

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: 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: 20260804T043503+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 [ASWG](#) .

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.

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

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

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-Wurttemberg, Germany), 12(22), e2417393.

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.

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

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.

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.

- 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 L, et al. (2025) Strawberry cryptochrome FvCRY1 and FvCRY2 transcriptionally regulate anthocyanin biosynthesis and sugar metabolism. *Molecular horticulture*, 5(1), 63.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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).
- 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.
- 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.
- Gracia C, et al. (2025) Genetic and QTL analyses of sugar and acid content in sweet cherry (*Prunus avium* L.). *Horticulture research*, 12(2), uhae310.