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

Funding:

Resource Name: TASSEL

Resource ID: SCR_012837

Alternate IDs: nlx_154674, biotools:tassel

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

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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 2119 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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.

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.

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

Rolling WR, et al. (2025) Combining genome-wide association and genomic prediction to unravel the genetic architecture of carotenoid accumulation in carrot. The plant genome, 18(1), e20560.

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

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.

Mastrangelo AM, et al. (2025) A new wild emmer wheat panel allows to map new loci associated with resistance to stem rust at seedling stage. The plant genome, 18(1), e20413.

Qin Y, et al. (2025) Integrated Genetic Diversity and Multi-Omics Analysis of Colour Formation in Safflower. International journal of molecular sciences, 26(2).

Kim MS, et al. (2025) A combination of upstream alleles involved in rice heading hastens natural long-day responses. Genes & genomics, 47(2), 245.

Mahaman Mourtala IZ, et al. (2025) Genetic diversity and population structure studies of West African sweetpotato [Ipomoea batatas (L.) Lam] collection using DArTseq. PloS one, 20(1), e0312384.

Mukuze C, et al. (2025) Genome-wide association mapping of bruchid resistance loci in soybean. PloS one, 20(1), e0292481.

Bajgain P, et al. (2025) Improving complex agronomic and domestication traits in the perennial grain crop intermediate wheatgrass with genetic mapping and genomic prediction. The plant genome, 18(1), e20498.

Subrahmaniam HJ, et al. (2025) Natural variation in root exudate composition in the genetically structured Arabidopsis thaliana in the Iberian Peninsula. The New phytologist, 245(4), 1437.

Lakkakula IP, et al. (2025) Identification of leaf rust resistance loci in hard winter wheat using genome-wide association mapping. The plant genome, 18(1), e20546.

Wang J, et al. (2025) Research note: A low-density SNP genotyping panel for Chinese native chickens. Poultry science, 104(1), 104609.

Zhang Y, et al. (2025) Identification of superior haplotypes and candidate gene for seed size-related traits in soybean (Glycine max L.). Molecular breeding : new strategies in plant improvement, 45(1), 3.

Guo H, et al. (2025) Natural variation of CTB5 confers cold adaptation in plateau japonica rice. Nature communications, 16(1), 1032.

Silva ACD, et al. (2025) Genetic diversity, population structure in a historical panel of Brazilian soybean cultivars. PloS one, 20(1), e0313151.

Biswas A, et al. (2025) Comparative genomic prediction of resistance to Fusarium wilt (Fusarium oxysporum f. sp. niveum race 2) in watermelon: parametric and nonparametric approaches. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(1), 35.