

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 28, 2026

## FlyBase

RRID:SCR\_006549

Type: Tool

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### Proper Citation

FlyBase (RRID:SCR\_006549)

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### Resource Information

**URL:** <http://flybase.org/>

**Proper Citation:** FlyBase (RRID:SCR\_006549)

**Description:** Database of Drosophila genetic and genomic information with information about stock collections and fly genetic tools. Gene Ontology (GO) terms are used to describe three attributes of wild-type gene products: their molecular function, the biological processes in which they play a role, and their subcellular location. Additionally, FlyBase accepts data submissions. FlyBase can be searched for genes, alleles, aberrations and other genetic objects, phenotypes, sequences, stocks, images and movies, controlled terms, and Drosophila researchers using the tools available from the "Tools" drop-down menu in the Navigation bar.

**Abbreviations:** FB

**Synonyms:** flybase A Drosophila Genomic and Genetic Database, FlyBase: A Database of Drosophila Genes and Genomes, FLYBASE, FlyBase: A Database of Drosophila Genes & Genomes, FB

**Resource Type:** data or information resource, data repository, database, organism-related portal, portal, service resource, storage service resource, topical portal

**Defining Citation:** [PMID:24234449](#), [PMID:22127867](#), [PMID:18948289](#), [PMID:18641940](#), [PMID:18160408](#), [PMID:17099233](#), [PMID:16381917](#), [PMID:15608223](#), [PMID:12519974](#), [PMID:11752267](#), [PMID:11465064](#), [PMID:9847148](#), [PMID:9399806](#), [PMID:9045212](#), [PMID:8594600](#), [PMID:8578603](#), [PMID:7937045](#), [PMID:7925011](#)

**Keywords:** RIN, Resource Information Network, mutant, gene, genome, blast, genotype, phenotype, allele, sequence, stock, image, movie, controlled term, video resource, image collection, life-cycle, genome, expression, rna-seq, genetics, drosophilidae, bio.tools, FASEB list, RRID Community Authority

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MRC ;  
NIH Blueprint for Neuroscience Research ;  
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NSF

**Resource Name:** FlyBase

**Resource ID:** SCR\_006549

**Alternate IDs:** nif-0000-00558, r3d100010591, OMICS\_01649, biotools:flybase

**Alternate URLs:** <https://bio.tools/flybase>, <https://doi.org/10.17616/R3903Q>

**Old URLs:** <http://flybase.net>

**License:** Creative Commons Attribution 4.0 International License (CC BY 4.0)

**License URLs:**  
[https://wiki.flybase.org/wiki/FlyBase>About#FlyBase\\_Licenses\\_and\\_Availability](https://wiki.flybase.org/wiki/FlyBase>About#FlyBase_Licenses_and_Availability)

**Record Creation Time:** 20220129T080236+0000

**Record Last Update:** 20260821T193811+0000

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## Ratings and Alerts

No rating or validation information has been found for FlyBase.

No alerts have been found for FlyBase.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4234 mentions in open access literature.

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

Khamvongsa-Charbonnier L, et al. (2026) Metabolism fine tuning and cardiokines secretion represent adaptative responses of the heart to High Fat and High Sugar Diets in flies. PLoS genetics, 22(6), e1012189.

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the Drosophila brain. Cell genomics, 101125.

Yan Y, et al. (2026) The transformer gene controls sexual development in Drosophila suzukii. Insect science, 33(2), 547.

Low TCH, et al. (2026) The ORB2 RNA-binding protein negatively regulates its target transcripts during the Drosophila maternal-to-zygotic transition via its functionally conserved Zinc-binding "ZZ" domain. *Genetics*, 232(2).

Ho S, et al. (2026) Aub, Vasa, and Armi concentration in phase-separated nuage is dispensable for piRNA biogenesis and transposon silencing. *RNA (New York, N.Y.)*, 32(3), 341.

Leichter SM, et al. (2026) Polycomb misregulation in enterocytes drives tissue decline in the aging Drosophila intestine. *Genome research*, 36(1), 102.

Yang M, et al. (2026) Molecular evolution of octopamine receptors in Drosophila. *G3 (Bethesda, Md.)*, 16(2).

Tan FHP, et al. (2026) Geroprotective effects of Salvianolic acid A through redox and detoxification pathway activation in an aging Drosophila Alzheimer's model. *Biogerontology*, 27(1), 39.

Balagurov KI, et al. (2026) Beyond DNA binding: single C2H2 zinc fingers with adjacent ??-strands mediate dimerization in Drosophila transcription factors. *Nucleic acids research*, 54(1).

Dhakad P, et al. (2026) Comparative gene annotation and orthology assignments across 301 species of Drosophilidae. *PLoS biology*, 24(2), e3003663.

Jain R, et al. (2026) Insulin signaling engages divergent transcriptional mechanisms in neural and metabolic tissues. *BMC molecular and cell biology*, 27(1).

Cruz J, et al. (2026) Single-cell transcriptomics of X-ray irradiated Drosophila wing discs reveals heterogeneity related to cell-cycle status and cell location. *eLife*, 14.

Peaslee C, et al. (2026) Mapping whole-organism genetic comorbidities across model Species using unified ontologies. *Genetics*, 232(4).

Mundhe G, et al. (2026) Spatial patterning of contractility by a self-organized mechanogen activity gradient underlies Drosophila gastrulation. *Nature communications*, 17(1), 1721.

Marion SB, et al. (2026) Transposable elements contribute substantially to naturally occurring genetic lethality in Drosophila melanogaster. *PLoS biology*, 24(3), e3003467.

Crabtree A, et al. (2026) Stress-Encoded Mitochondrial Plasticity: ATF4 Control of Mega-Mitochondria and Nanotunnel Communication. *bioRxiv : the preprint server for biology*.

Yu YH, et al. (2026) CRM-TI: an enhanced pipeline for computationally assigning the target genes of cis-regulatory modules by considering comprehensive long-range regulation mechanisms. *BioData mining*, 19(1).

Daigle A, et al. (2026) The distribution of fitness effects of new mutations in regulatory regions of the D. melanogaster genome. *bioRxiv : the preprint server for biology*.

Turcotte CA, et al. (2026) Chromosome-specific differences in the recombination landscape of spontaneous meiotic nondisjunction. *Genetics*, 233(1).

Mouren JC, et al. (2026) Exonic enhancers are a widespread class of dual-function regulatory elements. *Nature communications*, 17(1).