

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: 20260729T044151+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 298 mentions in open access literature.

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

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.

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

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.

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.

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.

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.

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 agromorphological 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.

Shariatipour N, et al. (2025) Genetic dissection of crown rust resistance in oat and the identification of key adult plant resistance genes. *The plant genome*, 18(2), e70059.

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

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.

- Yang X, et al. (2025) MADS31 supports female germline development by repressing the post-fertilization programme in cereal ovules. *Nature plants*, 11(3), 543.
- Xu C, et al. (2025) Glutathione S-transferase in mediating adaptive responses of oats (*Avena sativa*) to osmotic and cadmium stress: genome-wide analysis. *BMC plant biology*, 25(1), 538.
- Murtaza M, et al. (2025) Transcriptome-based meta-analysis of drought stress regulatory genes in tomato. *BMC plant biology*, 25(1), 1347.
- Jaegle B, et al. (2025) k-mer-based GWAS in a wheat collection reveals novel and diverse sources of powdery mildew resistance. *Genome biology*, 26(1), 172.
- Pan Y, et al. (2024) Genome-wide analysis of the SWEET gene family and its response to powdery mildew and leaf spot infection in the common oat (*Avena sativa* L.). *BMC genomics*, 25(1), 995.
- 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.
- Li T, et al. (2024) The E3 ligase TaE3V-B1 ubiquitinates proteins encoded by the vernalization gene TaVRN1 and regulates developmental processes in wheat. *Plant physiology*, 197(1).
- Malik AS, et al. (2024) Conversion of superior bread wheat genotype HD3209 carrying Lr19/Sr25 into CMS line for development of rust-resistant wheat hybrids. *Scientific reports*, 14(1), 14112.