

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Gene Regulation Programs

RRID:SCR\_007787

Type: Tool

### Proper Citation

Gene Regulation Programs (RRID:SCR\_007787)

### Resource Information

**URL:** <http://www.gene-regulation.com/pub/programs.html>

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**Description:** In an effort to strongly support the collaborative nature of scientific research, BIOBASE offers access to their tools. Programs that are available through this portal are: \* AliBaba 2.1: AliBaba2 is a program for predicting binding sites of transcription factor binding sites in an unknown DNA sequence. Therefore it uses the binding sites collected in TRANSFAC. AliBaba2 is currently the most specific tool for predicting sites. \* Boxshade 3.3.1: Pretty Printing and Shading of Multiple-Alignment files. \* ClustalW 1.8: ClustalW Multiple Sequence Alignment Program. \* Dialign2.0: Multiple Sequence Alignment Program. \* F-Match 1.0: F-MATCH is a program for identifying statistically overrepresented Transcription Factor Binding Sites (TFBS) in a set of sequences compared against a control set, assuming a binomial distribution of TFBS frequency. The program reads MATCH output files for the query and control sets. F-Match uses a library of mononucleotide weight matrices from TRANSFAC 6.0 \* Match 1.0 Public: Match is designed for searching potential binding sites for transcription factors (TF binding sites) nucleotide sequences. MatchTM uses a library of mononucleotide weight matrices from TRANSFAC 6.0 \* molwSearch 1.0: Search for transcription factors with a certain molecular weight. \* P-Match 1.0: P-Match is a new tool for identifying transcription factor binding sites (TF binding sites) in DNA sequences. It combines pattern matching and weight matrix approaches thus providing higher accuracy of recognition than each of the methods alone. P-Match uses a library of mononucleotide weight matrices from TRANSFAC 6.0 along with the site alignments associated with these matrices. \* Patch 1.0: Search for potential transcription factor binding sites in your own sequences with the pattern search program using TRANSFAC 6.0 public sites. \* m2transfac 1.0: m2transfac is a PWM-PWM alignment interface for the TRANSFAC(R) database. For given user motifs, m2transfac reports all non-overlapping pairwise alignments to a TRANSFAC(R) matrix which satisfy a specified threshold. \* MatrixCatch 2.7: The MatrixCatch tool is designed for searching potential composite elements (CEs) for transcription factors (TFs) in any DNA sequence, which may be of interest. MatrixCatch uses a library of CE matrix models, which were compiled on a basis of experimentally identified CEs collected in

TRANSCOMPEL database and mononucleotide weight matrices for single TF-binding sites collected in TRANSFAC 6.0 public database. \* Composite Module Analyst (CMA) 1.0: CMA reads output of Match program and applies a genetic algorithm in order to define promoter models based on the composition of transcription factor binding sites and their pairs. \* PolyA Scan 0.000707: Scanning a Sequence for potential Polyadenylation Sites. \* ReadSeq 2.0: ReadSeq reads and writes nucleic/protein sequences in various formats. \* SignalScan: Analysis of DNA Sequences for known Eukaryotic Signals \* SbBlast 1.0: Search Tool for Sequence Search in the S/MARt Binder Database. SbBlast makes use of the BLAST Sequence Similarity Search Tool - Version 2.0.13 (May-26-2000). \* SnpFind 0.3: SNPFIND is a tool for searches in the Database of Single Nucleotide Polymorphisms. The search algorithm used for the database search is the BLAST algorithm. \* TfBlast 0.1: Search Tool for Sequence Search in the TRANSFAC Factor Table. SbBlast makes use of the BLAST Sequence Similarity Search Tool - Version 2.0.13 (May-26-2000).

**Abbreviations:** Gene Regulation Programs

**Synonyms:** gene-regulation.com: Programs

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

**Funding:** BIOBASE

**Resource Name:** Gene Regulation Programs

**Resource ID:** SCR\_007787

**Alternate IDs:** nlx\_143607

**Record Creation Time:** 20220129T080243+0000

**Record Last Update:** 20260905T132615+0000

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## Ratings and Alerts

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

No alerts have been found for Gene Regulation Programs.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 73 mentions in open access literature.

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

Nishiike Y, et al. (2026) Brain-derived estrogens facilitate male-typical behaviors by potentiating androgen receptor signaling in medaka. eLife, 13.

Androniki R, et al. (2025) Early Life Mild Adversity Affects in a Sexually Dimorphic Way the Oxytocinergic System Reducing Close Social Interaction in Adult Male Rats. *Journal of neurochemistry*, 169(12), e70326.

Liu B, et al. (2024) A Preliminary Study on Transcriptional Regulation of SNP Site C-1888T in the Promoter Region of Human PLUNC Gene and Nasopharyngeal Carcinoma Susceptibility. *Genetics research*, 2024, 5148918.

Penninger P, et al. (2024) HDAC1 fine-tunes Th17 polarization in vivo to restrain tissue damage in fungal infections. *Cell reports*, 43(12), 114993.

Desouza LA, et al. (2021) The Hallucinogenic Serotonin2A Receptor Agonist, 2,5-Dimethoxy-4-Iodoamphetamine, Promotes cAMP Response Element Binding Protein-Dependent Gene Expression of Specific Plasticity-Associated Genes in the Rodent Neocortex. *Frontiers in molecular neuroscience*, 14, 790213.

Elgendy AM, et al. (2021) Involvement of Cis-Acting Elements in Molecular Regulation of JH-Mediated Vitellogenin Gene 2 of Female *Periplaneta americana*. *Frontiers in physiology*, 12, 723072.

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).

Nishiike Y, et al. (2021) Estrogen receptor 2b is the major determinant of sex-typical mating behavior and sexual preference in medaka. *Current biology : CB*, 31(8), 1699.

Ohtsuka Y, et al. (2020) In silico identification and functional validation of linear cationic  $\alpha$ -helical antimicrobial peptides in the ascidian *Ciona intestinalis*. *Scientific reports*, 10(1), 12619.

Wu X, et al. (2019) Functional analysis of 5 upstream polymorphic variations of the human dopamine D1 receptor gene. *Journal of cellular and molecular medicine*, 23(8), 5813.

Guo T, et al. (2018) Cloning and Transcriptional Activity Analysis of the Porcine Abcb1 Gene Promoter: Transcription Factor Sp1 Regulates the Expression of Porcine Abcb1. *Frontiers in pharmacology*, 9, 373.

Han J, et al. (2018) Inducible microRNA-122 modulates RIG-I signaling pathway via targeting DAK in miiuy croaker after poly(I:C) stimulation. *Developmental and comparative immunology*, 78, 52.

Wei K, et al. (2018) Global identification, structural analysis and expression characterization of cytochrome P450 monooxygenase superfamily in rice. *BMC genomics*, 19(1), 35.

Navarro-Sánchez L, et al. (2018) Epigenetic Study in Parkinson's Disease: A Pilot Analysis of DNA Methylation in Candidate Genes in Brain. *Cells*, 7(10).

Liu H, et al. (2018) Trps1 is associated with the multidrug resistance of lung cancer cell by regulating MGMT gene expression. *Cancer medicine*, 7(5), 1921.

Wu Y, et al. (2018) Long noncoding RNA hypoxia-inducible factor 1 alpha-antisense RNA 1 promotes tumor necrosis factor- $\alpha$ -induced apoptosis through caspase 3 in Kupffer cells. *Medicine*, 97(4), e9483.

Rana A, et al. (2017) The transcriptional regulation of the human angiotensinogen gene after high-fat diet is haplotype-dependent: Novel insights into the gene-regulatory networks and implications for human hypertension. *PloS one*, 12(5), e0176373.

Kupsco A, et al. (2017) Developmental expression and regulation of flavin-containing monooxygenase by the unfolded protein response in Japanese medaka (*Oryzias latipes*). *Comparative biochemistry and physiology. Toxicology & pharmacology : CBP*, 191, 7.

Huang S, et al. (2017) Isolation and characterization of the 5'-flanking region of the human PDXK gene. *Gene*, 628, 218.

Borsatto T, et al. (2017) Biotinidase deficiency: Genotype-biochemical phenotype association in Brazilian patients. *PloS one*, 12(5), e0177503.