

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

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: data or information resource, database

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

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: 20260912T200208+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 662 mentions in open access literature.

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

mejlová J, et al. (2026) The Development of New SSR Markers and an Assay for Genotyping Sweet Cherry (*Prunus avium* L.) in One Reaction. International journal of molecular sciences, 27(5).

Sun H, et al. (2026) FveDAD2 negatively regulates branch crowns by affecting abscisic acid metabolism through FveHB7 in woodland strawberry. Horticulture research, 13(1), uhaf250.

Liu D, et al. (2026) Genome-wide Identification and expression analysis of TOR signaling pathway components in apple in response to low nitrogen. The plant genome, 19(1), e70215.

Zhang S, et al. (2026) Whole-genome resequencing of 495 *Pyrus* accessions provides insights into the genetics of agronomic traits and evolutionary history of pear. Horticulture research, 13(5), uhag042.

Cheng X, et al. (2026) Haplotype-resolved genome assembly provides insights into the unique floral scent of *Rosa rugosa* originated in China. Molecular horticulture, 6(1).

Yan J, et al. (2026) Uncovering novel loci and developing functional Kompetitive Allele Specific PCR markers for chilling requirement in peach via genome-wide association study. Horticulture research, 13(6), uhag069.

Xu X, et al. (2026) Identification of the RcbZIP gene family in *Rubus Chingii* and analysis of the regulation of flavonoid synthesis by RcbZIP1 and RcbZIP12. Frontiers in plant science, 17, 1769751.

Zhang X, et al. (2026) Pangenomic analyses of rose uncover widespread structure variation and empower genomics-directed breeding. *Nature genetics*, 58(5), 1164.

Jin J, et al. (2026) Salicylic acid reduces MdPUB24-mediated ubiquitination of MdWRKY40 to suppress ethylene biosynthesis in apple fruit. *Horticulture research*, 13(2), uhaf303.

Zhang Z, et al. (2026) Deciphering the Temporal Transcriptional Dynamics and Key Regulatory Networks of *Pyrus betulifolia* in Response to PEG-Induced Osmotic Stress. *Biology*, 15(6).

Wang Y, et al. (2026) Reduced MdFLS Expression Decreases Flavonol Content in Apple Flesh. *Plants (Basel, Switzerland)*, 15(5).

Wei HT, et al. (2026) Two pear phytoctokines PbePep4 and PdrPep6 interfamiliially elicit broad-spectrum immunity against various pathogens in crops. *Horticulture research*, 13(5), uhag027.

Humann JL, et al. (2026) Genome Database for *Vaccinium*: a knowledgebase for genetics, genomics, and breeding research. *Genetics*, 232(4).

Zhao C, et al. (2026) Genome-Wide Identification of R2R3-MYB Gene Family in Strawberry (*Fragaria vesca* L.) and Functional Characterization of FvMYB103 in Cold Stress. *International journal of molecular sciences*, 27(2).

Ren H, et al. (2026) Arabica coffee SBP transcription factor family members respond to brown leaf spot stress by regulating their expression. *BMC plant biology*, 26(1).

Zhang T, et al. (2026) Multi-omics analyses shed lights on the evolution and fruit development of Chinese raspberries (*Rubus* spp.). *Journal of integrative plant biology*, 68(4), 1032.

Li M, et al. (2026) De Novo Chromosome-Level Genome Assembly of 'Qing Zhou Mi' Landrace Peach and Analysis of Late Maturity and Fruit Weight Traits in Peach. *Plants (Basel, Switzerland)*, 15(7).

Sheng L, et al. (2026) Genome-wide identification of CONSTANS-LIKE genes and functional analysis of FaCOL57 and FaCOL59 in regulating anthocyanin and sugar synthesis in cultivated strawberry. *BMC genomics*, 27(1).

Han C, et al. (2026) Identification of the Auxin Response Factor gene family in kernel consumption apricot and association analysis of related genes regulating fruit size in distant hybridization. *BMC plant biology*, 26(1), 302.

Li X, et al. (2026) Genome-wide analysis of leucine-rich repeat-only proteins gene family revealed FaLRPop26 responding *Colletotrichum Siamense* infection by regulated lignin synthesis in cultivated strawberry (*Fragaria × ananassa*). *BMC plant biology*, 26(1), 328.