

Resource Summary Report

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[AnimalTFDB](#)

RRID:SCR_001624

Type: Tool

Proper Citation

AnimalTFDB (RRID:SCR_001624)

Resource Information

URL: <http://www.bioguo.org/AnimalTFDB/>

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Description: A comprehensive transcription factor (TF) database in which they identified and classified all the genome-wide TFs in 50 sequenced animal genomes (Ensembl release version 60). In addition to TFs, it also collects transcription co-factors and chromatin remodeling factors of those genomes, which play regulatory roles in transcription. Here they defined the TFs as proteins containing a sequence-specific DNA-binding domain (DBD) and regulating target gene expression. Currently, the AnimalTFDB classifies all the animal TFs into 72 families according to their conserved DBDs. Gene lists of transcription factors, transcription co-factors and chromatin remodeling factors of each species are available for downloading., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: AnimalTFDB

Synonyms: Animal Transcription Factor Database

Resource Type: database, data or information resource

Defining Citation: [PMID:22080564](#)

Keywords: transcription factor, dna-binding domain, transcription co-factor, chromatin remodeling factor, gene structure, functional domain, go annotation, protein interaction, ortholog, paralog, 3d structure, pathway, protein-protein interaction, binding site, target, data set, image collection, 3d spatial image, bio.tools, FASEB list

Funding: Huazhong University of Science and Technology; Wuhan; China ; Fundamental Research Funds for the Central Universities 2010MS045; National Natural Science Foundation of China 31171271

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AnimalTFDB

Resource ID: SCR_001624

Alternate IDs: nlx_153892, OMICS_01856, biotools:animal_tfdb

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

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260821T042529+0000

Ratings and Alerts

No rating or validation information has been found for AnimalTFDB.

No alerts have been found for AnimalTFDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 292 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Choudhury PR, et al. (2026) Atorvastatin pre-exposure in hypercholesterolemia remedies 27HC mediated dendritic cell dysfunctions in triple-negative breast cancer. Molecular therapy. Oncology, 34(3), 201250.

Yang S, et al. (2025) Exogenous TSG-6 treatment alleviates DSS-induced colitis in mice by modulating Pou2f3 and promoting tuft cells differentiation. Molecular medicine (Cambridge, Mass.), 31(1), 157.

Emili E, et al. (2025) Allometry of cell types in planarians by single-cell transcriptomics. Science advances, 11(19), eadm7042.

Shi Y, et al. (2025) Multi-omics exploration of CAV1+ tumor epithelial subcelltype in oral squamous cell carcinoma and its impact on the immune microenvironment. Discover oncology, 16(1), 1006.

Salamanca-D??az DA, et al. (2025) The Hydractinia cell atlas reveals cellular and molecular principles of cnidarian coloniality. Nature communications, 16(1), 2121.

Jiang C, et al. (2025) Telomere-to-telomere reference genome of Rhinogobio nasutus, an endangered endemic fish from the Yellow River. Scientific data, 12(1), 462.

Li L, et al. (2025) Spatiotemporal single-cell architecture of gene expression in the Caenorhabditis elegans germ cells. Cell discovery, 11(1), 26.

- Yu Z, et al. (2025) Analysis of post-transcriptional regulatory signatures and immune cell subsets in premature ovarian insufficiency based on full-length transcriptome. *Scientific reports*, 15(1), 5533.
- Ahn J, et al. (2025) Evolutionary lineage-specific genomic imprinting at the ZNF791 locus. *PLoS genetics*, 21(1), e1011532.
- Wang S, et al. (2025) Single-cell transcriptomic analysis of the senescent microenvironment in bone metastasis. *Cell proliferation*, 58(1), e13743.
- Yang ZZ, et al. (2025) DCAF13-mediated K63-linked ubiquitination of RNA polymerase I promotes uncontrolled proliferation in Breast Cancer. *Nature communications*, 16(1), 557.
- Zhang G, et al. (2025) TRAPT: a multi-stage fused deep learning framework for predicting transcriptional regulators based on large-scale epigenomic data. *Nature communications*, 16(1), 3611.
- Li B, et al. (2025) Zygotic activation of transposable elements during zebrafish early embryogenesis. *Nature communications*, 16(1), 3692.
- Jie M, et al. (2025) Single cell RNA sequencing analysis of mice hindlimb muscles identifies transcriptional heterogeneity in aging and physical frailty. *Scientific reports*, 15(1), 24828.
- Liu H, et al. (2025) ScRNA-seq combined with ATAC-seq analysis to explore the metabolic balance mechanism of CCl4-induced liver inflammatory injury. *Frontiers in immunology*, 16, 1600685.
- Arreola-Aldape CA, et al. (2025) A systematic review and functional in-silico analysis of genes and variants associated with amyotrophic lateral sclerosis. *Frontiers in neuroscience*, 19, 1598336.
- Loaiza-Moss J, et al. (2025) Transcriptome Analysis Suggests PKD3 Regulates Proliferative Glucose Metabolism, Calcium Homeostasis and Microtubule Dynamics After MEF Spontaneous Immortalization. *International journal of molecular sciences*, 26(2).
- Alexandre PA, et al. (2025) A high-resolution bovine mitochondrial co-expression network. *Biology open*, 14(2).
- Colt ME, et al. (2025) Male caregiving experience alters hippocampal neuroplasticity and transcription independent of reproduction in a biparental species. *Communications biology*, 8(1), 1212.
- O'Grady JF, et al. (2025) Integrative genomics sheds light on the immunogenetics of tuberculosis in cattle. *Communications biology*, 8(1), 479.