

Resource Summary Report

Generated by [dkNET](#) on Aug 15, 2026

MariaDB

RRID:SCR_021763

Type: Tool

Proper Citation

MariaDB (RRID:SCR_021763)

Resource Information

URL: <https://mariadb.org/>

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Description: Open source relational database management system that is compatible drop in replacement for MySQL database technology. Includes selection of storage engines, including high performance storage engines, for working with other RDBMS data sources. Uses standard and popular querying language. Runs on number of operating systems and supports wide variety of programming languages. Modern Relational Database SQL on JSON support.

Abbreviations: RDBMS

Synonyms: MariaDB Server, Relational DataBase Management System

Resource Type: data or information resource, database

Keywords: Relational database, management system, MySQL replacement

Availability: Free, Available for download, Freely available

Resource Name: MariaDB

Resource ID: SCR_021763

License: GNU General Public License

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260815T182934+0000

Ratings and Alerts

No rating or validation information has been found for MariaDB.

No alerts have been found for MariaDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Baskaran SP, et al. (2026) sCentInDB: a database of essential oil chemical profiles of Indian medicinal plants. *Molecular diversity*, 30(1), 789.

Camerini L, et al. (2026) Harsh parenting and rs11621961 at the SERPINA6/1 locus: gene-environment interaction effects on hair cortisol in a Brazilian population-based longitudinal study. *Stress (Amsterdam, Netherlands)*, 29(1), 2611613.

Zeng J, et al. (2025) CancerSCEM 2.0: an updated data resource of single-cell expression map across various human cancers. *Nucleic acids research*, 53(D1), D1278.

Bobrovskikh AV, et al. (2025) Identification of Key Differentially Expressed Genes in *Arabidopsis thaliana* Under Short- and Long-Term High Light Stress. *International journal of molecular sciences*, 26(16).

Haruay S, et al. (2025) Amoebic Dysentery in Northeastern Thailand: Contributing Factors in Border Provinces (2019-2023). *Iranian journal of parasitology*, 20(2), 268.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Boileau E, et al. (2025) Sci-ModoM: a quantitative database of transcriptome-wide high-throughput RNA modification sites. *Nucleic acids research*, 53(D1), D310.

Gorczyca M, et al. (2024) 'Mother(Nature) knows best' - hijacking nature-designed transcriptional programs for enhancing stress resistance and protein production in *Yarrowia lipolytica*; presentation of YaliFunTome database. *Microbial cell factories*, 23(1), 26.

Conceição HB, et al. (2024) RCPedia: a global resource for studying and exploring retrocopies in diverse species. *Bioinformatics (Oxford, England)*, 40(9).

Chou RT, et al. (2024) Positive-unlabeled learning identifies vaccine candidate antigens in the malaria parasite *Plasmodium falciparum*. *NPJ systems biology and applications*, 10(1), 44.

Salihoglu R, et al. (2024) Cat-E: A comprehensive web tool for exploring cancer targeting strategies. *Computational and structural biotechnology journal*, 23, 1376.

Ichihara H, et al. (2023) Plant GARDEN: a portal website for cross-searching between different types of genomic and genetic resources in a wide variety of plant species. *BMC plant biology*, 23(1), 391.

Kakoulidis P, et al. (2023) Identifying and profiling structural similarities between Spike of SARS-CoV-2 and other viral or host proteins with Machaon. *Communications biology*, 6(1), 752.

Choi Y, et al. (2023) HGTTree v2.0: a comprehensive database update for horizontal gene transfer (HGT) events detected by the tree-reconciliation method. *Nucleic acids research*, 51(D1), D1010.

Jarvi S, et al. (2022) Numbers, characteristics, and medical complexity of children with life-limiting conditions reaching age of transition to adult care in England: a repeated cross-sectional study [version 1; peer review: 2 approved]. *NIHR open research*, 2, 27.

Surachat K, et al. (2022) aTAP: automated transcriptome analysis platform for processing RNA-seq data by de novo assembly. *Heliyon*, 8(8), e10255.

Surles-Zeigler MC, et al. (2022) Extending and using anatomical vocabularies in the stimulating peripheral activity to relieve conditions project. *Frontiers in neuroinformatics*, 16, 819198.

Kim J, et al. (2022) MRA Toolbox v. 1.0: a web-based toolbox for predicting mixture toxicity of chemical substances in chemical products. *Scientific reports*, 12(1), 8880.

Ko?cielniak P, et al. (2022) OakRootRNADB-a consolidated RNA-seq database for coding and noncoding RNA in roots of pedunculate oak (*Quercus robur*). *Database : the journal of biological databases and curation*, 2022.

Pike M, et al. (2022) TAFFIES: Tailored Automated Feedback Framework for Developing Integrated and Extensible Feedback Systems. *SN computer science*, 3(2), 159.