Resource Summary Report

Generated by NIF on May 21, 2025

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 Recherce (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: 20250521T061620+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 9 mentions in open access literature.

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

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.