Resource Summary Report

Generated by dkNET on Aug 26, 2026

Binding and Expression Target Analysis

RRID:SCR_005396
Type: Tool

Proper Citation

Binding and Expression Target Analysis (RRID:SCR_005396)

Resource Information

URL: http://cistrome.org/BETA/

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Description: A software package that integrates ChIP-seq of transcription factors or chromatin regulators with differential gene expression data to infer direct target genes. BETA has three functions: (1) to predict whether the factor has activating or repressive function; (2) to infer the factor""s target genes; and (3) to identify the motif of the factor and its collaborators which might modulate the factor""s activating or repressive function. BETA requires ~2GB RAM and 1h for the whole procedure. BETA may run on the web server at Cistrome or may be downloaded.

Abbreviations: BETA

Synonyms: BETA - Binding and Expression Target Analysis

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource

Defining Citation: PMID:24263090

Keywords: transcription factor, chromatin regulator, transcriptome, chip-seq, cistrome, gene expression, target gene, motif, differential gene expression

Availability: Registration required, Open unspecified license

Resource Name: Binding and Expression Target Analysis

Resource ID: SCR_005396

Alternate IDs: OMICS_00515

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260821T193744+0000

Ratings and Alerts

No rating or validation information has been found for Binding and Expression Target Analysis.

No alerts have been found for Binding and Expression Target Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 455 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Foidart P, et al. (2026) Whole-genome doubling drives immune evasion by silencing antigen presentation. Cancer cell, 44(7), 1418.

Li B, et al. (2025) Genetic insights into cardiac conduction disorders from genome-wide association studies. Human genomics, 19(1), 20.

Vora M, et al. (2025) Genome-wide analysis of Smad and Schnurri transcription factors in C. elegans demonstrates widespread interaction and a function in collagen secretion. eLife, 13.

Parihar AK, et al. (2025) Adaptive responses of large-seeded lentils across diverse Indian climates. Heliyon, 11(3), e42184.

Wuergezhen D, et al. (2025) An eGFP-Col4a2 mouse model reveals basement membrane dynamics underlying hair follicle morphogenesis. The Journal of cell biology, 224(2).

Chambers TL, et al. (2025) Methylome-proteome integration after late-life voluntary exercise training reveals regulation and target information for improved skeletal muscle health. The Journal of physiology, 603(1), 211.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. iScience, 28(3), 112081.

Tang Q, et al. (2025) p63 co-opts the skin Krt8-to-Krt5 transition for enamel organ development. bioRxiv : the preprint server for biology.

Londono-Correa D, et al. (2025) Crystallized and fluid cognitive abilities have different genetic associations with neuropsychiatric disorders. Research square.

Harvey C, et al. (2025) Evaluation of a biomarker for amyotrophic lateral sclerosis derived from a hypomethylated DNA signature of human motor neurons. BMC medical genomics, 18(1), 10.

Lai Y, et al. (2025) Transcriptomic analysis reveals the function of m6A regulators in aged cochlea. Brazilian journal of otorhinolaryngology, 91(3), 101578.

Wei Q, et al. (2025) Enhancing the performance of SSVEP-based BCIs by combining task-related component analysis and deep neural network. Scientific reports, 15(1), 365.

Houten R, et al. (2025) Digital Versus Paper-Based Consent from the UK NHS Perspective: A Micro-costing Analysis. PharmacoEconomics - open, 9(1), 27.

Li Z, et al. (2024) EstroGene2.0: A multi-omic database of response to estrogens, ER-modulators, and resistance to endocrine therapies in breast cancer. bioRxiv : the preprint server for biology.

von Bechtolsheim F, et al. (2024) The development of tissue handling skills is sufficient and comparable after training in virtual reality or on a surgical robotic system: a prospective randomized trial. Surgical endoscopy, 38(5), 2900.

Ismaeel A, et al. (2024) Coordinated Regulation of Myonuclear DNA Methylation, mRNA, and miRNA Levels Associates With the Metabolic Response to Rapid Synergist Ablation-Induced Skeletal Muscle Hypertrophy in Female Mice. Function (Oxford, England), 5(1), zqad062.

Liu M, et al. (2024) Mapping the causal associations of cytokines with sarcopenia and aging traits: Evidence from bidirectional Mendelian randomization. Journal of cachexia, sarcopenia and muscle, 15(3), 1121.

Gu W, et al. (2024) A MTA2-SATB2 chromatin complex restrains colonic plasticity toward small intestine by retaining HNF4A at colonic chromatin. Nature communications, 15(1), 3595.

DiCiaccio B, et al. (2024) ZBTB7A is a modulator of KDM5-driven transcriptional networks in basal breast cancer. Cell reports, 43(12), 114991.

Saoud M, et al. (2024) Advancing Anticancer Drug Discovery: Leveraging Metabolomics and Machine Learning for Mode of Action Prediction by Pattern Recognition. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(47), e2404085.