

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

ChEA

RRID:SCR_005403

Type: Tool

Proper Citation

ChEA (RRID:SCR_005403)

Resource Information

URL: <http://amp.pharm.mssm.edu/lib/chea.jsp>

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Description: Data analysis service for gene-list enrichment analysis against a manual database. It allows users to input lists of mammalian gene symbols for which the program computes over-representation of transcription factor targets from the ChIP-X database. The database integrates interaction data from ChIP-chip, ChIP-seq, ChIP-PET and DamID studies and contains 189,933 interactions, manually extracted from 87 publications, describing the binding of 92 transcription factors to 31,932 target genes.

Abbreviations: ChEA

Synonyms: ChIP Enrichment Analysis

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource, software application, software resource

Defining Citation: [PMID:20709693](#)

Keywords: chip, transcription factor, interaction, mrna expression, gene, target gene, command-line, chip-chip, chip-seq

Resource Name: ChEA

Resource ID: SCR_005403

Alternate IDs: OMICS_00526

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260905T132958+0000

Ratings and Alerts

No rating or validation information has been found for ChEA.

No alerts have been found for ChEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 280 mentions in open access literature.

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

Wang R, et al. (2026) SAMS1 restrains NK cell mediated anti-tumor immunity in hepatocellular carcinoma. Nature communications, 17(1).

Abdelmoez AM, et al. (2026) Thromboxane signalling links immune activation to enhanced glucose uptake in skeletal muscle. Diabetologia, 69(6), 1643.

Manoukian P, et al. (2026) Estrogen Production in Pancreatic Cancer Shapes a Tumor-Suppressive Stromal Microenvironment. Cancer research, 86(3), 571.

Xu ZY, et al. (2026) In vitro experiments and bioinformatic analyses implicate KAT2A in the occurrence and development of hepatocellular carcinoma. Scientific reports, 16(1), 5737.

Cicha E, et al. (2026) The Effects of ACTH and Dexamethasone on the Transcriptomic Profile of the Rat Adrenal Gland: An In Vivo Study. Current issues in molecular biology, 48(2).

Radyk MD, et al. (2026) NADPH-producing enzymes restrict the formation of pancreatic precancerous lesions. Nature metabolism, 8(4), 824.

Zhu X, et al. (2026) Bioinformatic analysis and experimental validation of the function of mitogen-activated protein kinase in esophageal cancer. Discover oncology, 17(1).

Mulvey B, et al. (2026) Spatially resolved molecular sex differences at single-cell resolution in the adult human ventromedial and arcuate hypothalamus. Cell reports, 45(2), 116877.

Kumar R, et al. (2026) Identifying regulatory driver motifs in non-small cell lung carcinoma via a systematic approach. PloS one, 21(2), e0340798.

Talla A, et al. (2026) Innate antiviral and immune functions associated with the HIV reservoir decay after anti-PD-1 therapy. Nature medicine, 32(2), 505.

Maher S, et al. (2026) MYCN inhibits TrkC-mediated differentiation in neuroblastoma cells via disruption of the PKA signalling pathway. Cell death discovery, 12(1).

Liu YJ, et al. (2026) Dissecting molecular heterogeneity in primary gastric cancer by IGFBP7-related analysis. *Journal of translational medicine*, 24(1).

Aggarwal D, et al. (2026) Patient-derived organoid xenografts reveal the multifaceted role of the lncRNA MALAT1 in breast cancer progression. *bioRxiv : the preprint server for biology*.

Manakkat Vijay GK, et al. (2026) BLIMP1 shapes germinal center B cell clonal diversity by gating chromatin accessibility during light-to-dark zone transition. *Nature immunology*, 27(6), 1294.

Liu Z, et al. (2026) Interferon-related inflammaging links epigenetic age acceleration to multimorbidity. *Cell genomics*, 6(6), 101218.

Bui TA, et al. (2026) Early Transcriptional Changes in Neutrophil-Mediated Processes Following Recanalization After Ischemic Stroke. *Journal of the American Heart Association*, 15(7), e043522.

Kelchtermans J, et al. (2026) Genetic susceptibility to PM2.5 exposure and transcriptional responses in pediatric asthma: insights from single-cell transcriptomics. *Frontiers in immunology*, 17, 1644537.

Zhang T, et al. (2026) MEF2A-mediated inhibition of ischemic stroke injury via the PI3K/AKT pathway: a comprehensive bioinformatics and in vitro study. *BMC neuroscience*, 27(1).

Chen Y, et al. (2026) Farnesyltransferase Deficiency in Cardiomyocytes Initiates Senescence and Contributes to Cardiac Fibrosis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(26), e11530.

Zhang C, et al. (2026) Superenhancer-mediated ferroptosis in age-related hearing loss: cochlear epigenomics. *Cellular and molecular life sciences : CMLS*, 83(1).