

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 2026

GigaScience

RRID:SCR_006565

Type: Tool

Proper Citation

GigaScience (RRID:SCR_006565)

Resource Information

URL: <http://www.gigasciencejournal.com/>

Proper Citation: GigaScience (RRID:SCR_006565)

Description: An online open-access open-data journal, publishing "big-data" studies from the entire spectrum of life and biomedical sciences whose publication format links standard manuscript publication with its affiliated database, GigaDB, that hosts all associated data, provides data analysis tools, cloud-computing resources, and a DOI assignment to every dataset. GigaScience covers not just "omic" type data and the fields of high-throughput biology currently serviced by large public repositories, but also the growing range of more difficult-to-access data, such as imaging, neuroscience, ecology, cohort data, systems biology and other new types of large-scale sharable data. Supporting the open-data movement, they require that all supporting data and source code be publicly available in a suitable public repository and/or under a public domain CC0 license in the BGI GigaScience database. Using the BGI cloud as a test environment, they also consider open-source software tools / methods for the analysis or handling of large-scale data. When submitting a manuscript, please contact them if you have datasets or cloud applications you would like them to host. To maximize data usability submitters are encouraged to follow best practice for metadata reporting and are given the opportunity to submit in ISA-Tab format.

Abbreviations: GigaScience

Synonyms: Giga Science

Resource Type: service resource, data or information resource, data repository, database, storage service resource, journal article

Keywords: genomics, biomedical, biological, dna, genome, biotechnology, medicine, health, digital object identifier, data sharing

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

Resource Name: GigaScience

Resource ID: SCR_006565

Alternate IDs: OMICS_01834, nlx_71355

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260729T044137+0000

Ratings and Alerts

No rating or validation information has been found for GigaScience.

No alerts have been found for GigaScience.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Kim J, et al. (2024) Expansion of the HSP70 gene family in *Tegillarca granosa* and expression profiles in response to zinc toxicity. *Cell stress & chaperones*, 29(1), 97.

Xiao SZ, et al. (2019) Increased interactivity and improvements to the GigaScience database, GigaDB. *Database : the journal of biological databases and curation*, 2019.

Siu-Ting K, et al. (2019) Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. *Molecular biology and evolution*, 36(6), 1344.

Damas J, et al. (2018) Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. *Genome biology*, 19(1), 155.

Alomair AO, et al. (2018) Colonic Mucosal Microbiota in Colorectal Cancer: A Single-Center Metagenomic Study in Saudi Arabia. *Gastroenterology research and practice*, 2018, 5284754.

Va?eka L, et al. (2017) Stacked Autoencoders for the P300 Component Detection. *Frontiers in neuroscience*, 11, 302.

Dumontier M, et al. (2016) The health care and life sciences community profile for dataset descriptions. *PeerJ*, 4, e2331.

Arend D, et al. (2016) PGP repository: a plant phenomics and genomics data publication infrastructure. *Database : the journal of biological databases and curation*, 2016.

Yin W, et al. (2016) Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. *Nature communications*, 7, 13107.

Szalkai B, et al. (2016) Nucleotide 9-mers characterize the type II diabetic gut metagenome. *Genomics*, 107(4), 120.

Tracz V, et al. (2016) Towards an open science publishing platform. *F1000Research*, 5, 130.

Yu H, et al. (2016) Genome-wide identification and characterization of long intergenic noncoding RNAs and their potential association with larval development in the Pacific oyster. *Scientific reports*, 6, 20796.

Rocca-Serra P, et al. (2016) Data standards can boost metabolomics research, and if there is a will, there is a way. *Metabolomics : Official journal of the Metabolomic Society*, 12, 14.

González-Beltrán A, et al. (2015) From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. *PloS one*, 10(7), e0127612.

Shen X, et al. (2015) PAV markers in *Sorghum bicolor*: genome pattern, affected genes and pathways, and genetic linkage map construction. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 128(4), 623.

Salek RM, et al. (2015) COordination of Standards in MetabOlogicS (COSMOS): facilitating integrated metabolomics data access. *Metabolomics : Official journal of the Metabolomic Society*, 11(6), 1587.

Walker R, et al. (2015) Emerging trends in peer review-a survey. *Frontiers in neuroscience*, 9, 169.

Lin J, et al. (2014) Recommendations for the role of publishers in access to data. *PLoS biology*, 12(10), e1001975.

Kratz J, et al. (2014) Data publication consensus and controversies. *F1000Research*, 3, 94.

Appels R, et al. (2014) Advances in genome studies in plants and animals. *Functional & integrative genomics*, 14(1), 1.