

Resource Summary Report

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PLABQTL

RRID:SCR_012789

Type: Tool

Proper Citation

PLABQTL (RRID:SCR_012789)

Resource Information

URL: https://plant-breeding.uni-hohenheim.de/software.html#jfmulticontent_c110647-2

Proper Citation: PLABQTL (RRID:SCR_012789)

Description: Software application (entry from Genetic Analysis Software)

Synonyms: PLAnt Breeding QTL analysis

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: PLABQTL

Resource ID: SCR_012789

Alternate IDs: nlx_154535

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260727T040548+0000

Ratings and Alerts

No rating or validation information has been found for PLABQTL.

No alerts have been found for PLABQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Sielemann K, et al. (2023) Genomic characterization of a nematode tolerance locus in sugar beet. BMC genomics, 24(1), 748.

Ence D, et al. (2022) NLR diversity and candidate fusiform rust resistance genes in loblolly pine. G3 (Bethesda, Md.), 12(2).

Talukder ZI, et al. (2020) Genetic Dissection of Phomopsis Stem Canker Resistance in Cultivated Sunflower Using High Density SNP Linkage Map. International journal of molecular sciences, 21(4).

Talukder ZI, et al. (2020) Unraveling the Sclerotinia Basal Stalk Rot Resistance Derived From Wild Helianthus argophyllus Using a High-Density Single Nucleotide Polymorphism Linkage Map. Frontiers in plant science, 11, 617920.

Kumar S, et al. (2018) Mapping Grain Iron and Zinc Content Quantitative Trait Loci in an Iniadi-Derived Immortal Population of Pearl Millet. Genes, 9(5).

Rosen A, et al. (2018) Genome-Based Prediction of Time to Curd Induction in Cauliflower. Frontiers in plant science, 9, 78.

Kumar S, et al. (2017) Mapping QTLs Controlling Flowering Time and Important Agronomic Traits in Pearl Millet. Frontiers in plant science, 8, 1731.

Walch-Liu P, et al. (2017) QTL analysis of the developmental response to L-glutamate in Arabidopsis roots and its genotype-by-environment interactions. Journal of experimental botany, 68(11), 2919.

Perez-Lara E, et al. (2016) QTLs Associated with Agronomic Traits in the Cutler × AC Barrie Spring Wheat Mapping Population Using Single Nucleotide Polymorphic Markers. PloS one, 11(8), e0160623.

Yao N, et al. (2016) QTL Mapping in Three Rice Populations Uncovers Major Genomic Regions Associated with African Rice Gall Midge Resistance. PloS one, 11(8), e0160749.

Francisco M, et al. (2015) Organ-Specific Quantitative Genetics and Candidate Genes of Phenylpropanoid Metabolism in Brassica oleracea. Frontiers in plant science, 6, 1240.

Wang Y, et al. (2015) First insights into the genotype-phenotype map of phenotypic stability in rye. Journal of experimental botany, 66(11), 3275.

Rodríguez VM, et al. (2013) Genetic regulation of cold-induced albinism in the maize inbred line A661. Journal of experimental botany, 64(12), 3657.

Arraouadi S, et al. (2012) QTL mapping of physiological traits associated with salt tolerance in Medicago truncatula Recombinant Inbred Lines. Genomics, 99(2), 118.