Resource Summary Report

Generated by NIF on Apr 21, 2025

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

Defining Citation: PMID:24263090

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

Funding:

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: 20250420T014250+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 445 mentions in open access literature.

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

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).

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.

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.

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.

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.

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.

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.

Valenzuela-Fuenzalida JJ, et al. (2024) The Association between Anatomical Variants of Musculoskeletal Structures and Nerve Compressions of the Lower Limb: A Systematic Review and Meta-Analysis. Diagnostics (Basel, Switzerland), 14(7).

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.

Ali D, et al. (2024) Direct targets of MEF2C are enriched for genes associated with schizophrenia and cognitive function and are involved in neuron development and mitochondrial function. PLoS genetics, 20(9), e1011093.

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.

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.

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.

Pulupa JM, et al. (2024) DNA sequence-induced solid phase transition as a solution to the genome folding paradox. Research square.

Mao G, et al. (2024) Unveiling the bioinformatic genes and their involved regulatory mechanisms in type 2 diabetes combined with osteoarthritis. Frontiers in immunology, 15, 1353915.

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

Sánchez-Yustos P, et al. (2024) Initial Upper Palaeolithic lithic industry at Cueva Millán in the hinterlands of Iberia. Scientific reports, 14(1), 21705.

Wong AH, et al. (2024) Formative evaluation of an emergency department clinical decision support system for agitation symptoms: a study protocol. BMJ open, 14(2), e082834.

Luo Y, et al. (2024) Ectopic expression of the transcription factor ONECUT3 drives a complex karyotype in myelodysplastic syndromes. The Journal of clinical investigation,

134(8).