

Resource Summary Report

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ChIP-X Enrichment Analysis 3

RRID:SCR_023159

Type: Tool

Proper Citation

ChIP-X Enrichment Analysis 3 (RRID:SCR_023159)

Resource Information

URL: <https://maayanlab.cloud/chea3/>

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Description: Web based transcription factor enrichment analysis. Web server ranks TFs associated with user-submitted gene sets. ChEA3 background database contains collection of gene set libraries generated from multiple sources including TF-gene co-expression from RNA-seq studies, TF-target associations from ChIP-seq experiments, and TF-gene co-occurrence computed from crowd-submitted gene lists. Enrichment results from these distinct sources are integrated to generate composite rank that improves prediction of correct upstream TF compared to ranks produced by individual libraries.

Abbreviations: ChEA3

Synonyms: ChIP-X Enrichment Analysis Version 3 (ChEA3)

Resource Type: software resource, web application

Defining Citation: [PMID:31114921](#)

Keywords: Transcription Factor, gene sets, transcription factor enrichment analysis, TF-gene co-expression from RNA-seq studies, TF-target associations from ChIP-seq experiments, TF-gene co-occurrence, prediction of correct upstream,

Funding: NHLBI U54HL127624;
NCI U24CA224260;
NIGMS T32GM062754;
NIH Office of the Director OT3OD025467

Availability: Free, Freely available

Resource Name: ChIP-X Enrichment Analysis 3

Resource ID: SCR_023159

Record Creation Time: 20230121T050159+0000

Record Last Update: 20260804T043808+0000

Ratings and Alerts

No rating or validation information has been found for ChIP-X Enrichment Analysis 3.

No alerts have been found for ChIP-X Enrichment Analysis 3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Liu D, et al. (2025) Polycystic ovary syndrome and epithelial-mesenchymal transition: Mendelian randomization and single-cell analysis insights. *Journal of ovarian research*, 18(1), 33.

Li Y, et al. (2025) Deciphering the transcriptomic landscape of systemic lupus erythematosus-associated pulmonary arterial hypertension. *Respiratory research*, 26(1), 106.

Jin Y, et al. (2025) Effects of hypoxia stress on the milk synthesis in bovine mammary epithelial cells. *Journal of animal science and biotechnology*, 16(1), 37.

Li YM, et al. (2025) Identification and Validation of Ferritinophagy-Related Biomarkers in Periodontitis. *International dental journal*, 75(3), 1781.

Jiang C, et al. (2025) NR4A1 suppresses breast cancer growth by repressing c-Fos-mediated lipid and redox dyshomeostasis. *Experimental & molecular medicine*, 57(4), 804.

Chen Y, et al. (2025) Identification of WDR74 and TNFRSF12A as biomarkers for early osteoarthritis using machine learning and immunohistochemistry. *Frontiers in immunology*, 16, 1517646.

Yu Y, et al. (2025) Ferroptosis and Sterol Biosynthesis Dysregulation in Granulosa Cells of Patients with Diminished Ovarian Reserve. *Antioxidants (Basel, Switzerland)*, 14(6).

Prenen F, et al. (2025) JAK/STAT inhibition protects glucocorticoid receptor knockout mice from lethal malaria-induced hypoglycemia and hyperinflammation. *EMBO molecular medicine*, 17(8), 2040.

Wang Y, et al. (2025) Diagnostic immune-related markers for diabetic kidney disease: a bioinformatics and machine learning approach. *Renal failure*, 47(1), 2525467.

Alexander SE, et al. (2025) Bioavailable testosterone and androgen receptor activation, but not total testosterone, are associated with muscle mass and strength in females. *The Journal of physiology*, 603(18), 5181.

Yang Y, et al. (2025) Dual Inhibition of CDK4/6 and CDK7 Suppresses Triple-Negative Breast Cancer Progression via Epigenetic Modulation of SREBP1-Regulated Cholesterol Metabolism. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(5), e2413103.

Wess M, et al. (2025) Versatile roles of annexin A4 in clear cell renal cell carcinoma: Impact on membrane repair, transcriptional signatures, and composition of the tumor microenvironment. *iScience*, 28(4), 112198.

Jiang H, et al. (2025) ETS2 aggravate allergic airway inflammation by regulating ANT2-mediated cytosolic mitochondrial DsRNA levels. *Respiratory research*, 26(1), 159.

Prenen F, et al. (2025) Resolution of experimental malaria-associated acute respiratory distress syndrome is Alox12 independent and shows residual inflammation. *Malaria journal*, 24(1), 216.

Liu Y, et al. (2025) C1q+ Macrophage-Tumor Cell Interaction Promoted Tumorigenesis via GPR17/PI3K/AKT Pathway Induced DNA Hypermethylation in Nasopharyngeal Carcinoma. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(26), e2503434.

Zhang L, et al. (2025) Impact of varying oxidative stress levels on the secretion characteristics and protein cargo profiling of extracellular vesicles derived from duck intestinal epithelial cells. *Poultry science*, 104(12), 106070.

Shen X, et al. (2025) Mechanisms responsible for the ability of enoxaparin sodium to inhibit inflammatory responses in the immune microenvironment of bone repair: A transcriptomic sequencing study. *PloS one*, 20(9), e0332041.

Niu S, et al. (2025) Identify the potential target of efferocytosis in knee osteoarthritis synovial tissue: a bioinformatics and machine learning-based study. *Frontiers in immunology*, 16, 1550794.

Chen J, et al. (2025) A novel Wnt/??-catenin signaling gene signature for progression and metastasis of gastric cancer. *Oncology research*, 33(5), 1199.

Liu W, et al. (2025) Identification of macrophage polarisation and mitochondria-related biomarkers in diabetic retinopathy. *Journal of translational medicine*, 23(1), 23.