

Resource Summary Report

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GrainGenes

RRID:SCR_007696

Type: Tool

Proper Citation

GrainGenes (RRID:SCR_007696)

Resource Information

URL: <http://wheat.pw.usda.gov>

Proper Citation: GrainGenes (RRID:SCR_007696)

Description: Grain Genes is a genome database for Triticeae and Avena. It contains tools that allow users to browse graingenes, search the MySQL database, and view maps, genetic markers, gene expression and sequences.

Synonyms: GrainGenes

Resource Type: data or information resource, database

Keywords: agriculture, avena, plant genome, triticeae, FASEB list

Resource Name: GrainGenes

Resource ID: SCR_007696

Alternate IDs: nif-0000-02925, r3d100012363

Alternate URLs: <https://doi.org/10.17616/R3D08J>, <https://doi.org/10.17616/R3D08J>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260811T043313+0000

Ratings and Alerts

No rating or validation information has been found for GrainGenes.

No alerts have been found for GrainGenes.

Data and Source Information

Usage and Citation Metrics

We found 322 mentions in open access literature.

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

Brooke M, et al. (2026) Identification and association mapping of sources of stem rust resistance in the wild barley diversity panel effective against virulent isolates from the Pacific Northwest. *G3* (Bethesda, Md.), 16(3).

Caguiat JD, et al. (2026) Development and characterization of near-isogenic lines for quantitative trait locus qDT.3B.1 underlying drought tolerance in wheat. *The plant genome*, 19(2), e70186.

Baumann U, et al. (2026) OzBarley: A genetic and phenotypic data resource capturing the Australian barley breeding history. *Scientific data*, 13(1).

Pandit M, et al. (2026) Exploring standing genetic variation for barley leaf rust resistance in Australian breeding panel. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(1), 31.

Nguyen DT, et al. (2026) QTL mapping of oat crown rust resistance in Australian fields and identification of a seedling resistance locus in oat line GS7. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(1), 41.

Ivanizs L, et al. (2026) Introgression of barley chromosome arms 4H and 6H into wheat via Robertsonian translocations: GBS-assisted structural analysis and impact on grain nutrient composition. *Plant molecular biology*, 116(2), 23.

Sun Y, et al. (2026) Systematic analysis of the Diacylglycerol acyltransferase (DGAT) genes in oat and functional characterization of AsDGAT2-1 involved in oil accumulation and cold stress tolerance. *BMC plant biology*, 26(1).

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

Osipova SV, et al. (2025) Drought tolerance of the photosynthetic apparatus of bread wheat (*Triticum aestivum* L.) lines with introgressions in chromosome 2D from *Aegilops tauschii* Coss. *Vavilovskii zhurnal genetiki i selektsii*, 29(4), 530.

Chouaibi Y, et al. (2025) Durum wheat nuclear factor Y (NF-Y) a subfamily: structure, phylogeny, and expression analysis in response to hormones and abiotic stresses. *Functional & integrative genomics*, 25(1), 102.

Miao Y, et al. (2025) Unravelling consensus genomic regions conferring stem-related traits in wheat via meta-QTL analysis. *BMC plant biology*, 25(1), 609.

Marcotuli I, et al. (2025) Identification of new QTLs for quality traits and yield using tetraploid wheat interspecific backcross inbred lines. *BMC genomics*, 26(1), 1111.

Malik AS, et al. (2025) Conversion of elite bread wheat cultivars HD3086 and HD2932 into cytoplasmic male sterile (CMS) lines and their genetic assessment to develop CMS-based hybrids. *BMC plant biology*, 25(1), 1539.

Pan Y, et al. (2025) Genome-wide analysis of the COMT gene family in *Avena sativa*: insights into lignin biosynthesis and disease defense mechanisms. *Frontiers in plant science*, 16, 1609698.

Hisano H, et al. (2025) Rapid development of naked malting barley germplasm through targeted mutagenesis. *Molecular breeding : new strategies in plant improvement*, 45(3), 32.

Peters Haugrud AR, et al. (2025) Identification of robust yield quantitative trait loci derived from cultivated emmer for durum wheat improvement. *The plant genome*, 18(1), e20398.

Shirvani H, et al. (2025) Genetic structure and marker-trait association analysis for agro-morphological and physiological characteristics in germplasm of wild barley (*Hordeum vulgare* subsp. *spontaneum*). *Scientific reports*, 15(1), 38706.

Shirvani H, et al. (2025) Marker-trait association analysis for root and shoot traits at the seedling stage of wild barley (*Hordeum vulgare* subsp. *spontaneum*) under water stress and normal conditions. *AoB PLANTS*, 17(4), plaf022.

Manan F, et al. (2025) Genome-wide association and biparental mapping revealed a major quantitative trait locus associated with seedling resistance to bacterial leaf streak in durum. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(1), 10.

Hewitt TC, et al. (2025) Divergent molecular pathways govern temperature-dependent wheat stem rust resistance genes. *Nature communications*, 16(1), 4905.