

Resource Summary Report

Generated by [NIF](#) on Aug 1, 2026

DGRP-189

RRID:BDSC_28152

Type: Organism

Proper Citation

RRID:BDSC_28152

Organism Information

URL: <https://n2t.net/bdsc:28152>

Proper Citation: RRID:BDSC_28152

Description: Drosophila melanogaster with name DGRP-189 from BDSC.

Species: Drosophila melanogaster

Notes: Drosophila Genetic Reference Panel strain - sequenced isogenic reference wild type strain (aka 'Raleigh' or 'Mackay' line). Donor: Trudy Mackay, North Carolina State University

Genomic Alteration: Chromosome wt

Catalog Number: 28152

Database: Bloomington Drosophila Stock Center (BDSC)

Database Abbreviation: BDSC

Availability: available

Alternate IDs: BDSC_28152, BL28152

Organism Name: DGRP-189

Record Creation Time: 20240911T222452+0000

Record Last Update: 20260725T195205+0000

Ratings and Alerts

No rating or validation information has been found for DGRP-189.

No alerts have been found for DGRP-189.

Data and Source Information

Source: [Integrated Animals](#)

Source Database: Bloomington Drosophila Stock Center (BDSC)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Sato DX, et al. (2025) Multifaceted and extensive behavioral trajectories of genomically diverse Drosophila lines. Scientific data, 12(1), 400.

Yamamoto A, et al. (2024) The genetic basis of variation in Drosophila melanogaster mating behavior. iScience, 27(5), 109837.

Spierer AN, et al. (2021) Natural variation in the regulation of neurodevelopmental genes modifies flight performance in Drosophila. PLoS genetics, 17(3), e1008887.

Patel SP, et al. (2021) Identification of genetic modifiers of lifespan on a high sugar diet in the Drosophila Genetic Reference Panel. Heliyon, 7(6), e07153.

Kurmangaliyev YZ, et al. (2020) Transcriptional Programs of Circuit Assembly in the Drosophila Visual System. Neuron, 108(6), 1045.

Everett LJ, et al. (2020) Gene expression networks in the Drosophila Genetic Reference Panel. Genome research, 30(3), 485.