

Resource Summary Report

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BARLEYMAP

RRID:SCR_015710

Type: Tool

Proper Citation

BARLEYMAP (RRID:SCR_015710)

Resource Information

URL: <http://floresta.eead.csic.es/barleymap>

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Description: Barleymap was designed to search the position of barley genetic markers on the Barley Physical Map and the POPSEQ map. Its three main functions are finding markers, aligning sequences, and locating by position.

Resource Type: data analysis software, data or information resource, data processing software, database, sequence analysis software, software application, software resource, standalone software, web application

Defining Citation: [DOI:10.1007/s11032-015-0253-1](https://doi.org/10.1007/s11032-015-0253-1)

Keywords: barley, genetic marker, barley physical map, popseq map

Funding: DGA GA-LC-059-2011;
MICINN AGL2010-21929;
MICINN RTA2009-00006-C04-02;
MICINN BES-2011-045905

Availability: Freely available, Free for academic use, Free, Available for download

Resource Name: BARLEYMAP

Resource ID: SCR_015710

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260905T132758+0000

Ratings and Alerts

No rating or validation information has been found for BARLEYMAP.

No alerts have been found for BARLEYMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Ksouri N, et al. (2025) Mapping the genomic landscape of Prunus spp. with PrunusMap. Horticulture research, 12(2), uhae301.

Afsharyan NP, et al. (2025) Comparative transcriptome analysis reveals candidate gene for flowering time QTL HvHeading in barley. BMC plant biology, 25(1), 782.

Noe SM, et al. (2025) Comparing wMAS, GWAS, and genomic prediction for selecting powdery mildew-resistant spring barley genotypes. BMC genomics, 26(1), 1091.

Amouzoune M, et al. (2024) Genome wide association study of seedling and adult plant leaf rust resistance in two subsets of barley genetic resources. Scientific reports, 14(1), 15428.

Cabeza A, et al. (2024) Genetic control of root/shoot biomass partitioning in barley seedlings. Frontiers in plant science, 15, 1408043.

Eckstein PE, et al. (2024) An island of receptor-like genes at the Rrs13 locus on barley chromosome 6HS co-locate with three novel sources of scald resistance. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(11), 249.

Du B, et al. (2024) Genome-wide screening of meta-QTL and candidate genes controlling yield and yield-related traits in barley (Hordeum vulgare L.). PloS one, 19(5), e0303751.

Rodríguez Del Río Á, et al. (2023) Diversity of gene expression responses to light quality in barley. Scientific reports, 13(1), 17143.

Elakhdar A, et al. (2023) Genome-wide association analysis provides insights into the genetic basis of photosynthetic responses to low-temperature stress in spring barley. Frontiers in plant science, 14, 1159016.

Xu T, et al. (2022) Integrated GWAS and transcriptomic analysis reveal the candidate salt-responding genes regulating Na⁺/K⁺ balance in barley (Hordeum vulgare L.). Frontiers in plant science, 13, 1004477.

Borrego-Benjumea A, et al. (2021) Genome-Wide Association Study of Waterlogging Tolerance in Barley (Hordeum vulgare L.) Under Controlled Field Conditions. Frontiers in

plant science, 12, 711654.

Hautsalo J, et al. (2021) Pyramiding of scald resistance genes in four spring barley MAGIC populations. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 134(12), 3829.

Büttner B, et al. (2020) Identification of QTLs conferring resistance to scald (*Rhynchosporium commune*) in the barley nested association mapping population HEB-25. BMC genomics, 21(1), 837.

Novakazi F, et al. (2020) You Had Me at "MAGIC"! Four Barley MAGIC Populations Reveal Novel Resistance QTL for Powdery Mildew. Genes, 11(12).

Ogrodowicz P, et al. (2020) Mapping of quantitative trait loci for traits linked to fusarium head blight in barley. PloS one, 15(2), e0222375.

Zhang M, et al. (2019) Response of Tibetan Wild Barley Genotypes to Drought Stress and Identification of Quantitative Trait Loci by Genome-Wide Association Analysis. International journal of molecular sciences, 20(3).

Wang Q, et al. (2019) Dissecting the Genetic Basis of Grain Size and Weight in Barley (*Hordeum vulgare* L.) by QTL and Comparative Genetic Analyses. Frontiers in plant science, 10, 469.

Åhman I, et al. (2019) Introgression of resistance to *Rhopalosiphum padi* L. from wild barley into cultivated barley facilitated by doubled haploid and molecular marker techniques. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 132(5), 1397.

Du B, et al. (2019) Identification of QTL underlying the leaf length and area of different leaves in barley. Scientific reports, 9(1), 4431.

Du B, et al. (2019) Mapping dynamic QTL dissects the genetic architecture of grain size and grain filling rate at different grain-filling stages in barley. Scientific reports, 9(1), 18823.