

Resource Summary Report

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ChIPBase

RRID:SCR_005404

Type: Tool

Proper Citation

ChIPBase (RRID:SCR_005404)

Resource Information

URL: <http://deepbase.sysu.edu.cn/chipbase/>

Proper Citation: ChIPBase (RRID:SCR_005404)

Description: A database for decoding transcription factor binding maps, expression profiles and transcriptional regulation of long non-coding RNAs (lncRNAs, lincRNAs), microRNAs, other ncRNAs (snoRNAs, tRNAs, snRNAs, etc.) and protein-coding genes from ChIP-Seq data. ChIPBase currently includes millions of transcription factor binding sites (TFBSs) among 6 species. ChIPBase provides several web-based tools and browsers to explore TF-lncRNA, TF-miRNA, TF-mRNA, TF-ncRNA and TF-miRNA-mRNA regulatory networks., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: ChIPBase

Resource Type: data or information resource, database

Keywords: chip-seq, gene, rna, microrna, long non-coding rna, non-coding, transcription factor binding site, protein, transcriptional regulation, annotation, regulatory element, transcription factor, genome, network, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ChIPBase

Resource ID: SCR_005404

Alternate IDs: OMICS_00527

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260829T182941+0000

Ratings and Alerts

No rating or validation information has been found for ChIPBase.

No alerts have been found for ChIPBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 145 mentions in open access literature.

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

Ge W, et al. (2025) Identifying Pyroptosis-Hub Genes and Inflammation Cell Type-Related Genes in Ischemic Stroke. *Molecular neurobiology*, 62(5), 6228.

Wang Z, et al. (2025) Integrated analysis of exosome-related genes and their role in psoriasis pathogenesis. *Frontiers in immunology*, 16, 1492012.

Cheng S, et al. (2025) Exploring hypoxia-related genes in spinal cord injury: a pathway to new therapeutic targets. *Frontiers in molecular neuroscience*, 18, 1565430.

Mao S, et al. (2025) Study on differentially expressed genes and pattern recognition receptors in osteoporosis based on bioinformatics analysis. *Scientific reports*, 15(1), 31287.

Wang Z, et al. (2025) Development of immune-derived molecular markers for preeclampsia based on multiple machine learning algorithms. *Scientific reports*, 15(1), 1767.

Wang Y, et al. (2025) Identification of key interactive genes and their potential biological functions in type 2 diabetes and Sjögren's syndrome. *Scientific reports*, 15(1), 28660.

Zheng L, et al. (2025) Exploring the molecular characteristics of inflammatory bowel disease from the perspective of hypoxia-related genes. *Frontiers in pharmacology*, 16, 1612676.

Li S, et al. (2025) Integrated Transcriptomic Analysis Provided Diagnostic and Pathophysiological Insights for Epilepsy. *Journal of immunology research*, 2025, 5925485.

Tu JL, et al. (2025) Identification of fatty acid metabolism hub genes in endometriosis using integrative bioinformatics analysis. *Frontiers in medicine*, 12, 1529074.

Zhu Z, et al. (2025) Exploration of differential expression and biological significance of amino acid metabolism genes in osteoarthritis. *Frontiers in immunology*, 16, 1588072.

Wang Y, et al. (2025) Identification of aging-related biomarkers and immune infiltration analysis in renal stones by integrated bioinformatics analysis. *Scientific reports*, 15(1), 21650.

Lu Y, et al. (2025) Decoding the diagnostic biomarkers of mitochondrial dysfunction related gene variants in pediatric T cell acute lymphoblastic leukemia. *Scientific reports*, 15(1), 21144.

Jiang H, et al. (2025) Prognostic and therapeutic insights from lactate metabolism and tumor immune microenvironment in head and neck squamous cell carcinoma. *Discover oncology*, 16(1), 909.

Wang S, et al. (2025) The impact of inflammation and iron metabolism on gene expression alterations in ischemic stroke: a bioinformatics approach. *Scientific reports*, 15(1), 15233.

Maimaiti Y, et al. (2025) FOXO regulation of TXNIP induces ferroptosis in satellite cells by inhibiting glutathione metabolism, promoting Sarcopenia. *Cellular and molecular life sciences : CMLS*, 82(1), 81.

Xu Y, et al. (2025) Identification of tacrolimus-related genes in familial combined hyperlipidemia and development of a diagnostic model using bioinformatics analysis. *Heliyon*, 11(3), e41705.

Shen J, et al. (2025) Glycolytic pathways: The hidden regulators in Parkinson's disease. *Heliyon*, 11(3), e41831.

Yao L, et al. (2025) Prediction model of mitochondrial energy metabolism related genes in idiopathic pulmonary fibrosis and its correlation with immune microenvironment. *Scientific reports*, 15(1), 16801.

Delgado-Chaves FM, et al. (2025) DRaCOon: a novel algorithm for pathway-level differential co-expression analysis in transcriptomics. *BMC bioinformatics*, 26(1), 137.

Yin X, et al. (2025) Unveiling the molecular mechanisms of recurrent miscarriage through endoplasmic reticulum stress related gene expression. *Scientific reports*, 15(1), 1452.