

Resource Summary Report

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

Defining Citation: [PMID:20709693](#)

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

Funding:

Resource Name: ChEA

Resource ID: SCR_005403

Alternate IDs: OMICS_00526

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250521T061032+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 229 mentions in open access literature.

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

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

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.

Lv ZB, et al. (2024) GDF10 and IDO1 as a thyroid cancer prognostic biomarker associated with immune infiltration. *Heliyon*, 10(6), e27651.

Zhou L, et al. (2024) Notch1 signaling pathway promotes growth and metastasis of gastric cancer via modulating CDH5. *Aging*, 16(16), 11893.

Li F, et al. (2024) Identifying cell type-specific transcription factor-mediated activity immune modules reveal implications for immunotherapy and molecular classification of pan-cancer. *Briefings in bioinformatics*, 25(5).

Peng D, et al. (2024) Circ_BBS9 as an early diagnostic biomarker for lung adenocarcinoma: direct interaction with IFIT3 in the modulation of tumor immune microenvironment. *Frontiers in immunology*, 15, 1344954.

Lv W, et al. (2024) Identification of key metabolism-related genes and pathways in spontaneous preterm birth: combining bioinformatic analysis and machine learning. *Frontiers in endocrinology*, 15, 1440436.

Radak M, et al. (2024) Unraveling molecular similarities between colorectal polyps and colorectal cancer: a systems biology approach. *Intestinal research*, 22(2), 199.

Bhattacharjya A, et al. (2024) Exploring gene regulatory interaction networks and predicting therapeutic molecules for hypopharyngeal cancer and EGFR-mutated lung adenocarcinoma. *FEBS open bio*, 14(7), 1166.

Imani S, et al. (2024) Exploration of drug repurposing for Mpox outbreaks targeting gene signatures and host-pathogen interactions. *Scientific reports*, 14(1), 29436.

Halimani N, et al. (2024) Knockdown of Hyaluronan synthase 2 suppresses liver fibrosis in mice via induction of transcriptomic changes similar to 4MU treatment. *Scientific reports*, 14(1), 2797.

Tijms BM, et al. (2024) Cerebrospinal fluid proteomics in patients with Alzheimer's disease reveals five molecular subtypes with distinct genetic risk profiles. *Nature aging*, 4(1), 33.

Bajpai AK, et al. (2024) Systems genetics and bioinformatics analyses using ESR1-correlated genes identify potential candidates underlying female bone development. *Genomics*, 116(1), 110769.

Yu D, et al. (2024) Feedforward cysteine regulation maintains melanoma differentiation state and limits metastatic spread. *Cell reports*, 43(7), 114484.

Sudalagunta PR, et al. (2024) The Functional Transcriptomic Landscape Informs Therapeutic Strategies in Multiple Myeloma. *Cancer research*.

Shao A, et al. (2024) The L27 domain of MPP7 enhances TAZ-YY1 cooperation to renew muscle stem cells. *EMBO reports*, 25(12), 5667.

Balcioglu O, et al. (2024) Mcam stabilizes a luminal progenitor-like breast cancer cell state via Ck2 control and Src/Akt/Stat3 attenuation. *NPJ breast cancer*, 10(1), 80.

Yang B, et al. (2024) Integrative transcriptome analysis identifies a crotonylation gene signature for predicting prognosis and drug sensitivity in hepatocellular carcinoma. *Journal of cellular and molecular medicine*, 28(20), e70083.

Lin G, et al. (2024) Key extracellular proteins and TF-miRNA co-regulatory network in diabetic foot ulcer: Bioinformatics and experimental insights. *PloS one*, 19(7), e0307205.

Folle AM, et al. (2024) Modulatory actions of *Echinococcus granulosus* antigen B on macrophage inflammatory activation. *Frontiers in cellular and infection microbiology*, 14, 1362765.