

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: 20260805T044305+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 2335 mentions in open access literature.

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

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.

Tiozon RN, et al. (2025) Lipidomics-based association study reveals genomic signatures of anti-cancer qualities of pigmented rice sprouts. *Frontiers in plant science*, 16, 1533442.

Kannababu N, et al. (2025) Role of functional genes for seed vigor related traits through genome-wide association mapping in finger millet (*Eleusine coracana* L. Gaertn.). *Scientific reports*, 15(1), 5569.

Yang Q, et al. (2025) Identification of QTL for branch traits in soybean (*Glycine max* L.) and its application in genomic selection. *Frontiers in genetics*, 16, 1484146.

Ishikawa N, et al. (2025) Allotetraploid Origin and Putative Ancient Introgression in *Plantago hakusanensis* (Plantaginaceae). *Ecology and evolution*, 15(3), e71144.

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.

Marla SR, et al. (2025) Mining sorghum pangenome enabled identification of new *dw3* alleles for breeding stable-dwarfing hybrids. *G3 (Bethesda, Md.)*, 15(5).

Johnson S, et al. (2025) Genomic Markers Associated With Soybean Resistance to the Stem Borer, *Dectes texanus* (Coleoptera: Cerambycidae). *Plant direct*, 9(3), e70040.

Deng X, et al. (2025) Genome-wide association study of salicylic acid provides genetic insights for tea plant selective breeding. *Horticulture research*, 12(4), uhae362.

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.

Li J, et al. (2025) Natural variation of indels in the CTB3 promoter confers cold tolerance in japonica rice. *Nature communications*, 16(1), 1613.

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.

Chen A, et al. (2025) Genetic parameter estimation and molecular foundation of Double-yolk eggs trait in white leghorn. *Poultry science*, 104(7), 105069.

Poutougnigni Matenchi Y, et al. (2025) Genomic diversity of Cameroonian Gudali and Gudali-cross cattle. *Scientific reports*, 15(1), 15066.