

Resource Summary Report

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footprintDB

RRID:SCR_015711

Type: Tool

Proper Citation

footprintDB (RRID:SCR_015711)

Resource Information

URL: <http://floresta.eead.csic.es/footprintdb>

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Description: Web application for predicting transcription factors which bind a specific DNA site or motif, as well as DNA motifs or sites likely to be recognized by a specific DNA-binding protein. footprintDB also lists several databases and repositories relevant to DNA transcription.

Resource Type: data or information resource, database, software resource, web application

Defining Citation: [PMID:24234003](#)

Keywords: prediction, transcription factor, dna site, dna motif, meta-database, annotation

Funding: Plant KBBE EUI2008-03612;
Ministerio de Ciencia e Innovación ;
Agence Nationale de la Recherche (ANR) ;
BMBF

Availability: Freely available

Resource Name: footprintDB

Resource ID: SCR_015711

License URLs: <http://floresta.eead.csic.es/footprintdb/index.php?credits>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260912T195829+0000

Ratings and Alerts

No rating or validation information has been found for footprintDB.

No alerts have been found for footprintDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Rakpenthai A, et al. (2025) Transcriptional Regulation of the Phenylalanine Ammonia-Lyase (PAL) Gene Family in Mulberry Under Chitosan-Induced Stress. *Plants* (Basel, Switzerland), 14(17).

Lüdtke TH, et al. (2021) Combined genomic and proteomic approaches reveal DNA binding sites and interaction partners of TBX2 in the developing lung. *Respiratory research*, 22(1), 85.

Xia Y, et al. (2021) MIRLET7BHG promotes hepatocellular carcinoma progression by activating hepatic stellate cells through exosomal SMO to trigger Hedgehog pathway. *Cell death & disease*, 12(4), 326.

Ksouri N, et al. (2021) Tuning promoter boundaries improves regulatory motif discovery in nonmodel plants: the peach example. *Plant physiology*, 185(3), 1242.

Karageorgiou C, et al. (2020) The Cyclically Seasonal *Drosophila subobscura* Inversion O7 Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. *Frontiers in genetics*, 11, 565836.

Santana-Garcia W, et al. (2019) RSAT variation-tools: An accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding. *Computational and structural biotechnology journal*, 17, 1415.

Battistini F, et al. (2019) How B-DNA Dynamics Decipher Sequence-Selective Protein Recognition. *Journal of molecular biology*, 431(19), 3845.

Mulugeta TD, et al. (2019) SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. *BMC genomics*, 20(1), 694.

Zhang H, et al. (2018) Molecular characterization of the TaWTG1 in bread wheat (*Triticum aestivum* L.). *Gene*, 678, 23.

Parvathaneni RK, et al. (2017) Parallel loss of introns in the ABCB1 gene in angiosperms. *BMC evolutionary biology*, 17(1), 238.