Resource Summary Report

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HMS Drosophila RNAi Screening Center

RRID:SCR_009794
Type: Tool

Proper Citation

HMS Drosophila RNAi Screening Center (RRID:SCR_009794)

Resource Information

URL: http://harvard.eagle-i.net/i/0000012d-4d06-be70-2162-17a280000000

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Description: Core facility that provides the following services: Drosophila genome-wide and focused cell-based RNAi libraries, Custom synthesis of double-stranded RNAs for Drosophila cell-based RNAi.

The DRSC facilitates genome-wide and related cell-based screening at our state-of-the-art facility. Since our beginnings in 2003, we have successfully guided screeners through the process, including help with assay development and optimization, data and image analysis, and planning of follow-up assays. Screens performed at the DRSC have resulted in an impressive number of publications on a wide range of topics in high-profile journals.

Resource Type: core facility, service resource, access service resource

Keywords: rnai screening

Funding:

Resource Name: HMS Drosophila RNAi Screening Center

Resource ID: SCR_009794

Alternate IDs: nlx_156261

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

Record Creation Time: 20220129T080254+0000

Record Last Update: 20250508T065243+0000

Ratings and Alerts

No rating or validation information has been found for HMS Drosophila RNAi Screening Center.

No alerts have been found for HMS Drosophila RNAi Screening Center.

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 dkNET.

Merigliano C, et al. (2024) "Off-pore" nucleoporins relocalize heterochromatic breaks through phase separation. bioRxiv : the preprint server for biology.

Fellmeth JE, et al. (2023) A dynamic population of prophase CENP-C is required for meiotic chromosome segregation. PLoS genetics, 19(11), e1011066.

Zirin J, et al. (2015) Regulators of autophagosome formation in Drosophila muscles. PLoS genetics, 11(2), e1005006.

Sopko R, et al. (2015) A systems-level interrogation identifies regulators of Drosophila blood cell number and survival. PLoS genetics, 11(3), e1005056.

Jafari S, et al. (2015) Cis-regulatory mechanisms for robust olfactory sensory neuron class-restricted odorant receptor gene expression in Drosophila. PLoS genetics, 11(3), e1005051.

Jang BY, et al. (2015) Role of Drosophila EDEMs in the degradation of the alpha-1-antitrypsin Z variant. International journal of molecular medicine, 35(4), 870.

Liu Y, et al. (2015) EHFPI: a database and analysis resource of essential host factors for pathogenic infection. Nucleic acids research, 43(Database issue), D946.

Lee JE, et al. (2015) Drosophila melanogaster activating transcription factor 4 regulates glycolysis during endoplasmic reticulum stress. G3 (Bethesda, Md.), 5(4), 667.

Perkins AD, et al. (2014) The systematic identification of cytoskeletal genes required for Drosophila melanogaster muscle maintenance. Scientific data, 1, 140002.

Bohla D, et al. (2014) A functional insulator screen identifies NURF and dREAM components to be required for enhancer-blocking. PloS one, 9(9), e107765.

Sanchez-Alvarez M, et al. (2014) Signaling networks converge on TORC1-SREBP activity to promote endoplasmic reticulum homeostasis. PloS one, 9(7), e101164.

Zacharogianni M, et al. (2014) A stress assembly that confers cell viability by preserving ERES components during amino-acid starvation. eLife, 3.

Pereira AM, et al. (2014) Plasticity of the MAPK signaling network in response to mechanical stress. PloS one, 9(7), e101963.

Flockhart IT, et al. (2012) FlyRNAi.org--the database of the Drosophila RNAi screening center: 2012 update. Nucleic acids research, 40(Database issue), D715.

Contrino S, et al. (2012) modMine: flexible access to modENCODE data. Nucleic acids research, 40(Database issue), D1082.