

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 17, 2026

CIS-BP

RRID:SCR_017236

Type: Tool

Proper Citation

CIS-BP (RRID:SCR_017236)

Resource Information

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

Proper Citation: CIS-BP (RRID:SCR_017236)

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

Defining Citation: [PMID:25215497](#)

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

Funding: Canadian Institute for Advanced Research Junior Fellows Genetic Networks Program ;

Canadian Institutes of Health Research ;

EU Marie Curie International Outgoing Fellowship ;

Fondo Nacional de Desarrollo Científico y Tecnológico ;

Gordon and Betty Moore Foundation ;

Howard Hughes Medical Institute ;

Millennium Nucleus for Fungal Integrative and Synthetic Biology ;

NICHD P01 HD39691;

NIGMS GM082971;

NSF MCB-1024999

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: 20260912T200217+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 115 mentions in open access literature.

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

Yuan X, et al. (2026) Fusobacterium nucleatum promotes tumor extravasation and metastasis in head and neck cancer via TLR4/MYB/ESPN axis. Communications biology, 9(1).

Nagel S, et al. (2026) Glycolytic Enzymes Are Part of an Oncogenic Network in AML. Cells, 15(6).

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4+ T cells. Cell reports, 45(4), 117103.

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

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

Zhao P, et al. (2025) Hypoxia-mediated HES4 promotes the proliferation and motility of hepatocellular carcinoma cell by enhancing COL4A2 transcription. Discover oncology, 16(1), 1405.

Liu S, et al. (2025) Predicting the DNA binding specificity of transcription factor mutants using family-level biophysically interpretable machine learning. Nucleic acids research, 53(16).

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

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

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

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

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

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.

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.

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.

Gralak AJ, et al. (2024) Identification of methylation-sensitive human transcription factors using meSMiLE-seq. *bioRxiv* : the preprint server for biology.

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.