

# Resource Summary Report

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## MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation

RRID:SCR\_003077

Type: Tool

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### Proper Citation

MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation  
(RRID:SCR\_003077)

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### Resource Information

**URL:** <http://genome.ufl.edu/mapper/>

**Proper Citation:** MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation (RRID:SCR\_003077)

**Description:** A platform composed of three modules: the Database, the Search Engine, and rSNPs, for the computational identification of transcription factor binding sites (TFBSs) in multiple genomes, that combines TRANSFAC and JASPAR data with the search power of profile hidden Markov models (HMMs). The Database contains putative TFBSs found in the upstream sequences of genes from the human, mouse and D.melanogaster genomes. For each gene, they scanned the region from 10,000 base pairs upstream of the transcript start to 50 base pairs downstream of the coding sequence start against all their models. Therefore, the database contains putative binding sites in the gene promoter and in the initial introns and non-coding exons. Information displayed for each putative binding site includes the transcription factor name, its position (absolute on the chromosome, or relative to the gene), the score of the prediction, and the region of the gene the site belongs to. If the selected gene has homologs in any of the other two organisms, the program optionally displays the putative TFBSs in the homologs. The Search Engine allows the identification, visualization and selection of putative TFBSs occurring in the promoter or other regions of a gene from the human, mouse, D.melanogaster, C.elegans or S.cerevisiae genomes. In addition, it allows the user to upload a sequence to query and to build a model by supplying a multiple sequence alignment of binding sites for a transcription factor of interest. rSNPs MAPPER is designed to identify Single Nucleotide Polymorphisms (SNPs) that may have an effect on the presence of one or more TFBSs.

**Abbreviations:** MAPPER, MAPPER 2,

**Synonyms:** Multi-genome Analysis of Positions and Patterns of Elements of Regulation, MAPPER 2 - Multi-genome Analysis of Positions and Patterns of Elements of Regulation, MAPPER database

**Resource Type:** data or information resource, database, service resource

**Defining Citation:** [PMID:15608292](#), [PMID:15799782](#)

**Keywords:** transcription factor binding site, gene promoter, intron, non-coding exon, transcription factor, chromosome, gene, homolog, rsnp, single nucleotide polymorphism, search engine

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation

**Resource ID:** SCR\_003077

**Alternate IDs:** OMICS\_01877, nif-0000-03101

**Old URLs:** <http://bio.chip.org/mapper>

**Record Creation Time:** 20220129T080217+0000

**Record Last Update:** 20260801T190918+0000

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## Ratings and Alerts

No rating or validation information has been found for MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation.

No alerts have been found for MAPPER - Multi-genome Analysis of Positions and Patterns of Elements of Regulation.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

Li T, et al. (2019) 1,25(OH)<sub>2</sub>D<sub>3</sub> Attenuates IL-1??-Induced Epithelial-to-Mesenchymal Transition Through Inhibiting the Expression of lncTCF7. *Oncology research*, 27(7), 739.

Arai Y, et al. (2019) Evolutionary Gain of Dbx1 Expression Drives Subplate Identity in the Cerebral Cortex. *Cell reports*, 29(3), 645.

Imawari Y, et al. (2018) Downregulation of dual-specificity tyrosine-regulated kinase 2 promotes tumor cell proliferation and invasion by enhancing cyclin-dependent kinase 14 expression in breast cancer. *Cancer science*, 109(2), 363.

Orlowska-Baranowska E, et al. (2017) Functional polymorphism of the renalase gene is associated with cardiac hypertrophy in female patients with aortic stenosis. PloS one, 12(10), e0186729.

Pasutto F, et al. (2017) Pseudoexfoliation syndrome-associated genetic variants affect transcription factor binding and alternative splicing of LOXL1. Nature communications, 8, 15466.

Chan CY, et al. (2017) Transcription factor HBP1 is a direct anti-cancer target of transcription factor FOXO1 in invasive oral cancer. Oncotarget, 8(9), 14537.

Satterstrom FK, et al. (2015) Nuclear respiratory factor 2 induces SIRT3 expression. Aging cell, 14(5), 818.

Mori S, et al. (2015) Identification of APOBEC3B promoter elements responsible for activation by human papillomavirus type 16 E6. Biochemical and biophysical research communications, 460(3), 555.

Satterstrom FK, et al. (2014) Luciferase-based reporter to monitor the transcriptional activity of the SIRT3 promoter. Methods in enzymology, 543, 141.

Knight JC, et al. (2014) Approaches for establishing the function of regulatory genetic variants involved in disease. Genome medicine, 6(10), 92.

Worsley-Hunt R, et al. (2011) Identification of cis-regulatory sequence variations in individual genome sequences. Genome medicine, 3(10), 65.