross-species dissection of saline-related genes by genetically deciphering a euryhaline microalga *Chlorella* sp. *Nature communications*, 17(1), 1577.

Li H, et al. (2026) Crop phenotype prediction using SNP context and whole-genome feature embedding based on DNABERT-2. *Plant methods*, 22(1), 15.

Zhang L, et al. (2026) Investigating the functions of glycosyl hydrolase family 1 in foxtail millet through an integrated genome-wide survey, expression profiling, and variation analysis. *BMC plant biology*, 26(1).

Hanson F, et al. (2026) Genetic diversity analysis of North Dakota public soybean breeding program cultivars. *Scientific reports*, 16(1), 6012.

Kumawat G, et al. (2026) Genome-wide association study for root-related traits at vegetative growth stages of soybean (*Glycine max* L. Merrill). *BMC genomics*, 27(1), 178.

Yang X, et al. (2026) ZmPEPCK2 enhances nutritional quality and yield potential by synchronizing carbon and nitrogen metabolism in maize kernels. *Plant communications*, 7(5), 101734.

Babu P, et al. (2026) Dissecting adult plant resistance to stripe and leaf rust in advanced Indian wheat breeding lines through a genome-wide association study. *BMC plant biology*, 26(1).

Lou Q, et al. (2026) Transcriptome Analysis Identifies OsWRKY26 as a Key Regulator for Cold Tolerance at the Seedling Stage in Rice. *Plants (Basel, Switzerland)*, 15(4).

Ontoy J, et al. (2026) Characterization of resistance to bacterial panicle blight in rice revealed by transcriptome and QTL mapping analyses. *Frontiers in plant science*, 17, 1857873.