

Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 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: software application, service resource, data or information resource, data analysis service, database, software resource, production service resource, analysis service 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: 20260729T044114+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 256 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. GigaScience, 14.

Shin GS, et al. (2025) Lamin B1 regulates RNA splicing factor expression by modulating the spatial positioning and chromatin interactions of the ETS1 gene locus. Animal cells and systems, 29(1), 149.

Sun B, et al. (2025) Acute hypoxia modulate macrophage phenotype accompanied with transcriptome re-programming and metabolic re-modeling. Frontiers in immunology, 16, 1534009.

Shafieizadegan S, et al. (2025) The molecular impact of miR-326 in acute lymphoblastic leukemia and its cross talk with P53. Annals of hematology, 104(4), 2417.

Lee C, et al. (2025) Insights into Convergent Evolution From Studying Amino Acid Patterns in Independent Lineages of Birds. Genome biology and evolution, 17(12).

Chauvir?? T, et al. (2025) Flavoproteins as native and genetically encoded spin probes for in cell ESR spectroscopy. Nature communications, 16(1), 5406.

Li X, et al. (2025) Integrating multi-omics to unveil PSMD12 as a critical gene in promoting brain metastases of lung adenocarcinoma. Journal of translational medicine, 23(1), 668.

Sun C, et al. (2025) DCN, NPM3 and SULF1 are hub genes related to vasculogenic mimicry in lung adenocarcinoma. Journal of cancer research and clinical oncology, 151(12), 318.

Seno A, et al. (2025) Genome-wide mapping of arsenic-activated Nrf2 reveals metabolic and epigenetic reprogramming in induced pluripotent stem cells. Redox biology, 86, 103773.

Bu F, et al. (2025) Biomarkers in glioblastoma and degenerative CNS diseases: defining new advances in clinical usefulness and therapeutic molecular target. Frontiers in molecular biosciences, 12, 1506961.

Chang YH, et al. (2025) Isoform-level analyses of 6 cancers uncover extensive genetic risk mechanisms undetected at the gene-level. *British journal of cancer*, 133(6), 874.

Watanabe H, et al. (2025) Lethal co-expression intolerance underlies the mutually exclusive expression of ASCL1 and NEUROD1 in SCLC cells. *NPJ precision oncology*, 9(1), 74.

Chaharlashkar Z, et al. (2025) Metastatic melanoma: An integrated analysis to identify critical regulators associated with prognosis, pathogenesis and targeted therapies. *PloS one*, 20(1), e0312754.

Zheng Q, et al. (2025) Bidirectional histone monoaminylation dynamics regulate neural rhythmicity. *Nature*, 637(8047), 974.

Shen Y, et al. (2025) Ints7 deficiency activates DNA damage response to elicit resurgence of endogenous retrovirus MERVL and anastasis of embryonic stem cells. *Nucleic acids research*, 53(15).

Lepore Signorile M, et al. (2025) Tailoring a novel colorectal cancer stem cell-targeted therapy by inhibiting the SMYD3/c-MYC axis. *Signal transduction and targeted therapy*, 10(1), 206.

Qadeer ZA, et al. (2025) Human stem cell models for group 3 medulloblastoma uncover JARID1B as a regulator of the chromatin landscape. *bioRxiv : the preprint server for biology*.

Falvo P, et al. (2025) Age-dependent differences in breast tumor microenvironment: challenges and opportunities for efficacy studies in preclinical models. *Cell death and differentiation*, 32(6), 1000.

Nie H, et al. (2025) Transcriptome Data Combined With Mendelian Randomization Analysis Identifies Key Genes Associated With Mitochondria and Programmed Cell Death in Intervertebral Disc Degeneration. *JOR spine*, 8(1), e70057.

Li J, et al. (2025) Elevated Expression of CHAF1A in Hepatocellular Carcinoma Progression and Immune Modulation. *Clinical and experimental gastroenterology*, 18, 25.