

# Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 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/>

**Proper Citation:** Genome Database for Rosaceae (RRID:SCR\_012756)

**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:** 20260801T191028+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 486 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#).

Liu RX, et al. (2026) MdHMGB15-MdXERICO-MdNRP module mediates salt tolerance of apple by regulating the expression of salt stress-related genes. *Journal of advanced research*, 79, 61.

Li C, et al. (2025) Melatonin suppresses ethylene biosynthesis by inhibiting transcription factor MdREM10 during apple fruit ripening. *Horticulture research*, 12(5), uhaf020.

Liu S, et al. (2025) Identification of the SWEET gene family and functional characterization of PsSWEET1a and PsSWEET17b in the regulation of sugar accumulation in 'Fengtang' plum (*Prunus salicina* Lindl.). *BMC plant biology*, 25(1), 407.

Li T, et al. (2025) Ethylene-Activated E3 Ubiquitin Ligase MdEAL1 Promotes Apple Fruit Softening by Facilitating the Dissociation of Transcriptional Repressor Complexes. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 12(22), e2417393.

Feng X, et al. (2025) Functional characterization of COMT genes in Chinese white pear (*Pyrus bretschneideri*) and their role in lignin synthesis. *Frontiers in plant science*, 16, 1614220.

Zhang H, et al. (2025) Identification of the U-box gene family in peach (*Prunus persica*) and functional analysis of PpPUB20 in response to salt stress. *Frontiers in genetics*, 16, 1549981.

Li Q, et al. (2025) PpMYC2 and PpJAM2/3 antagonistically regulate lignin synthesis to cope with the disease in peach fruit. *Plant biotechnology journal*, 23(9), 3524.

Wang ?? C, et al. (2025) PSIA: A Comprehensive Knowledgebase of Plant Self-incompatibility. *Genomics, proteomics & bioinformatics*, 23(3).

Wu X, et al. (2025) Two gap-free genomes of Argentina provide insights into their genetic relationships. *Molecular horticulture*, 5(1), 50.

Zhang L, et al. (2025) Strawberry cryptochrome FvCRY1 and FvCRY2 transcriptionally regulate anthocyanin biosynthesis and sugar metabolism. *Molecular horticulture*, 5(1), 63.

Bai X, et al. (2025) Genome-wide identification of WOX family members in rose and functional analysis of RcWUS1 in embryogenic transformation. *The plant genome*, 18(1), e70012.

Jung S, et al. (2025) Building resource-efficient community databases using open-source software. *Database : the journal of biological databases and curation*, 2025.

Yang X, et al. (2025) Major Facilitator Superfamily transporters balance sugar metabolism in peach. *Plant physiology*, 198(1).

Gu S, et al. (2025) The Ste20 Homologue FvM4K1 Regulates Organ Size via Hippo Signalling Pathway in Woodland Strawberry (*Fragaria vesca*). *Plant biotechnology journal*, 23(11), 5094.

Guo Z, et al. (2025) Identification of the AKR gene family in sweet cherry and its response to different abiotic stresses. *Scientific reports*, 15(1), 29251.

Meng J, et al. (2025) Identification of PpTHE1, a cell wall integrity sensor regulating the increased duration of harvest window in slow-melting flesh peach, through the assembly of a chromosome-level reference genome of *Prunus persica*. *Plant biotechnology journal*, 23(10), 4228.

Liu L, et al. (2025) The pan genome analysis of WOX gene family in apple and the two sides of MdWUS-1 in promoting leaf-borne shoot. *Horticulture research*, 12(8), uhaf117.

Wang J, et al. (2025) Integration of volatile and non-volatile metabolites and the transcriptome reveals the formation mechanisms of differential aroma compounds between *Pyrus communis* and *Pyrus pyrifolia* cultivars. *Frontiers in plant science*, 16, 1559012.

Bai Y, et al. (2025) Identification and expression analysis of papain-like cysteine proteases gene family and response to B. cinerea stress in *F. vesca*. *BMC plant biology*, 25(1), 1294.

Itam M, et al. (2025) Genetic architecture of key traits for *Prunus* crop improvement: an overview of 25 years of curated genomic and breeding data. *Horticulture research*, 12(8), uhaf142.