# **Resource Summary Report**

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# **Genome Database for Rosaceae**

RRID:SCR\_012756 Type: Tool

### **Proper Citation**

Genome Database for Rosaceae (RRID:SCR\_012756)

### **Resource Information**

URL: http://www.rosaceae.org/

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**Description:** GDR is a curated and integrated web-based relational database. GDR contains comprehensive data of the genetically anchored peach physical map, annotated EST databases of apple, peach, almond, cherry, rose, raspberry and strawberry, Rosaceae maps and markers and all publicly available Rosaceae sequences. Annotations of ESTs include contig assembly, putative function, simple sequence repeats, ORFs, Gene Ontology and anchored position to the peach physical map where applicable. Our integrated map viewer provides graphical interface to the genetic, transcriptome and physical mapping information. We continue to add Rosaceae map data to CMap, a web-based tool that allows users to view comparisons of genetic and physical maps. ESTs, BACs and markers can be queried by various categories and the search result sites are linked to the integrated map viewer or to the WebFPC physical map sites. In addition to browsing and querying the database, users can compare their sequences with the annotated GDR sequences via a dedicated sequence similarity server running either the BLAST or FASTA algorithm, search their sequences for microsatellites using the SSR server or assemble their ESTs using the CAP3 Server.

#### Synonyms: GDR

Resource Type: database, data or information resource

Keywords: est, genome sequence, rosaceae, bio.tools, FASEB list

Funding:

Resource Name: Genome Database for Rosaceae

Resource ID: SCR\_012756

Alternate IDs: nif-0000-02896, biotools:gdr

Alternate URLs: https://bio.tools/gdr

Old URLs: http://www.bioinfo.wsu.edu/gdr/

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250503T060334+0000

## **Ratings and Alerts**

No rating or validation information has been found for Genome Database for Rosaceae.

No alerts have been found for Genome Database for Rosaceae.

## Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 441 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Zhong Y, et al. (2025) Transcriptome sequencing reveals jasmonate playing a key role in ALA-induced osmotic stress tolerance in strawberry. BMC plant biology, 25(1), 41.

Huang R, et al. (2025) The Identification of Auxin Response Factors and Expression Analyses of Different Floral Development Stages in Roses. Genes, 16(1).

Liu Z, et al. (2025) Genomes and integrative genomic insights into the genetic architecture of main agronomic traits in the edible cherries. Horticulture research, 12(1), uhae269.

Brainard SH, et al. (2024) The first two chromosome-scale genome assemblies of American hazelnut enable comparative genomic analysis of the genus Corylus. Plant biotechnology journal, 22(2), 472.

Pei T, et al. (2024) MdWRKY71 promotes the susceptibility of apple to Glomerella leaf spot by controlling salicylic acid degradation. Molecular plant pathology, 25(4), e13457.

Minamikawa MF, et al. (2024) Genomic prediction and genome-wide association study using combined genotypic data from different genotyping systems: application to apple fruit quality

traits. Horticulture research, 11(7), uhae131.

da Silva Linge C, et al. (2024) Ppe.RPT/SSC-1: from QTL mapping to a predictive KASP test for ripening time and soluble solids concentration in peach. Scientific reports, 14(1), 1453.

Wang N, et al. (2024) A Functional InDel in the WRKY10 Promoter Controls the Degree of Flesh Red Pigmentation in Apple. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(30), e2400998.

Liu M, et al. (2024) Expression analysis of the apple HSP70 gene family in abiotic stress and phytohormones and expression validation of candidate MdHSP70 genes. Scientific reports, 14(1), 23975.

Tang R, et al. (2024) The FvABF3-FvALKBH10B-FvSEP3 cascade regulates fruit ripening in strawberry. Nature communications, 15(1), 10912.

Gupta P, et al. (2024) Plant Reactome Knowledgebase: empowering plant pathway exploration and OMICS data analysis. Nucleic acids research, 52(D1), D1538.

Liu Z, et al. (2024) Molecular characterization of PSEUDO RESPONSE REGULATOR family in Rosaceae and function of PbPRR59a and PbPRR59b in flowering regulation. BMC genomics, 25(1), 794.

Zhou L, et al. (2024) Multi-omics analyzes of Rosa gigantea illuminate tea scent biosynthesis and release mechanisms. Nature communications, 15(1), 8469.

Xie L, et al. (2024) Genome-wide identification and analysis of anthocyanin synthesis-related R2R3-MYB genes in Fragaria pentaphylla. BMC genomics, 25(1), 952.

Wang L, et al. (2024) Genome-Wide Identification and Expression Analysis of the Sweet Cherry Whirly Gene Family. Current issues in molecular biology, 46(8), 8015.

Huang D, et al. (2024) Genome-wide analysis of the passion fruit invertase gene family reveals involvement of PeCWINV5 in hexose accumulation. BMC plant biology, 24(1), 836.

Hu DG, et al. (2024) A linker histone acts as a transcription factor to orchestrate malic acid accumulation in apple in response to sorbitol. The Plant cell, 37(1).

Zhou Z, et al. (2024) The MdERF61-mdm-miR397b-MdLAC7b module regulates apple resistance to Fusarium solani via lignin biosynthesis. Plant physiology, 197(1).

Shum C, et al. (2024) Untying the knot: Unraveling genetic mechanisms behind black knot disease resistance in Prunus salicina (Japanese plum). Plant-environment interactions (Hoboken, N.J.), 5(6), e70016.

Lin Y, et al. (2024) Genome-wide analysis and functional validation reveal the role of late embryogenesis abundant genes in strawberry (Fragaria?×?ananassa) fruit ripening. BMC genomics, 25(1), 228.