Resource Summary Report

Generated by <u>NIF</u> on May 15, 2025

InterMine

RRID:SCR_001772 Type: Tool

Proper Citation

InterMine (RRID:SCR_001772)

Resource Information

URL: http://intermine.github.io/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: GNU Lesser General Public License, v2

Resource Name: InterMine

Resource ID: SCR_001772

Alternate IDs: OMICS_03840, biotools:intermine

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

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014038+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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

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

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

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

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

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

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).

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

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.

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

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

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).

Dharshini SAP, et al. (2019) Investigating the energy crisis in Alzheimer disease using transcriptome study. Scientific reports, 9(1), 18509.

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

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

Komkova D, et al. (2018) The InterMine Android app: Cross-organism genomic data in your pocket. F1000Research, 7, 1837.

Boldyreva LV, et al. (2017) Protein and Genetic Composition of Four Chromatin Types in Drosophila melanogaster Cell Lines. Current genomics, 18(2), 214.

Chen YA, et al. (2016) An integrative data analysis platform for gene set analysis and knowledge discovery in a data warehouse framework. Database : the journal of biological databases and curation, 2016.

Boussaha M, et al. (2015) Genome-Wide Study of Structural Variants in Bovine Holstein, Montbéliarde and Normande Dairy Breeds. PloS one, 10(8), e0135931.