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: data or information resource, database

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

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

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250508T065434+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 457 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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.

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.

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.

Li X, et al. (2023) Double Hyperautofluorescence Rings as a Sign of CFAP410-related Retinopathy. Investigative ophthalmology & visual science, 64(15), 44.

Wang P, et al. (2023) Missense Mutations in MAB21L1: Causation of Novel Autosomal Dominant Ocular BAMD Syndrome. Investigative ophthalmology & visual science, 64(3), 19.

Wen X, et al. (2023) A detoxification pathway initiated by a nuclear receptor TcHR96h in Tetranychus cinnabarinus (Boisduval). PLoS genetics, 19(9), e1010911.

Bertani-Torres W, et al. (2023) Waardenburg Syndrome: The Contribution of Next-Generation Sequencing to the Identification of Novel Causative Variants. Audiology research, 14(1), 9.

Shi X, et al. (2023) Minigene splicing assays reveal new insights into exonic variants of the SLC12A3 gene in Gitelman syndrome. Molecular genetics & genomic medicine, 11(4), e2128.

Wang Y, et al. (2023) Genetic and clinical landscape of ARR3-associated MYP26: the most common cause of Mendelian early-onset high myopia with a unique inheritance. The British journal of ophthalmology, 107(10), 1545.

Fisher WW, et al. (2023) A modERN resource: identification of Drosophila transcription factor candidate target genes using RNAi. Genetics, 223(4).

Wang Y, et al. (2022) Different Phenotypes Represent Advancing Stages of ABCA4-Associated Retinopathy: A Longitudinal Study of 212 Chinese Families From a Tertiary Center. Investigative ophthalmology & visual science, 63(5), 28.

Wu S, et al. (2022) Internal Transcription Terminators Control Stoichiometry of ABC Transporters in Cellulolytic Clostridia. Microbiology spectrum, 10(2), e0165621.

Emtenani S, et al. (2022) Macrophage mitochondrial bioenergetics and tissue invasion are boosted by an Atossa-Porthos axis in Drosophila. The EMBO journal, 41(12), e109049.

Sharrock TE, et al. (2022) Different temporal requirements for tartan and wingless in the formation of contractile interfaces at compartmental boundaries. Development (Cambridge, England), 149(21).

Mulyanti D, et al. (2021) Insertion of prpoD_rpoS fragment enhances expression of recombinant protein by dps auto-inducible promoter in Escherichia coli. Molecular biology reports, 48(8), 5833.

Wang P, et al. (2021) An Early Diagnostic Clue for COL18A1- and LAMA1-Associated Diseases: High Myopia With Alopecia Areata in the Cranial Midline. Frontiers in cell and developmental biology, 9, 644947.

Jiang Y, et al. (2021) Novel BMP4 Truncations Resulted in Opposite Ocular Anomalies: Pathologic Myopia Rather Than Microphthalmia. Frontiers in cell and developmental biology, 9, 769636.

Yi Z, et al. (2021) Novel variants in GUCY2D causing retinopathy and the genotype-phenotype correlation. Experimental eye research, 208, 108637.