

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

GigaDB

RRID:SCR_004002

Type: Tool

Proper Citation

GigaDB (RRID:SCR_004002)

Resource Information

URL: <http://gigadb.org/>

Proper Citation: GigaDB (RRID:SCR_004002)

Description: Repository to host data and tools associated with articles published by GigaScience & GigaByte journals. GigaDB defines a dataset as a group of files (e.g., sequencing data, analyses, imaging files, software programs) that are related to and support an article or study. Through their association with DataCite, each dataset will be assigned a DOI that can be used as a standard citation for future use of these data in other articles by the authors and other researchers. Datasets in GigaDB all require a title that is specific to the dataset, an author list, and an abstract that provides information specific to the data included within the dataset. Detailed information about the dataset is curated by dedicated biocurators in collaboration with the article authors at the time of publication of the associated manuscript to ensure full transparency and reproducibility of all journal articles published in GigaScience and GigaByte journals.

Abbreviations: GigaDB

Synonyms: GigaScience Database, Giga DB

Resource Type: service resource, software resource, storage service resource, data repository, software repository, data or information resource

Defining Citation: [PMID:30753480](#), [PMID:23587345](#), [PMID:24622612](#), [PMID:35701374](#)

Keywords: data set, isa-tab, digital object identifier, FAIR, DOI, transparency,

Funding: BGI

Availability: Creative Commons Zero License, The community can contribute to this resource

Resource Name: GigaDB

Resource ID: SCR_004002

Alternate IDs: DOI:10.25504/FAIRsharing.rcbwsf, r3d100010692, nlx_158413, DOI:10.5524, DOI:10.17616/R3TG83

Alternate URLs: <https://doi.org/10.17616/r3tg83>, <https://fairsharing.org/10.25504/FAIRsharing.rcbwsf>, <https://doi.org/10.17616/R3X89B>

Record Creation Time: 20220129T080222+0000

Record Last Update: 20260728T043154+0000

Ratings and Alerts

No rating or validation information has been found for GigaDB.

No alerts have been found for GigaDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 194 mentions in open access literature.

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

Liu J, et al. (2025) Insights into angiosperm evolution and lineage-specialized lignan biosynthesis from the early-diverging Schisandra genome. *Science advances*, 11(33), eadw0486.

Jiang L, et al. (2025) Genome-Wide Characterization and Expression Analysis of the Cysteine-Rich Polycomb-like Protein Gene Family in Response to Hormone Signaling in Apple (*Malus domestica*). *International journal of molecular sciences*, 26(12).

Yoder EB, et al. (2025) Multiple Pathways of Visual Adaptations for Water Column Usage in an Antarctic Adaptive Radiation. *Ecology and evolution*, 15(3), e70867.

Guo K, et al. (2025) Comparative analysis of genotype imputation strategies for SNPs calling from RNA-seq. *BMC genomics*, 26(1), 245.

Gao YF, et al. (2025) Chromosome-level genome assembly of the longhorn beetle *Arhopalus rusticus* (Coleoptera: Cerambycidae). *Scientific data*, 12(1), 1171.

Wang LY, et al. (2025) A chromosomal-level genome assembly of *Araneus marmoreus* Schenkel, 1953 (Araneae: Araneidae). *Scientific data*, 12(1), 859.

Wiredu-Boakye D, et al. (2025) Evolutionary Insights into the Length Variation of DNA Damage Response Proteins Across Eukaryotes. *Genome biology and evolution*, 17(6).

- Kumari A, et al. (2025) Genome-wide identification, characterization, and expression pattern analysis of the glyoxalase gene family in *Phyllostachys pubescens* during abiotic stresses. *BMC plant biology*, 25(1), 1364.
- Tan ZW, et al. (2025) Genome-Wide Analysis of the APETALA2/Ethylene-Responsive Factor Gene Family in *Carthamus tinctorius* L. *Plant direct*, 9(1), e70032.
- McHale F, et al. (2025) Evolution of Duplicated Hox Gene Clusters in Land Snails and Slugs. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 344(6), 363.
- Ohm H, et al. (2025) Comprehensive identification of the PEBP gene family in *Vicia faba* highlighting VtTFL1a variation and phenotypic insights into determinate growth. *Scientific reports*, 15(1), 28687.
- Guo H, et al. (2024) Genome-wide identification and expression analysis of the HAK/KUP/KT gene family in Moso bamboo. *Frontiers in plant science*, 15, 1331710.
- Wang YH, et al. (2024) Comprehensive analysis of B3 family genes in pearl millet (*Pennisetum glaucum*) and the negative regulator role of PgRAV-04 in drought tolerance. *Frontiers in plant science*, 15, 1400301.
- Wang Q, et al. (2024) A consensus genome of sika deer (*Cervus nippon*) and transcriptome analysis provided novel insights on the regulation mechanism of transcript factor in antler development. *BMC genomics*, 25(1), 617.
- Yu J, et al. (2024) A plant virus manipulates the long-winged morph of insect vectors. *Proceedings of the National Academy of Sciences of the United States of America*, 121(3), e2315341121.
- Hockens C, et al. (2024) Chromosome segregation during spermatogenesis occurs through a unique center-kinetic mechanism in holocentric moth species. *PLoS genetics*, 20(6), e1011329.
- Zietz M, et al. (2024) The probability of edge existence due to node degree: a baseline for network-based predictions. *GigaScience*, 13.
- Cao Y, et al. (2024) Expansion and diversity of caspases in *Mytilus coruscus* contribute to larval metamorphosis and environmental adaptation. *BMC genomics*, 25(1), 314.
- Wang XD, et al. (2024) Integrated transcriptomic analysis reveals evolutionary and developmental characteristics of tendon ossification in teleost. *BMC biology*, 22(1), 304.
- Zhu F, et al. (2024) Polyploidization of *Indotyphlops braminus*: evidence from isoform-sequencing. *BMC genomic data*, 25(1), 23.