

Resource Summary Report

Generated by T1D on Sep 6, 2026

Df(1)Sxl-bt, y[1]/Binsinscy

RRID:BDSC_3196

Type: Organism

Proper Citation

RRID:BDSC_3196

Organism Information

URL: <https://n2t.net/bdsc:3196>

Proper Citation: RRID:BDSC_3196

Description: Drosophila melanogaster with name Df(1)Sxl-bt, y[1]/Binsinscy from BDSC.

Species: Drosophila melanogaster

Notes: Donor: Thomas Cline, University of California, Berkeley

Affected Gene: CG12541, CG1958, CG2059, CG3032, CG4593, CG4607, CG4615, CG4617, CG8300, cm, Cph, fz4, Inx2, Inx7, lncRNA:CR43837, lncRNA:CR44357, lncRNA:CR45532, lncRNA:CR46245, lncRNA:CR46494, lncRNA:lol, mir-4956, moat, nullo, ogre, sloth1, sloth2, Sxl, unc-119, ZC3H18, y

Genomic Alteration: Chromosome 1

Catalog Number: 3196

Database: Bloomington Drosophila Stock Center (BDSC)

Database Abbreviation: BDSC

Availability: available

Alternate IDs: BDSC_3196, BDSC:3196, BL3196

Organism Name: Df(1)Sxl-bt, y[1]/Binsinscy

Record Creation Time: 20240911T222136+0000

Record Last Update: 20260905T135747+0000

Ratings and Alerts

No rating or validation information has been found for Df(1)Sxl-bt, y[1]/Binsinscy.

No alerts have been found for Df(1)Sxl-bt, y[1]/Binsinscy.

Data and Source Information

Source: [Integrated Animals](#)

Source Database: Bloomington Drosophila Stock Center (BDSC)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Ribeiro V, et al. (2026) Genome-wide screen for deficiencies modifying Cyclin G-induced developmental instability in *Drosophila melanogaster*. *Genetics*, 232(3).

Messer CL, et al. (2025) A deficiency screen of the X chromosome for Rap1 GTPase dominant interacting genes in *Drosophila* border cell migration. *G3* (Bethesda, Md.), 15(5).

Hammond M, et al. (2020) fs(1)A13041 is a 5' UTR deletion of the essential gene small ovary in *Drosophila*. *microPublication biology*, 2020.

Li X, et al. (2020) The Mediator CDK8-Cyclin C complex modulates Dpp signaling in *Drosophila* by stimulating Mad-dependent transcription. *PLoS genetics*, 16(5), e1008832.

Sawyer JK, et al. (2020) Exploiting codon usage identifies intensity-specific modifiers of Ras/MAPK signaling in vivo. *PLoS genetics*, 16(12), e1009228.