# Resource Summary Report

Generated by RRID on Apr 10, 2025

## Gene Regulation Databases

RRID:SCR_008033
Type: Tool

### Proper Citation

Gene Regulation Databases (RRID:SCR_008033)

### Resource Information

**URL:** http://www.gene-regulation.com/pub/databases.html

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**Description:** In an effort to strongly support the collaborative nature of scientific research, BIOBASE offers academic and non-profit organizations free access to reduced functionality versions of their products. TRANSFAC Professional provides gene regulation analysis solutions, offering the most comprehensive collection of eukaryotic gene regulation data. The professional paid subscription gives customers access to up-to-date data and tools not available in the free version. The public databases currently available for academic and non-profit organizations are: * TRANSFAC: contains data on transcription factors, their experimentally-proven binding sites, and regulated genes. Its broad compilation of binding sites allows the derivation of positional weight matrices. * TRANSPATH: provides data about molecules participating in signal transduction pathways and the reactions they are involved in, resulting in a complex network of interconnected signaling components.TRANSPATH focuses on signaling cascades that change the activities of transcription factors and thus alter the gene expression profile of a given cell. * PathoDB: is a database on pathologically relevant mutated forms of transcription factors and their binding sites. It comprises numerous cases of defective transcription factors or mutated transcription factor binding sites, which are known to cause pathological defects. * S/MARt DB: presents data on scaffold or matrix attached regions (S/MARs) of eukaryotic genomes, as well as about the proteins that bind to them. S/MARs organize the chromatin in the form of functionally independent loop domains gained increasing support. Scaffold or Matrix Attached Regions (S/MARs) are genomic DNA sequences through which the chromatin is tightly attached to the proteinaceous scaffold of the nucleus. * TRANSCompel: is a database on composite regulatory elements affecting gene transcription in eukaryotes. Composite regulatory elements consist of two closely situated binding sites for distinct transcription factors, and provide cross-coupling of different signaling pathways. * PathoSign Public: is a database which collects information about defective cell signaling molecules causing human diseases. While constituting a useful data

repository in itself, PathoSign is also aimed at being a foundational part of a platform for modeling human disease processes.

**Abbreviations:** Gene Regulation Public Databases

**Synonyms:** gene-regulation.com: Public Databases for Academic and Non-profit Organizations

**Resource Type:** topical portal, portal, data or information resource

**Keywords:** element, eukaryote, eukaryotic, expression, functionally, gene, genome, alignment, bind, binding site, cell, chromatin, collaborative, component, coupling, disease, dna, domain, human, matrix, molecular weight, molecule, mononucleotide, network, nucleotide, nucleus, pathological, protein, region, regulated, regulatory, scientific research, sequence, signaling, signal pathway, transcription factor, molecular neuroanatomy resource

**Funding:** BIOBASE

**Resource Name:** Gene Regulation Databases

**Resource ID:** SCR_008033

**Alternate IDs:** nif-0000-10230

**Record Creation Time:** 20220129T080245+0000

**Record Last Update:** 20250410T065656+0000

## Ratings and Alerts

No rating or validation information has been found for Gene Regulation Databases.

No alerts have been found for Gene Regulation Databases.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 127 mentions in open access literature.

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

Jeong MS, et al. (2023) Exploring the Relationship between CLPTM1L-MS2 Variants and Susceptibility to Bladder Cancer. Genes, 15(1).

Hitomi Y, et al. (2022) rs9459874 and rs1012656 in CCR6/FGFR1OP confer susceptibility to primary biliary cholangitis. Journal of autoimmunity, 126, 102775.

Tsai KK, et al. (2022) Screening of organoids derived from patients with breast cancer implicates the repressor NCOR2 in cytotoxic stress response and antitumor immunity. Nature cancer, 3(6), 734.

López-Márquez A, et al. (2022) Sox9 is involved in the thyroid differentiation program and is regulated by crosstalk between TSH, TGF? and thyroid transcription factors. Scientific reports, 12(1), 2144.

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).

Kim MH, et al. (2021) VNTR polymorphism in the breakpoint region of ABL1 and susceptibility to bladder cancer. BMC medical genomics, 14(1), 121.

Hitomi Y, et al. (2021) rs1944919 on chromosome 11q23.1 and its effector genes COLCA1/COLCA2 confer susceptibility to primary biliary cholangitis. Scientific reports, 11(1), 4557.

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.

Ashraf A, et al. (2019) Evolution of Deeper Rooting 1-like homoeologs in wheat entails the C-terminus mutations as well as gain and loss of auxin response elements. PloS one, 14(4), e0214145.

Zhang J, et al. (2019) Cmah deficiency may lead to age-related hearing loss by influencing miRNA-PPAR mediated signaling pathway. PeerJ, 7, e6856.

Trescher S, et al. (2019) Estimation of Transcription Factor Activity in Knockdown Studies. Scientific reports, 9(1), 9593.

Hitomi Y, et al. (2019) NFKB1 and MANBA Confer Disease Susceptibility to Primary Biliary Cholangitis via Independent Putative Primary Functional Variants. Cellular and molecular gastroenterology and hepatology, 7(3), 515.

Wang X, et al. (2019) Molecular characterization of ABHD5 gene promoter in intramuscular preadipocytes of Qinchuan cattle: Roles of Evi1 and C/EBP?. Gene, 690, 38.

Hitomi Y, et al. (2019) POGLUT1, the putative effector gene driven by rs2293370 in primary biliary cholangitis susceptibility locus chromosome 3q13.33. Scientific reports, 9(1), 102.

Diao C, et al. (2018) Identification and analysis of key genes in osteosarcoma using bioinformatics. Oncology letters, 15(3), 2789.

Wei L, et al. (2018) Bioinformatics analysis of microarray data to reveal the pathogenesis of diffuse intrinsic pontine glioma. Biological research, 51(1), 26.

Guo J, et al. (2018) Ultraconserved element uc.372 drives hepatic lipid accumulation by suppressing miR-195/miR4668 maturation. Nature communications, 9(1), 612.

Wang C, et al. (2018) Comparative gene expression profile and DNA methylation status in diabetic patients of Kazak and Han people. Medicine, 97(36), e11982.

Kobayashi K, et al. (2018) In vitro analysis of the transcriptional regulatory mechanism of zebrafish pou5f3. Experimental cell research, 364(1), 28.

Shi Z, et al. (2018) Exploring the molecular pathogenesis associated with T-cell prolymphocytic leukemia based on a comprehensive bioinformatics analysis. Oncology letters, 16(1), 301.