

Resource Summary Report

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Berkeley Drosophila Genome Project

RRID:SCR_013094

Type: Tool

Proper Citation

Berkeley Drosophila Genome Project (RRID:SCR_013094)

Resource Information

URL: <http://www.fruitfly.org>

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Description: Database on the sequence of the euchromatic genome of *Drosophila melanogaster*. In addition to genomic sequencing, the BDGP is 1) producing gene disruptions using P element-mediated mutagenesis on a scale unprecedented in metazoans; 2) characterizing the sequence and expression of cDNAs; and 3) developing informatics tools that support the experimental process, identify features of DNA sequence, and allow us to present up-to-date information about the annotated sequence to the research community. Resources * Universal Proteomics Resource: Search for clones for expression and tissue culture * Materials: Request genomic or cDNA clones, library filters or fly stocks * Download Sequence data sets and annotations in fasta or xml format by http or ftp * Publications: Browse or download BDGP papers * Methods: BDGP laboratory protocols and vector maps * Analysis Tools: Search sequences for CRMs, promoters, splice sites, and gene predictions * Apollo: Genome annotation viewer and editor September 15, 2009 Illumina RNA-Seq data from 30 developmental time points of *D. melanogaster* has been submitted to the Short Read Archive at NCBI as part of the modENCODE project. The data set currently contains 2.2 billion single-end and paired reads and over 201 billion base pairs.

Abbreviations: BDGP, BDGP EST, BDGP INS

Resource Type: database, data or information resource

Defining Citation: [PMID:21177961](#)

Keywords: drosophila genome, cdna, est, transposon insertions, genomic sequencing, gene, FASEB list

Funding: NHGRI ;
NIGMS

Resource Name: Berkeley Drosophila Genome Project

Resource ID: SCR_013094

Alternate IDs: nif-0000-02867, r3d100010624

Alternate URLs: <http://www.bdgp.org/>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260808T190519+0000

Ratings and Alerts

No rating or validation information has been found for Berkeley Drosophila Genome Project.

No alerts have been found for Berkeley Drosophila Genome Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 478 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Wu P, et al. (2026) A novel TetR-type repressor directly modulates precursor supply and utilization for erythromycin biosynthesis. Synthetic and systems biotechnology, 13, 132.

Kokubo S, et al. (2026) Tomato lipocalins mediate ABA (abscisic acid)- and ethylene-dependent regulation of stress tolerance and fruit ripening. Plant biotechnology (Tokyo, Japan), 43(1), 61.

Dong Y, et al. (2026) Unravelling the progression of the zebrafish primary body axis with reconstructed spatiotemporal transcriptomics. Genome biology, 27(1), 11.

You Q, et al. (2025) Splicing Analysis of Exonic TSC1 and TSC2 Gene Variants Causing Tuberous Sclerosis Complex. Human mutation, 2025, 1497712.

Zhou S, et al. (2025) Identification and functional characteristics of a novel splice site variant in L1CAM caused X-linked hydrocephalus. Frontiers in genetics, 16, 1588709.

Liu Z, et al. (2025) Cloning and Transcriptional Activity Analysis of the Bovine CDH11 Gene Promoter: Transcription Factors Sp1 and GR Regulate Bovine CDH11 Expression. Animals : an open access journal from MDPI, 15(9).

Zhang B, et al. (2025) Identified five variants in CFTR gene that alter RNA splicing by minigene assay. Frontiers in genetics, 16, 1543623.

Wang H, et al. (2025) An insect symbiotic virus promotes the transmission of a phytoarbovirus via inhibiting E3 ubiquitin ligase Sina. *PLoS pathogens*, 21(5), e1013178.

Qiao D, et al. (2025) Three intronic variants altering RNA splicing were identified in the CLCN5 gene by minigene assay. *BMC medical genomics*, 18(1), 158.

Coba-Males MA, et al. (2025) Identification of transposable elements and satellite DNA in the Neotropical species *Drosophila amaguana* from the Ecuadorian Andean Forests. *PLoS one*, 20(12), e0337390.

Li H, et al. (2025) A comprehensive splicing characterization of COL4A5 mutations and prognostic significance in a single cohort with X-linked alport syndrome. *Frontiers in genetics*, 16, 1564343.

Shao Y, et al. (2025) Identifying six single nucleotide variants in the COL17A1 gene that alter RNA splicing: database analysis and minigene assays. *Scientific reports*, 15(1), 11387.

Mikami K, et al. (2025) A fast in situ hybridization chain reaction method in *Drosophila* embryos and ovaries. *Fly*, 19(1), 2428499.

Ye M, et al. (2024) Promoter engineering enables precise metabolic regulation towards efficient ??-elemene production in *Ogataea polymorpha*. *Synthetic and systems biotechnology*, 9(2), 234.

Bruhn H, et al. (2024) Novel Synonymous and Deep Intronic Variants Causing Primary and Secondary Pyruvate Dehydrogenase Complex Deficiency. *Human mutation*, 2024, 1611838.

Zhang XY, et al. (2024) COG6-CDG: Two Novel Variants and Milder Phenotype in a Chinese Patient. *Human mutation*, 2024, 9857442.

Shao LN, et al. (2024) Characterization of a novel AEL allele harboring a c.28 + 5G>A mutation on the ABO*A2.01 background: a study utilizing PacBio third-generation sequencing and functional assays. *Frontiers in immunology*, 15, 1396426.

Pan F, et al. (2024) Three exonic variants in the PHEX gene cause aberrant splicing in a minigene assay. *Frontiers in genetics*, 15, 1353674.

Hu M, et al. (2023) Identification of an Arylnaphthalene Lignan Derivative as an Inhibitor against Dengue Virus Serotypes 1 to 4 (DENV-1 to -4) Using a Newly Developed DENV-3 Infectious Clone and Replicon. *Microbiology spectrum*, 11(4), e0042323.

Huang Y, et al. (2023) MIGGRI: A multi-instance graph neural network model for inferring gene regulatory networks for *Drosophila* from spatial expression images. *PLoS computational biology*, 19(11), e1011623.