

# 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](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 resource, software application

**Keywords:** gene, genetic, genomic

**Resource Name:** PLABQTL

**Resource ID:** SCR\_012789

**Alternate IDs:** nlx\_154535

**Record Creation Time:** 20220129T080312+0000

**Record Last Update:** 20260731T042854+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 [PRECISE-TBI](#) .

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.