

Resource Summary Report

Generated by [NIF](#) on Aug 20, 2026

PAZAR

RRID:SCR_005410

Type: Tool

Proper Citation

PAZAR (RRID:SCR_005410)

Resource Information

URL: <http://www.pazar.info/>

Proper Citation: PAZAR (RRID:SCR_005410)

Description: Database that unites independently created and maintained data collections of transcription factor and regulatory sequence annotation. The flexible PAZAR schema permits the representation of diverse information derived from experiments ranging from biochemical protein-DNA binding to cellular reporter gene assays. Data collections can be made available to the public, or restricted to specific system users. The data "boutiques" within the shopping-mall-inspired system facilitate the analysis of genomics data and the creation of predictive models of gene regulation., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PAZAR

Resource Type: data or information resource, data repository, database, storage service resource, service resource, software resource

Defining Citation: [PMID:18971253](#)

Keywords: transcription factor, target gene, regulatory sequence, transcription factor profile, annotation, sequence, profile, transcription factor binding profile, chip, chip-seq, gene, cis-regulatory element, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PAZAR

Resource ID: SCR_005410

Alternate IDs: OMICS_00540, biotools:pazar

Alternate URLs: <https://bio.tools/pazar>

License: GNU Lesser General Public License

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260820T054501+0000

Ratings and Alerts

No rating or validation information has been found for PAZAR.

No alerts have been found for PAZAR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Zang W, et al. (2025) The MIR181A2HG/miR-5680/VCAN-CD44 Axis Regulates Gastric Cancer Lymph Node Metastasis by Promoting M2 Macrophage Polarization. Cancer medicine, 14(2), e70600.

Hu Y, et al. (2025) Accurate Transcription Factor Activity Inference to Decipher Cell Identity from Single-Cell Transcriptomic Data with MetaTF. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e10745.

Barker HR, et al. (2025) TFBSFootprinter: a multiomics tool for prediction of transcription factor binding sites in vertebrate species. Transcription, 16(2-3), 204.

Zhang T, et al. (2024) Germline cis variant determines epigenetic regulation of the anti-cancer drug metabolism gene dihydropyrimidine dehydrogenase (DPYD). eLife, 13.

Zhang T, et al. (2023) Germline cis variant determines epigenetic regulation of the anti-cancer drug metabolism gene dihydropyrimidine dehydrogenase (DPYD). bioRxiv : the preprint server for biology.

Buki G, et al. (2023) Correlation between large FBN1 deletions and severe cardiovascular phenotype in Marfan syndrome: Analysis of two novel cases and analytical review of the literature. Molecular genetics & genomic medicine, 11(7), e2166.

Wang L, et al. (2023) A functional mechanism for a non-coding variant near AGTR2 associated with risk for preterm birth. BMC medicine, 21(1), 258.

Liao W, et al. (2023) Bioinformatics and experimental analyses of glutamate receptor and its targets genes in myocardial and cerebral ischemia. BMC genomics, 24(1), 300.

Büki G, et al. (2023) Identification of an NF1 Microdeletion with Optical Genome Mapping. *International journal of molecular sciences*, 24(17).

Schmidt AF, et al. (2022) Fetal maturation revealed by amniotic fluid cell-free transcriptome in rhesus macaques. *JCI insight*, 7(18).

Quan Y, et al. (2020) Genome-wide pathogenesis interpretation using a heat diffusion-based systems genetics method and implications for gene function annotation. *Molecular genetics & genomic medicine*, 8(10), e1456.

Caliskan A, et al. (2020) Novel molecular signatures and potential therapeutics in renal cell carcinomas: Insights from a comparative analysis of subtypes. *Genomics*, 112(5), 3166.

Hörhold F, et al. (2020) Reprogramming of macrophages employing gene regulatory and metabolic network models. *PLoS computational biology*, 16(2), e1007657.

Poos AM, et al. (2019) Modelling TERT regulation across 19 different cancer types based on the MIPRIIP 2.0 gene regulatory network approach. *BMC bioinformatics*, 20(1), 737.

Garcia-Alonso L, et al. (2019) Benchmark and integration of resources for the estimation of human transcription factor activities. *Genome research*, 29(8), 1363.

Rivera C, et al. (2018) Agrin has a pathological role in the progression of oral cancer. *British journal of cancer*, 118(12), 1628.

Zhang X, et al. (2018) Diesel exhaust and house dust mite allergen lead to common changes in the airway methylome and hydroxymethylome. *Environmental epigenetics*, 4(3), dvy020.

Vafaei F, et al. (2016) ORTI: An Open-Access Repository of Transcriptional Interactions for Interrogating Mammalian Gene Expression Data. *PloS one*, 11(10), e0164535.

Jayaram N, et al. (2016) Evaluating tools for transcription factor binding site prediction. *BMC bioinformatics*, 17(1), 547.

Huang Y, et al. (2016) ARN: analysis and prediction by adipogenic professional database. *BMC systems biology*, 10(1), 57.