

Resource Summary Report

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[FlyTF.org](#)

RRID:SCR_004123

Type: Tool

Proper Citation

FlyTF.org (RRID:SCR_004123)

Resource Information

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

Proper Citation: FlyTF.org (RRID:SCR_004123)

Description: A database of genomic and protein data for Drosophila site-specific transcription factors.

Abbreviations: FlyTF

Synonyms: FlyTF.org - The Drosophila Transcription Factor Database

Resource Type: data or information resource, database

Defining Citation: [PMID:16613907](#)

Keywords: transcription factor, gene, annotation, genome, protein

Availability: The community can contribute to this resource, Acknowledgement requested

Resource Name: FlyTF.org

Resource ID: SCR_004123

Alternate IDs: OMICS_00534

Record Creation Time: 20220129T080222+0000

Record Last Update: 20260729T044054+0000

Ratings and Alerts

No rating or validation information has been found for FlyTF.org.

No alerts have been found for FlyTF.org.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Tang JLY, et al. (2022) NanoDam identifies Homeobrain (ARX) and Scarecrow (NKX2.1) as conserved temporal factors in the Drosophila central brain and visual system. *Developmental cell*, 57(9), 1193.

Arguello JR, et al. (2021) Targeted molecular profiling of rare olfactory sensory neurons identifies fate, wiring, and functional determinants. *eLife*, 10.

Ouma WZ, et al. (2018) Topological and statistical analyses of gene regulatory networks reveal unifying yet quantitatively different emergent properties. *PLoS computational biology*, 14(4), e1006098.

Alyagor I, et al. (2018) Combining Developmental and Perturbation-Seq Uncovers Transcriptional Modules Orchestrating Neuronal Remodeling. *Developmental cell*, 47(1), 38.

Wessels HH, et al. (2016) The mRNA-bound proteome of the early fly embryo. *Genome research*, 26(7), 1000.

Nitta KR, et al. (2015) Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. *eLife*, 4.

Parrish JZ, et al. (2014) Kr^{ppel} mediates the selective rebalancing of ion channel expression. *Neuron*, 82(3), 537.

Jafari S, et al. (2012) Combinatorial activation and repression by seven transcription factors specify Drosophila odorant receptor expression. *PLoS biology*, 10(3), e1001280.

Xie W, et al. (2012) Tissue-specific transcriptome profiling of *Plutella xylostella* third instar larval midgut. *International journal of biological sciences*, 8(8), 1142.

Garcia M, et al. (2011) Lateral gene expression in Drosophila early embryos is supported by Grainyhead-mediated activation and tiers of dorsally-localized repression. *PloS one*, 6(12), e29172.

Charoensawan V, et al. (2010) Genomic repertoires of DNA-binding transcription factors across the tree of life. *Nucleic acids research*, 38(21), 7364.

Wilson D, et al. (2008) DBD--taxonomically broad transcription factor predictions: new content and functionality. *Nucleic acids research*, 36(Database issue), D88.