# 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:** database, data or information resource

**Defining Citation:** PMID:16613907

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

**Funding:**

**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:** 20250519T204647+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 dkNET.


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) Krüppel 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.