Resource Summary Report

Generated by NIF on Apr 16, 2025

FlyFactorSurvey

RRID:SCR_002113
Type: Tool

Proper Citation

FlyFactorSurvey (RRID:SCR_002113)

Resource Information

URL: http://pgfe.umassmed.edu/ffs/

Proper Citation: FlyFactorSurvey (RRID:SCR_002113)

Description: Database of Drosophila transcription factor DNA binding specificity using the bacterial one-hybrid method, DNase I or SELEX methods. The database provides community access to recognition motifs and position weight matrices for transcription factors (TFs), including many unpublished motifs. Search tools and flat file downloads are provided to retrieve binding site information (as sequences, matrices and sequence logos) for individual TFs, groups of TFs or for all TFs with characterized binding specificities. Linked analysis tools allow users to identify motifs within the database that share similarity to a query matrix or to view the distribution of occurrences of an individual motif throughout the Drosophila genome. This database and its associated tools provide computational and experimental biologists with resources to predict interactions between Drosophila TFs and target cis-regulatory sequences.

Abbreviations: FlyFactorSurvey

Resource Type: database, data or information resource

Defining Citation: PMID:21097781

Keywords: transcription factor, motif, cis-regulatory module, transcription factor binding site, bio.tools

Funding: NHGRI 1R01HG005287-01A1

Resource Name: FlyFactorSurvey

Resource ID: SCR_002113

Alternate IDs: biotools:flyfactorsurvey, OMICS_01879

Alternate URLs: https://bio.tools/flyfactorsurvey

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250412T054650+0000

Ratings and Alerts

No rating or validation information has been found for FlyFactorSurvey.

No alerts have been found for FlyFactorSurvey.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Poupault C, et al. (2021) A combinatorial cis-regulatory logic restricts color-sensing Rhodopsins to specific photoreceptor subsets in Drosophila. PLoS genetics, 17(6), e1009613.

Yamada TG, et al. (2020) Identification of a master transcription factor and a regulatory mechanism for desiccation tolerance in the anhydrobiotic cell line Pv11. PloS one, 15(3), e0230218.

Ma Y, et al. (2019) Changes in chromatin accessibility ensure robust cell cycle exit in terminally differentiated cells. PLoS biology, 17(9), e3000378.

Kapheim KM, et al. (2019) Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: Nomia melanderi). G3 (Bethesda, Md.), 9(3), 625.

Park J, et al. (2019) Dissecting the sharp response of a canonical developmental enhancer reveals multiple sources of cooperativity. eLife, 8.

Shokri L, et al. (2019) A Comprehensive Drosophila melanogaster Transcription Factor Interactome. Cell reports, 27(3), 955.

Zandvakili A, et al. (2018) Degenerate Pax2 and Senseless binding motifs improve detection of low-affinity sites required for enhancer specificity. PLoS genetics, 14(4), e1007289.

Vincent BJ, et al. (2018) Hunchback is counter-repressed to regulate even-skipped stripe 2 expression in Drosophila embryos. PLoS genetics, 14(9), e1007644.

Vizcaya-Molina E, et al. (2018) Damage-responsive elements in Drosophila regeneration. Genome research, 28(12), 1852.

Wang X, et al. (2018) Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection. Molecular biology and evolution, 35(8), 1958.

Neto M, et al. (2017) Nuclear receptors connect progenitor transcription factors to cell cycle control. Scientific reports, 7(1), 4845.

Castro-Mondragon JA, et al. (2017) RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections. Nucleic acids research, 45(13), e119.

Khoueiry P, et al. (2017) Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. eLife, 6.

Ribeiro L, et al. (2017) Evolution and multiple roles of the Pancrustacea specific transcription factor zelda in insects. PLoS genetics, 13(7), e1006868.

Koenecke N, et al. (2016) Genome-wide identification of Drosophila dorso-ventral enhancers by differential histone acetylation analysis. Genome biology, 17(1), 196.

Stroebele E, et al. (2016) Integration of Orthogonal Signaling by the Notch and Dpp Pathways in Drosophila. Genetics, 203(1), 219.

Ma X, et al. (2015) Reliable scaling of position weight matrices for binding strength comparisons between transcription factors. BMC bioinformatics, 16, 265.

Sun BF, et al. (2015) Regulation of transcription factors on sexual dimorphism of fig wasps. Scientific reports, 5, 10696.

Nadimpalli S, et al. (2015) Pervasive variation of transcription factor orthologs contributes to regulatory network evolution. PLoS genetics, 11(3), e1005011.

Persikov AV, et al. (2015) A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. Nucleic acids research, 43(3), 1965.