Resource Summary Report

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Distant Regulatory Elements

RRID:SCR_003058
Type: Tool

Proper Citation

Distant Regulatory Elements (RRID:SCR_003058)

Resource Information

URL: http://dire.dcode.org

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Description: Web server based on the Enhancer Identification (EI) method, to determine the chromosomal location and functional characteristics of distant regulatory elements (REs) in higher eukaryotic genomes. The server uses gene co-expression data, comparative genomics, and combinatorics of transcription factor binding sites (TFBSs) to find TFBS-association signatures that can be used for discriminating specific regulatory functions. DiRE's unique feature is the detection of REs outside of proximal promoter regions, as it takes advantage of the full gene locus to conduct the search. DiRE can predict common REs for any set of input genes for which the user has prior knowledge of co-expression, co-function, or other biologically meaningful grouping. The server predicts function-specific REs consisting of clusters of specifically-associated TFBSs, and it also scores the association of individual TFs with the biological function shared by the group of input genes. Its integration with the Array2BIO server allows users to start their analysis with raw microarray expression data.

Abbreviations: DiRE

Synonyms: Distant Regulatory Elements of co-regulated genes

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

Defining Citation: PMID:18487623

Keywords: regulatory element, enhancer identification, genome, prediction, transcription factor binding site, gene, co-expression, co-function, function, transcription factor,

comparative genomics, regulatory function, gene locus, chromosome, bio.tools

Funding: NLM ;
Intramural Research Program

Availability: Public

Resource Name: Distant Regulatory Elements

Resource ID: SCR_003058

Alternate IDs: nif-0000-30448, biotools:dire

Alternate URLs: https://bio.tools/dire

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250514T061238+0000

Ratings and Alerts

No rating or validation information has been found for Distant Regulatory Elements.

No alerts have been found for Distant Regulatory Elements.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lopes-Paciencia S, et al. (2024) A senescence restriction point acting on chromatin integrates oncogenic signals. Cell reports, 43(4), 114044.

Ye T, et al. (2021) Combination of Danshen and ligustrazine has dual anti-inflammatory effect on macrophages and endothelial cells. Journal of ethnopharmacology, 266, 113425.

Qian J, et al. (2021) Babaodan controls excessive immune responses and may represent a cytokine-targeted agent suitable for COVID-19 treatment. Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie, 139, 111586.

Chen J, et al. (2020) Genetic regulatory subnetworks and key regulating genes in rat hippocampus perturbed by prenatal malnutrition: implications for major brain disorders.

Aging, 12(9), 8434.

Braun L, et al. (2019) The Toxoplasma effector TEEGR promotes parasite persistence by modulating NF-?B signalling via EZH2. Nature microbiology, 4(7), 1208.

Mitxelena J, et al. (2018) An E2F7-dependent transcriptional program modulates DNA damage repair and genomic stability. Nucleic acids research, 46(9), 4546.

Ornelles DA, et al. (2016) Limited but durable changes to cellular gene expression in a model of latent adenovirus infection are reflected in childhood leukemic cell lines. Virology, 494, 67.

Liu D, et al. (2016) A comprehensive transcriptomic analysis of differentiating embryonic stem cells in response to the overexpression of Mesogenin 1. Aging, 8(10), 2324.

Liu P, et al. (2016) Identification of targets of miRNA-221 and miRNA-222 in fulvestrant-resistant breast cancer. Oncology letters, 12(5), 3882.

Infante A, et al. (2016) Pathologically Relevant Prelamin A Interactions with Transcription Factors. Methods in enzymology, 569, 485.

Duffy DJ, et al. (2016) Wnt signalling is a bi-directional vulnerability of cancer cells. Oncotarget, 7(37), 60310.

He K, et al. (2015) Gene set enrichment analysis of pathways and transcription factors associated with diabetic retinopathy using a microarray dataset. International journal of molecular medicine, 36(1), 103.

He K, et al. (2015) The stromal genome heterogeneity between breast and prostate tumors revealed by a comparative transcriptomic analysis. Oncotarget, 6(11), 8687.

El Taghdouini A, et al. (2015) In vitro reversion of activated primary human hepatic stellate cells. Fibrogenesis & tissue repair, 8, 14.

Infante A, et al. (2014) Prelamin A accumulation and stress conditions induce impaired Oct-1 activity and autophagy in prematurely aged human mesenchymal stem cell. Aging, 6(4), 264.

He K, et al. (2014) Comprehensive identification of essential pathways and transcription factors related to epilepsy by gene set enrichment analysis on microarray datasets. International journal of molecular medicine, 34(3), 715.

Teng S, et al. (2013) Genome-wide prediction and analysis of human tissue-selective genes using microarray expression data. BMC medical genomics, 6 Suppl 1(Suppl 1), S10.

Minami I, et al. (2012) A small molecule that promotes cardiac differentiation of human pluripotent stem cells under defined, cytokine- and xeno-free conditions. Cell reports, 2(5), 1448.

Wu JQ, et al. (2012) Tcf7 is an important regulator of the switch of self-renewal and

differentiation in a multipotential hematopoietic cell line. PLoS genetics, 8(3), e1002565.

Lee MP, et al. (2011) Twist1 directly regulates genes that promote cell proliferation and migration in developing heart valves. PloS one, 6(12), e29758.