

Resource Summary Report

Generated by [T1D](#) on Aug 7, 2026

InterMine

RRID:SCR_001772

Type: Tool

Proper Citation

InterMine (RRID:SCR_001772)

Resource Information

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

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Description: An open source data warehouse system built for the integration and analysis of complex biological data that enables the creation of biological databases accessed by sophisticated web query tools. Parsers are provided for integrating data from many common biological data sources and formats, and there is a framework for adding data. InterMine includes a user-friendly web interface that works "out of the box" and can be easily customized for specific needs, as well as a powerful, scriptable web-service API to allow programmatic access to data.

Resource Type: software resource

Defining Citation: [PMID:24753429](#)

Keywords: mac os x, unix/linux, windows, java, bio.tools

Funding: Wellcome Trust

Availability: Free, Freely available

Resource Name: InterMine

Resource ID: SCR_001772

Alternate IDs: OMICS_03840, biotools:intermine

Alternate URLs: <https://github.com/intermine/intermine>, <https://bio.tools/intermine>

Old URLs: <http://intermine.github.io/intermine.org/>

License: GNU Lesser General Public License, v3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260801T190150+0000

Ratings and Alerts

No rating or validation information has been found for InterMine.

No alerts have been found for InterMine.

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 [T1D](#) .

Gadiya Y, et al. (2026) pyBiodatafuse: extending interoperability of data using modular queries across biomedical resources. Bioinformatics (Oxford, England), 42(3).

Gural B, et al. (2026) LocusPackRat: an R package to support prioritizing candidate genes from large GWAS intervals with standardized evidence aggregation. G3 (Bethesda, Md.), 16(6).

Gural B, et al. (2025) LocusPackRat: a Semi-Automated Framework for Prioritizing Candidate Genes from Large GWAS Intervals. bioRxiv : the preprint server for biology.

Roth L, et al. (2025) The FIP 1.0 Data Set: Highly resolved annotated image time series of 4,000 wheat plots grown in 6 years. GigaScience, 14.

Glaser-Schmitt A, et al. (2024) Pervasive tissue-, genetic background-, and allele-specific gene expression effects in Drosophila melanogaster. PLoS genetics, 20(8), e1011257.

Mansueto L, et al. (2024) Building a community-driven bioinformatics platform to facilitate Cannabis sativa multi-omics research. GigaByte (Hong Kong, China), 2024, gigabyte137.

Baldarelli RM, et al. (2024) Mouse Genome Informatics: an integrated knowledgebase system for the laboratory mouse. Genetics, 227(1).

, et al. (2022) Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 220(4).

De Jes??s-Kim L, et al. (2021) DDK regulates replication initiation by controlling the multiplicity of Cdc45-GINS binding to Mcm2-7. eLife, 10.

Ferreira-Neto JRC, et al. (2021) The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. Frontiers in plant science, 12, 667013.

Bastian FB, et al. (2021) The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. *Nucleic acids research*, 49(D1), D831.

Nowotarski SH, et al. (2021) Planarian Anatomy Ontology: a resource to connect data within and across experimental platforms. *Development (Cambridge, England)*, 148(15).

Sharma B, et al. (2021) Genome-wide analysis of HECT E3 ubiquitin ligase gene family in *Solanum lycopersicum*. *Scientific reports*, 11(1), 15891.

Shamimuzzaman M, et al. (2020) MaizeMine: A Data Mining Warehouse for the Maize Genetics and Genomics Database. *Frontiers in plant science*, 11, 592730.

Szymczak S, et al. (2020) DNA methylation QTL analysis identifies new regulators of human longevity. *Human molecular genetics*, 29(7), 1154.

Medeiros C, et al. (2020) Molecular diversity and genetic structure of *Saccharum* complex accessions. *PloS one*, 15(5), e0233211.

Wehrs M, et al. (2020) Investigation of Bar-seq as a method to study population dynamics of *Saccharomyces cerevisiae* deletion library during bioreactor cultivation. *Microbial cell factories*, 19(1), 167.

Halajyan A, et al. (2019) NetR and AttR, Two New Bioinformatic Tools to Integrate Diverse Datasets into Cytoscape Network and Attribute Files. *Genes*, 10(6).

Lonardi S, et al. (2019) The genome of cowpea (*Vigna unguiculata* [L.] Walp.). *The Plant journal : for cell and molecular biology*, 98(5), 767.

Chen YA, et al. (2019) Assessing drug target suitability using TargetMine. *F1000Research*, 8, 233.