

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org/) on Apr 27, 2024

TASSEL

RRID:SCR_012837

Type: Tool

Proper Citation

TASSEL (RRID:SCR_012837)

Resource Information

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

Proper Citation: TASSEL (RRID:SCR_012837)

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>

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 1913 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Gnanapragasam N, et al. (2024) Extreme trait GWAS (Et-GWAS): Unraveling rare variants in the 3,000 rice genome. Life science alliance, 7(3).

Fan Y, et al. (2024) Genome-Wide Association Study Identifies Rice Panicle Blast-Resistant Gene Pb4 Encoding a Wall-Associated Kinase. International journal of molecular sciences, 25(2).

Nouraei S, et al. (2024) Genome-wide association study of drought tolerance in wheat (*Triticum aestivum* L.) identifies SNP markers and candidate genes. Molecular genetics and genomics : MGG, 299(1), 22.

Huang CC, et al. (2024) Application of bulk segregant RNA-Seq (BSR-Seq) and allele-specific primers to study soybean powdery mildew resistance. BMC plant biology, 24(1), 155.

Sehgal D, et al. (2024) Genomic characterisation and dissection of the onset of resistance to acetyl CoA carboxylase-inhibiting herbicides in a large collection of *Digitaria insularis* from Brazil. Frontiers in genetics, 15, 1340852.

Yadav J, et al. (2024) Unravelling the novel genetic diversity and marker-trait associations of corn leaf aphid resistance in wheat using microsatellite markers. PloS one, 19(2), e0289527.

Dai D, et al. (2024) Identification of a Branch Number Locus in Soybean Using BSA-Seq and GWAS Approaches. International journal of molecular sciences, 25(2).

Li C, et al. (2024) Uncovering Novel QTLs and Candidate Genes for Salt Tolerance at the Bud Burst Stage in Rice through Genome-Wide Association Study. Plants (Basel, Switzerland), 13(2).

Shah LR, et al. (2024) Mapping phenotypic performance and novel SNPs for cold tolerance in tomato (*Solanum lycopersicum*) genotypes through GWAS and population genetics. BMC genomic data, 25(1), 9.

Sowadan O, et al. (2024) Genome-Wide Association Analysis Unravels New Quantitative

Trait Loci (QTLs) for Eight Lodging Resistance Constituent Traits in Rice (*Oryza sativa* L.). *Genes*, 15(1).

Jia M, et al. (2024) The pan-plastome of *Hemerocallis citrina* reveals new insights into the genetic diversity and cultivation history of an economically important food plant. *BMC plant biology*, 24(1), 44.

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of *Sesamum* species. *Plant communications*, 5(1), 100729.

Dong Y, et al. (2024) Genome-Wide Association Study for Maize Hybrid Performance in a Typical Breeder Population. *International journal of molecular sciences*, 25(2).

Wu F, et al. (2024) ZmARF1 positively regulates low phosphorus stress tolerance via modulating lateral root development in maize. *PLoS genetics*, 20(2), e1011135.

Sallam A, et al. (2024) Genome-wide analysis for root and leaf architecture traits associated with drought tolerance at the seedling stage in a highly ecologically diverse wheat population. *Computational and structural biotechnology journal*, 23, 870.

Ho WK, et al. (2024) A genomic toolkit for winged bean *Psophocarpus tetragonolobus*. *Nature communications*, 15(1), 1901.

Kohli M, et al. (2024) Genome-wide association studies for earliness, MYMIV resistance, and other associated traits in mungbean (*Vigna radiata* L. Wilczek) using genotyping by sequencing approach. *PeerJ*, 12, e16653.

Reyes-Ardila WL, et al. (2024) Exploring Genomics and Microbial Ecology: Analysis of *Bidens pilosa* L. Genetic Structure and Soil Microbiome Diversity by RAD-Seq and Metabarcoding. *Plants (Basel, Switzerland)*, 13(2).

Qiu Y, et al. (2024) Identification of loci conferring resistance to 4 foliar diseases of maize. *G3 (Bethesda, Md.)*, 14(2).

Zaïm M, et al. (2024) Genomic regions of durum wheat involved in water productivity. *Journal of experimental botany*, 75(1), 316.