

Resource Summary Report

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cisTarget

RRID:SCR_024808

Type: Tool

Proper Citation

cisTarget (RRID:SCR_024808)

Resource Information

URL: <https://resources.aertslab.org/cistarget/>

Proper Citation: cisTarget (RRID:SCR_024808)

Description: Web application to download database for motif enrichment, motif annotations, cluster-buster implementation, precomputed regions for creating gene-based databases and to download lists of transcription factors for human, mouse and fly, chip-seq tracks annotations.

Resource Type: data or information resource, database

Keywords: motif enrichment, motif annotations, cluster-buster implementation, precomputed regions for creating gene-based databases, transcription factors for human, mouse and fly, chip-seq tracks annotations,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: cisTarget

Resource ID: SCR_024808

Record Creation Time: 20240103T212525+0000

Record Last Update: 20250521T061947+0000

Ratings and Alerts

No rating or validation information has been found for cisTarget.

No alerts have been found for cisTarget.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Yu Q, et al. (2025) Causal genes identification of giant cell arteritis in CD4+?Memory t cells: an integration of multi-omics and expression quantitative trait locus analysis. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 74(1), 3.

Yoffe L, et al. (2025) Acquisition of discrete immune suppressive barriers contributes to the initiation and progression of preinvasive to invasive human lung cancer. bioRxiv : the preprint server for biology.

Yan Z, et al. (2024) A time-resolved multi-omics atlas of transcriptional regulation in response to high-altitude hypoxia across whole-body tissues. Nature communications, 15(1), 3970.

Kim S, et al. (2024) Innate immune responses against mRNA vaccine promote cellular immunity through IFN-? at the injection site. Nature communications, 15(1), 7226.

Matsuda T, et al. (2024) Deciphering craniopharyngioma subtypes: Single-cell analysis of tumor microenvironment and immune networks. iScience, 27(11), 111068.

Li J, et al. (2024) Single-cell transcriptomics reveals IRF7 regulation of the tumor microenvironment in isocitrate dehydrogenase wild-type glioma. MedComm, 5(11), e754.

Zhou Z, et al. (2024) Single cell atlas reveals multilayered metabolic heterogeneity across tumour types. EBioMedicine, 109, 105389.

Tang L, et al. (2024) Single-cell and Bulk RNA-Seq reveal angiogenic heterogeneity and microenvironmental features to evaluate prognosis and therapeutic response in lung adenocarcinoma. Frontiers in immunology, 15, 1352893.

Zhang M, et al. (2024) Integrated analysis of single-cell RNA sequencing and bulk RNA data reveals gene regulatory networks and targets in dilated cardiomyopathy. Scientific reports, 14(1), 13942.

Xu K, et al. (2024) Single-Cell RNA Sequencing Identifies Crucial Genes Influencing the

Polarization of Tumor-Associated Macrophages in Liver Cancer. *International journal of genomics*, 2024, 7263358.

Licón-Muñoz Y, et al. (2024) Single-nucleus and spatial landscape of the sub-ventricular zone in human glioblastoma. *bioRxiv : the preprint server for biology*.

Zhang L, et al. (2024) Single-cell analysis reveals the stromal dynamics and tumor-specific characteristics in the microenvironment of ovarian cancer. *Communications biology*, 7(1), 20.

Hashemi E, et al. (2024) Transcriptomic diversity of innate lymphoid cells in human lymph nodes compared to BM and spleen. *Communications biology*, 7(1), 769.

Zhao S, et al. (2024) Exploring the prognostic value of BRMS1^{hi} microglia based on single-cell anoikis regulator patterns in the immunologic microenvironment of GBM. *Journal of neuro-oncology*, 170(1), 101.

Wang S, et al. (2024) Single-cell RNA-Seq reveals the heterogeneity of fibroblasts within the tympanojugular paraganglioma microenvironment. *Heliyon*, 10(15), e35478.

Jiang C, et al. (2024) Unveiling Dynamic Changes and Regulatory Mechanisms of T Cell Subsets in Sepsis Pathogenesis. *ImmunoTargets and therapy*, 13, 29.

Yates J, et al. (2024) Cell states and neighborhoods in distinct clinical stages of primary and metastatic esophageal adenocarcinoma. *bioRxiv : the preprint server for biology*.

Zhang W, et al. (2024) Single-cell analysis uncovers high-proliferative tumour cell subtypes and their interactions in the microenvironment of gastric cancer. *Journal of cellular and molecular medicine*, 28(12), e18373.

Chai YC, et al. (2024) Spatially Self-Organized Three-Dimensional Neural Concentroid as a Novel Reductionist Humanized Model to Study Neurovascular Development. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(5), e2304421.

Rytkönen KT, et al. (2024) Gene Regulatory Network Analysis of Decidual Stromal Cells and Natural Killer Cells. *Reproductive sciences (Thousand Oaks, Calif.)*, 31(10), 3159.