

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 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: 20260912T200011+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 [SPARC SAWG](#) .

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

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

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

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

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).

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.

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.

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.

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).

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.

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

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