

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

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: web application, software resource

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: 20260815T182733+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 193 mentions in open access literature.

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

Lao Y, et al. (2026) Dietary Supplementation with Chrysanthemum morifolium Ramat cv. 'Hangju' Flower Extract Alleviates Skin Photoaging in SKH-1 Hairless Mice. *Nutrients*, 18(2).

Wang Y, et al. (2026) Exploration Novel Therapeutic Targets for Periodontitis via Stress Granules Biomarkers. *International dental journal*, 76(2), 109390.

Pan S, et al. (2026) PURE-seq integrates FACS and PIP-seq for single-cell genomics of ultra-rare cells. *Nature communications*, 17(1), 1408.

Singh P, et al. (2026) Decoding Prognostic Signatures in Brain Metastatic Non-Small-Cell Lung Cancer via Integrated Multi-Omics and Network Analysis. *International journal of molecular sciences*, 27(8).

Tang J, et al. (2026) Development and validation of an immune-related diagnostic signature for breast cancer bone metastasis. *Scientific reports*, 16(1).

Xie J, et al. (2026) Critical Biological Functions and Clinical Implications of Epigenetic-Related Candidate Biomarkers in Chronic Obstructive Pulmonary Disease: Integrated Machine Learning Screening and Basic Experimental Validation. *International journal of chronic obstructive pulmonary disease*, 21, 592045.

de Assis LVM, et al. (2026) Hepatocyte Circadian Clocks Control Cholesterol Metabolism and Protect From Metabolic Dysfunction-Associated Steatohepatitis. *Cellular and molecular gastroenterology and hepatology*, 20(8), 101806.

Hao W, et al. (2026) Integrative Multi-Omics Analysis Unveils Biomarkers Linking the Gut Microbiota, Blood Metabolites, and Recurrent Pregnancy Loss. *International journal of women's health*, 18, 598767.

Xue Q, et al. (2026) Copper deprivation reprograms antioxidant defense to suppress ferroptosis via SLC7A11. *Redox biology*, 92, 104130.

Sun M, et al. (2026) FOS drives podocyte injury and renal fibrosis in diabetic kidney disease via direct Smad3 binding. *Cellular and molecular life sciences : CMLS*, 83(1).

Xiao G, et al. (2026) Defect in lysosomal enzyme trafficking and sorting is associated with irreversibility of pulmonary arterial hypertension. *Frontiers in cardiovascular medicine*, 13, 1763556.

Sharma RK, et al. (2026) Mechanotransduction-Induced Gene Expression Reveals Activation of TGF β /SKIL/TAZ Axis and Supports Invasive Phenotype in Triple-Negative Breast Cancer. *International journal of molecular sciences*, 27(5).

Jeon Y, et al. (2026) Uncovering a Glaucoma-Linked Lysophosphatidic Acid-MAPK/AP-1 Fibrosis Axis in Human Trabecular Meshwork Cells and Its Modulation by Diospyros kaki Leaf Extract. *International journal of molecular sciences*, 27(3).

Li P, et al. (2026) Multi-stage transcriptome analysis identifies hub genes and regulatory mechanisms driving cervical cancer progression. *PeerJ*, 14, e21255.

Albuz O, et al. (2026) Host Gene Signatures Associated with Gastric Cancer-Associated Microbial Taxa: A Descriptive Microbiome-Transcriptome Study. *Medicina (Kaunas, Lithuania)*, 62(5).

Jackson-Strong M, et al. (2026) GATA2 controls alveolar macrophage inflammatory gene expression and metabolic function. *JCI insight*, 11(7).

Yue B, et al. (2026) STUB1 downregulates TOP2A through a dual mechanism of ubiquitination and FOXM1-mediated transcription repression, suppressing breast cancer growth and enhancing sensitivity to chemotherapy. *Cellular & molecular biology letters*, 31(1).

Sarver DC, et al. (2026) Time-restricted feeding enhances cross-tissue temporal coordination of mitochondrial-associated transcripts. *iScience*, 29(6), 115957.

Ha YE, et al. (2026) Antioxidant Activities and Lipid Accumulation-Inhibitory Effects of Seed and Callus Extracts of *Impatiens balsamina* L. *Plants (Basel, Switzerland)*, 15(11).

Cheng A, et al. (2026) Environmental Fluoride Compromises Male Fertility: Differentially Modulated miR-34a-5p Targets REST to Regulate Autophagy in Testicular Somatic Cells. *Research (Washington, D.C.)*, 9, 1113.