

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Intergrated Transcription Factor Platform

RRID:SCR_008119

Type: Tool

Proper Citation

Intergrated Transcription Factor Platform (RRID:SCR_008119)

Resource Information

URL: <http://itfp.biosino.org/itfp/>

Proper Citation: Intergrated Transcription Factor Platform (RRID:SCR_008119)

Description: ITFP is an integrated transcription factor (TF) platform, which included abundant TFs and targets message of mammalian. Support vector machine (SVM) algorithm combined with error-correcting output coding (ECOC) algorithm was utilized to identify and classify transcription factor from protein sequence of Human, Mouse and Rat. For transcription factor targets, a reverse engineering method named ARACNE was used to derive potential interaction pairs between transcription factor and downstream regulated gene from Human, Mouse and Rat gene expression profile data. Detailed information of gene expression profile data can be found in help page. Moreover, all data provided by the platform is free for non-commercial users and can be downloaded through links on help page.

Synonyms: ITFP

Resource Type: data or information resource, database

Keywords: expression, gene, human, message, mouse, protein, rat, sequence, target, transcription factor

Resource Name: Intergrated Transcription Factor Platform

Resource ID: SCR_008119

Alternate IDs: nif-0000-20862

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260729T044203+0000

Ratings and Alerts

No rating or validation information has been found for Intergrated Transcription Factor Platform.

No alerts have been found for Intergrated Transcription Factor Platform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ruiz E, et al. (2023) An Integrative Multi-Omics Analysis of The Molecular Links between Aging and Aggressiveness in Thyroid Cancers. *Aging and disease*, 14(3), 992.

Singh P, et al. (2020) Transcriptomic analysis delineates potential signature genes and miRNAs associated with the pathogenesis of asthma. *Scientific reports*, 10(1), 13354.

Yeh SJ, et al. (2019) Investigating Common Pathogenic Mechanisms between Homo sapiens and Different Strains of *Candida albicans* for Drug Design: Systems Biology Approach via Two-Sided NGS Data Identification. *Toxins*, 11(2).

Wang Z, et al. (2019) Dynamics of transcriptome changes during subcutaneous preadipocyte differentiation in ducks. *BMC genomics*, 20(1), 688.

Tan H, et al. (2019) Pan-cancer analysis on microRNA-associated gene activation. *EBioMedicine*, 43, 82.

Yin H, et al. (2019) Identification of the targets of hematoporphyrin derivative in lung adenocarcinoma using integrated network analysis. *Biological research*, 52(1), 4.

Liu Y, et al. (2019) Investigation of transcriptome mechanism associated with osteoporosis explored by microarray analysis. *Experimental and therapeutic medicine*, 17(5), 3459.

Gao LW, et al. (2018) Comprehensive bioinformatics analysis identifies several potential diagnostic markers and potential roles of cyclin family members in lung adenocarcinoma. *OncoTargets and therapy*, 11, 7407.

Yang H, et al. (2018) Investigation of mechanisms of mesenchymal stem cells for treatment of diabetic nephropathy via construction of a miRNA-TF-mRNA network. *Renal failure*, 40(1), 136.

Zhao W, et al. (2018) Gene module analysis of juvenile myelomonocytic leukemia and screening of anticancer drugs. *Oncology reports*, 40(6), 3155.

Li CW, et al. (2018) Investigating Pathogenic and Hepatocarcinogenic Mechanisms from Normal Liver to HCC by Constructing Genetic and Epigenetic Networks via Big Genetic

and Epigenetic Data Mining and Genome-Wide NGS Data Identification. Disease markers, 2018, 8635329.

Mao Z, et al. (2018) Identification of key genes and miRNAs associated with carotid atherosclerosis based on mRNA-seq data. Medicine, 97(13), e9832.

Li Y, et al. (2018) Identification of potential genes and miRNAs associated with sepsis based on microarray analysis. Molecular medicine reports, 17(5), 6227.

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.

Keller S, et al. (2017) Evaluation of epidermal growth factor receptor signaling effects in gastric cancer cell lines by detailed motility-focused phenotypic characterization linked with molecular analysis. BMC cancer, 17(1), 845.

Migliara G, et al. (2017) PIF* promotes brain re-myelination locally while regulating systemic inflammation- clinically relevant multiple sclerosis M.smegmatis model. Oncotarget, 8(13), 21834.

Mager LF, et al. (2017) The ESRP1-GPR137 axis contributes to intestinal pathogenesis. eLife, 6.

Tan X, et al. (2016) miR-671-5p inhibits epithelial-to-mesenchymal transition by downregulating FOXM1 expression in breast cancer. Oncotarget, 7(1), 293.

Shainer R, et al. (2016) PreImplantation factor (PIF) therapy provides comprehensive protection against radiation induced pathologies. Oncotarget, 7(37), 58975.

Li CW, et al. (2016) Investigating the specific core genetic-and-epigenetic networks of cellular mechanisms involved in human aging in peripheral blood mononuclear cells. Oncotarget, 7(8), 8556.