

Resource Summary Report

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CIS-BP

RRID:SCR_017236

Type: Tool

Proper Citation

CIS-BP (RRID:SCR_017236)

Resource Information

URL: <http://cisbp.cabr.utoronto.ca>

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Description: Software tool as catalog of inferred sequence binding preferences. Online library of transcription factors and their DNA binding motifs.

Synonyms: Catalog of Inferred Sequence Binding Preferences

Resource Type: web service, software resource, data access protocol, database, data or information resource

Defining Citation: [PMID:25215497](#)

Keywords: catalog, inferred, sequence, binding, preference, transcription, factor, DNA, motif, FASEB list

Funding: Canadian Institutes of Health Research ;
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Availability: Free, Freely available

Resource Name: CIS-BP

Resource ID: SCR_017236

Alternate IDs: r3d100013971

Alternate URLs: <https://doi.org/10.17616/R31NJN9V>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260805T044406+0000

Ratings and Alerts

No rating or validation information has been found for CIS-BP.

No alerts have been found for CIS-BP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 104 mentions in open access literature.

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

Drescher F, et al. (2025) Transcriptomic and genetic analysis reveals a Zn2Cys6 transcription factor specifically required for conidiation in submerged cultures of *Thermothelomyces thermophilus*. *mBio*, 16(1), e0311124.

Yakovenko I, et al. (2025) Telomemore enables single-cell analysis of cell cycle and chromatin condensation. *Nucleic acids research*, 53(3).

Xie Z, et al. (2025) DNA-guided transcription factor interactions extend human gene regulatory code. *Nature*, 641(8065), 1329.

Fanfani V, et al. (2025) Reproducible processing of TCGA regulatory networks. *GigaScience*, 14.

Yeo IS, et al. (2025) An integrated transcriptomic approach for identifying enhancers in limb motor pools. *Scientific reports*, 15(1), 34813.

Kim W, et al. (2025) Transcription factor-dependent regulatory networks of sexual reproduction in *Fusarium graminearum*. *mBio*, 16(1), e0303024.

Saha E, et al. (2025) Aging-associated alterations in gene regulatory networks associate with risk, prognosis and response to therapy in lung adenocarcinoma. *npj aging*, 11(1), 61.

Li B, et al. (2025) Zygotic activation of transposable elements during zebrafish early embryogenesis. *Nature communications*, 16(1), 3692.

Llanquinao-Sandoval J, et al. (2025) Identifying a novel Mecp2-mediated epigenetic mechanism controlling *Lonp1* in the hippocampus and its disruption by aging. *Scientific*

reports, 15(1), 40887.

Baek M, et al. (2024) Accurate prediction of protein-nucleic acid complexes using RoseTTAFoldNA. *Nature methods*, 21(1), 117.

Ounadjela JR, et al. (2024) Spatial multiomic landscape of the human placenta at molecular resolution. *Nature medicine*, 30(12), 3495.

Mindel V, et al. (2024) Revisiting the model for coactivator recruitment: Med15 can select its target sites independent of promoter-bound transcription factors. *Nucleic acids research*, 52(20), 12093.

Wang G, et al. (2024) Identification of endothelial and mesenchymal FOXF1 enhancers involved in alveolar capillary dysplasia. *Nature communications*, 15(1), 5233.

Mandros P, et al. (2024) node2vec2rank: Large Scale and Stable Graph Differential Analysis via Multi-Layer Node Embeddings and Ranking. *bioRxiv : the preprint server for biology*.

Vo NNT, et al. (2024) Transcription factor binding specificities of the oomycete *Phytophthora infestans* reflect conserved and divergent evolutionary patterns and predict function. *BMC genomics*, 25(1), 710.

Fanfani V, et al. (2024) Reproducible processing of TCGA regulatory networks. *bioRxiv : the preprint server for biology*.

Haque R, et al. (2024) Sex-specific developmental gene expression atlas unveils dimorphic gene networks in *C. elegans*. *Nature communications*, 15(1), 4273.

Zhimulev I, et al. (2024) Developmental and Housekeeping Genes: Two Types of Genetic Organization in the *Drosophila* Genome. *International journal of molecular sciences*, 25(7).

Han D, et al. (2024) Comparative analysis of models in predicting the effects of SNPs on TF-DNA binding using large-scale in vitro and in vivo data. *Briefings in bioinformatics*, 25(2).

Roehrig A, et al. (2024) Single-cell multiomics reveals the interplay of clonal evolution and cellular plasticity in hepatoblastoma. *Nature communications*, 15(1), 3031.