

Resource Summary Report

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TRANSFAC

RRID:SCR_005620

Type: Tool

Proper Citation

TRANSFAC (RRID:SCR_005620)

Resource Information

URL: <http://www.gene-regulation.com/pub/databases.html#transfac>

Proper Citation: TRANSFAC (RRID:SCR_005620)

Description: Manually curated database of eukaryotic transcription factors, their genomic binding sites and DNA binding profiles. Used to predict potential transcription factor binding sites.

Abbreviations: TRANSFAC

Resource Type: data or information resource, database

Defining Citation: [PMID:12520026](#)

Keywords: Curated, eucaryotic, transcription, factor, genomic, binding, site, sequence, regulated, gene, bio.tools

Funding: European Commission ;
German Ministry of Education and Research

Availability: Free, Freely available

Resource Name: TRANSFAC

Resource ID: SCR_005620

Alternate IDs: biotools:transfac, nif-0000-03576

Alternate URLs: <http://www.biobase-international.com/pages/index.php?id=transfac>,
<http://gene-regulation.com/pub/databases.html>, <https://bio.tools/transfac>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260729T044126+0000

Ratings and Alerts

No rating or validation information has been found for TRANSFAC.

No alerts have been found for TRANSFAC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 261 mentions in open access literature.

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

Lu YY, et al. (2025) High APEX1 Expression Facilitates Osteosarcoma Cell Proliferation. Asian Pacific journal of cancer prevention : APJCP, 26(2), 453.

Subedi A, et al. (2024) Nerve injury inhibits Oprd1 and Cnr1 transcription through REST in primary sensory neurons. Scientific reports, 14(1), 26612.

Modahl CM, et al. (2024) Distinct regulatory networks control toxin gene expression in elapid and viperid snakes. BMC genomics, 25(1), 186.

Hariprakash JM, et al. (2024) Leveraging Tissue-Specific Enhancer-Target Gene Regulatory Networks Identifies Enhancer Somatic Mutations That Functionally Impact Lung Cancer. Cancer research, 84(1), 133.

Qi LF, et al. (2024) Ginsenoside Rg3 Restores Mitochondrial Cardiolipin Homeostasis via GRB2 to Prevent Parkinson's Disease. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(39), e2403058.

Husso A, et al. (2023) Impacts of maternal microbiota and microbial metabolites on fetal intestine, brain, and placenta. BMC biology, 21(1), 207.

Florentin J, et al. (2022) Loss of Amphiregulin drives inflammation and endothelial apoptosis in pulmonary hypertension. Life science alliance, 5(11).

Li HT, et al. (2022) Characterizing DNA methylation signatures of retinoblastoma using aqueous humor liquid biopsy. Nature communications, 13(1), 5523.

Raji Sathyan K, et al. (2022) Antiviral radical SAM enzyme viperin homologue from Asian seabass (*Lates calcarifer*): Molecular characterisation and expression analysis. Developmental and comparative immunology, 136, 104499.

Han S, et al. (2021) Proneural genes define ground-state rules to regulate neurogenic patterning and cortical folding. Neuron, 109(18), 2847.

Kim SS, et al. (2021) Transcription Factor HSF1 Suppresses the Expression of Surfactant Protein D in Cells Infected with *Aspergillus fumigatus*. Pathogens (Basel, Switzerland),

10(6).

Aladdin A, et al. (2021) The baculovirus promoter OpIE2 sequence has inhibitory effect on the activity of the cytomegalovirus (CMV) promoter in HeLa and HEK-293 T cells. *Gene*, 781, 145541.

Hefzy EM, et al. (2021) miR-155 T/A (rs767649) and miR-146a A/G (rs57095329) single nucleotide polymorphisms as risk factors for chronic hepatitis B virus infection among Egyptian patients. *PloS one*, 16(8), e0256724.

Daley EJ, et al. (2021) β -Catenin mediates glucose-dependent insulinotropic polypeptide increases in lysyl oxidase expression in osteoblasts. *Bone reports*, 14, 101063.

Vrettou M, et al. (2021) DNA methylation of Vesicular Glutamate Transporters in the mesocorticolimbic brain following early-life stress and adult ethanol exposure-an explorative study. *Scientific reports*, 11(1), 15322.

Su Y, et al. (2021) Identification of genes, pathways and transcription factor-miRNA-target gene networks and experimental verification in venous thromboembolism. *Scientific reports*, 11(1), 16352.

Haeussler S, et al. (2021) Genome-wide RNAi screen for regulators of UPRmt in *Caenorhabditis elegans* mutants with defects in mitochondrial fusion. *G3 (Bethesda, Md.)*, 11(7).

Mueller RC, et al. (2021) A high-quality genome and comparison of short- versus long-read transcriptome of the palaeartic duck *Aythya fuligula* (tufted duck). *GigaScience*, 10(12).

Zhang X, et al. (2021) Prioritization of Osteoporosis-Associated Genome-wide Association Study (GWAS) Single-Nucleotide Polymorphisms (SNPs) Using Epigenomics and Transcriptomics. *JBMR plus*, 5(5), e10481.

Bruscadin JJ, et al. (2021) Muscle allele-specific expression QTLs may affect meat quality traits in *Bos indicus*. *Scientific reports*, 11(1), 7321.