

# Resource Summary Report

Generated by [dkNET](#) on Apr 24, 2025

## Factorbook

RRID:SCR\_004086

Type: Tool

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### Proper Citation

Factorbook (RRID:SCR\_004086)

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### 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

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### Ratings and Alerts

No rating or validation information has been found for Factorbook.

No alerts have been found for Factorbook.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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.