Resource Summary Report

Generated by dkNET on Apr 23, 2025

Factorbook

RRID:SCR_004086
Type: Tool

Proper Citation

Factorbook (RRID:SCR_004086)

Resource Information

URL: http://www.factorbook.org/

Proper Citation: Factorbook (RRID:SCR_004086)

Description: A Wiki-based database for transcription factor-binding data generated by the ENCODE consortium.

Abbreviations: Factorbook

Resource Type: database, data or information resource

Defining Citation: PMID:22955990

Keywords: transcription factor, genome, transcription factor binding region, chip-seq

Funding:

Resource Name: Factorbook

Resource ID: SCR_004086

Alternate IDs: OMICS_00533

Record Creation Time: 20220129T080222+0000

Record Last Update: 20250423T060144+0000

Ratings and Alerts

No rating or validation information has been found for Factorbook.

No alerts have been found for Factorbook.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Villaplana-Velasco A, et al. (2023) Fine-mapping of retinal vascular complexity loci identifies Notch regulation as a shared mechanism with myocardial infarction outcomes. Communications biology, 6(1), 523.

Herburg L, et al. (2023) Chronic Voluntary Alcohol Consumption Alters Promoter Methylation and Expression of Fgf-2 and Fgfr1. International journal of molecular sciences, 24(4).

Del Giudice G, et al. (2023) An ancestral molecular response to nanomaterial particulates. Nature nanotechnology, 18(8), 957.

Pratt HE, et al. (2022) Factorbook: an updated catalog of transcription factor motifs and candidate regulatory motif sites. Nucleic acids research, 50(D1), D141.

Ginno PA, et al. (2020) A genome-scale map of DNA methylation turnover identifies site-specific dependencies of DNMT and TET activity. Nature communications, 11(1), 2680.

Cejas RB, et al. (2019) Contribution of DNA methylation to the expression of FCGRT in human liver and myocardium. Scientific reports, 9(1), 8674.

Harwood JC, et al. (2019) Nucleosome dynamics of human iPSC during neural differentiation. EMBO reports, 20(6).

DeRycke MS, et al. (2019) An expanded variant list and assembly annotation identifies multiple novel coding and noncoding genes for prostate cancer risk using a normal prostate tissue eQTL data set. PloS one, 14(4), e0214588.

Schmeier S, et al. (2017) TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. Nucleic acids research, 45(D1), D145.

Yevshin I, et al. (2017) GTRD: a database of transcription factor binding sites identified by ChIP-seq experiments. Nucleic acids research, 45(D1), D61.

Li J, et al. (2017) Roles of alternative splicing in modulating transcriptional regulation. BMC systems biology, 11(Suppl 5), 89.

Thibodeau SN, et al. (2015) Identification of candidate genes for prostate cancer-risk SNPs utilizing a normal prostate tissue eQTL data set. Nature communications, 6, 8653.

Zheng Y, et al. (2015) Comprehensive discovery of DNA motifs in 349 human cells and tissues reveals new features of motifs. Nucleic acids research, 43(1), 74.

Griffon A, et al. (2015) Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. Nucleic acids research, 43(4), e27.

Lu Y, et al. (2015) DELTA: A Distal Enhancer Locating Tool Based on AdaBoost Algorithm and Shape Features of Chromatin Modifications. PloS one, 10(6), e0130622.

Yao L, et al. (2014) Functional annotation of colon cancer risk SNPs. Nature communications, 5, 5114.

Qu H, et al. (2013) A brief review on the Human Encyclopedia of DNA Elements (ENCODE) project. Genomics, proteomics & bioinformatics, 11(3), 135.