Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

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: software resource, data or information resource, service resource, data repository, software repository, storage service 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, nlx_158413, DOI:10.5524, DOI:10.17616/R3TG83

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

Record Creation Time: 20220129T080222+0000

Record Last Update: 20250416T063336+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 184 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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.

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.

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.

Wu Y, et al. (2024) Chromosome-level genome assembly of Plagiognathops microlepis based on PacBio HiFi and Hi-C sequencing. Scientific data, 11(1), 802.

Zhu F, et al. (2024) Polyploidization of Indotyphlops braminus: evidence from isoform-sequencing. BMC genomic data, 25(1), 23.

Fu Q, et al. (2024) Large-scale analysis of the N-terminal regulatory elements of the kinase domain in plant Receptor-like kinase family. BMC plant biology, 24(1), 174.

Zheng L, et al. (2024) PP2 gene family in Phyllostachys edulis: identification, characterization, and expression profiles. BMC genomics, 25(1), 1081.

Hu J, et al. (2023) PearMODB: a multiomics database for pear (Pyrus) genomics, genetics and breeding study. Database : the journal of biological databases and curation, 2023.

Chen S, et al. (2023) The identification, adaptive evolutionary analyses and mRNA expression levels of homeobox (hox) genes in the Chinese mitten crab Eriocheir sinensis. BMC genomics, 24(1), 436.

Pinto BJ, et al. (2023) A lizard is never late: squamate genomics as a recent catalyst for understanding sex chromosome and microchromosome evolution. bioRxiv : the preprint server for biology.

Derrien M, et al. (2023) Gut microbiome function and composition in infants from rural Kenya and association with human milk oligosaccharides. Gut microbes, 15(1), 2178793.

Zhao Y, et al. (2023) Dispersal from the Qinghai-Tibet plateau by a high-altitude butterfly is associated with rapid expansion and reorganization of its genome. Nature communications, 14(1), 8190.

Tung CC, et al. (2023) Single-cell transcriptomics unveils xylem cell development and evolution. Genome biology, 24(1), 3.

Fan C, et al. (2023) Temporal-frequency-phase feature classification using 3D-convolutional neural networks for motor imagery and movement. Frontiers in neuroscience, 17, 1250991.