

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

REDfly Regulatory Element Database for Drosophila

RRID:SCR_006790

Type: Tool

Proper Citation

REDfly Regulatory Element Database for Drosophila (RRID:SCR_006790)

Resource Information

URL: <http://redfly.ccr.buffalo.edu>

Proper Citation: REDfly Regulatory Element Database for Drosophila (RRID:SCR_006790)

Description: Curated collection of known Drosophila transcriptional cis-regulatory modules (CRMs) and transcription factor binding sites (TFBSs). Includes experimentally verified fly regulatory elements along with their DNA sequence, associated genes, and expression patterns they direct. Submission of experimentally verified cis-regulatory elements that are not included in REDfly database are welcome.

Abbreviations: REDfly

Synonyms: Regulatory Element Database for Drosophila, Regulatory Element Database

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

Defining Citation: [PMID:20965965](#), [PMID:18039705](#), [PMID:16303794](#)

Keywords: transcriptional cis-regulatory module, transcription factor binding site, dna sequence, gene, expression pattern, genome, gene expression, transcription factor, cis-regulatory module, bio.tools

Funding: NIGMS U24 GM144232;
NSF EF0843229

Availability: Acknowledgement requested

Resource Name: REDfly Regulatory Element Database for Drosophila

Resource ID: SCR_006790

Alternate IDs: OMICS_01870, biotools:redfly, nif-0000-03393

Alternate URLs: <https://bio.tools/redfly>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260829T182242+0000

Ratings and Alerts

No rating or validation information has been found for REDfly Regulatory Element Database for Drosophila.

No alerts have been found for REDfly Regulatory Element Database for Drosophila.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Alberti B, et al. (2025) Spatial-scERA: a method for reconstructing spatial single-cell enhancer activity in multicellular organisms. Nucleic acids research, 53(14).

Asma H, et al. (2024) Regulatory genome annotation of 33 insect species. eLife, 13.

Sabarís G, et al. (2024) The Density of Regulatory Information Is a Major Determinant of Evolutionary Constraint on Noncoding DNA in Drosophila. Molecular biology and evolution, 41(2).

Asma H, et al. (2021) Annotating the Insect Regulatory Genome. Insects, 12(7).

Small S, et al. (2020) Transcriptional Enhancers in Drosophila. Genetics, 216(1), 1.

Karageorgiou C, et al. (2020) The Cyclically Seasonal Drosophila subobscura Inversion O7 Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. Frontiers in genetics, 11, 565836.

Hall BS, et al. (2019) Identification of novel genes associated with longevity in Drosophila melanogaster - a computational approach. Aging, 11(23), 11244.

Rivera J, et al. (2019) REDfly: the transcriptional regulatory element database for Drosophila. Nucleic acids research, 47(D1), D828.

Symonenko AV, et al. (2018) Reduced Neuronal Transcription of Escargot, the Drosophila Gene Encoding a Snail-Type Transcription Factor, Promotes Longevity. Frontiers in genetics, 9, 151.

Seong KM, et al. (2017) Changes in Neuronal Signaling and Cell Stress Response Pathways are Associated with a Multigenic Response of *Drosophila melanogaster* to DDT Selection. *Genome biology and evolution*, 9(12), 3356.

Jiang P, et al. (2014) CCAT: Combinatorial Code Analysis Tool for transcriptional regulation. *Nucleic acids research*, 42(5), 2833.

Kim AR, et al. (2013) Rearrangements of 2.5 kilobases of noncoding DNA from the *Drosophila* even-skipped locus define predictive rules of genomic cis-regulatory logic. *PLoS genetics*, 9(2), e1003243.

Tsurumi A, et al. (2011) STAT is an essential activator of the zygotic genome in the early *Drosophila* embryo. *PLoS genetics*, 7(5), e1002086.

Leung G, et al. (2009) Identifying cis-regulatory sequences by word profile similarity. *PloS one*, 4(9), e6901.

Macdonald SJ, et al. (2006) Fine scale structural variants distinguish the genomes of *Drosophila melanogaster* and *D. pseudoobscura*. *Genome biology*, 7(7), R67.