

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

[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: 20260912T200130+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 [SPARC SAWG](#) .

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.