

Resource Summary Report

Generated by T1D on Jul 31, 2026

footprintDB

RRID:SCR_005368

Type: Tool

Proper Citation

footprintDB (RRID:SCR_005368)

Resource Information

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

Proper Citation: footprintDB (RRID:SCR_005368)

Description: Database with 2797 unique DNA-binding proteins (mostly transcription factors, TFs), 4196 Position Weight Matrices (PWMs) and 13161 DNA Binding Sites extracted from the literature and other repositories. The binding interfaces of (most) proteins in the database are inferred from the collection of protein-DNA complexes described in 3D-footprint. The database predicts transcription factors which bind a specific DNA site or motif and DNA motifs or sites likely to be recognized by a specific DNA-binding protein.

Abbreviations: footprintDB

Resource Type: data or information resource, database

Keywords: transcription factor, dna motif, dna, motif, dna-binding protein, position weight matrix, protein

Availability: Free

Resource Name: footprintDB

Resource ID: SCR_005368

Alternate IDs: OMICS_00535

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260729T044121+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 [T1D](#) .

Rodríguez Del Río Á, et al. (2023) Diversity of gene expression responses to light quality in barley. Scientific reports, 13(1), 17143.

Huang Y, et al. (2023) Longevity-Associated Transcription Factor ATF7 Promotes Healthspan by Suppressing Cellular Senescence and Systematic Inflammation. Aging and disease, 14(4), 1374.

Li J, et al. (2021) Mechanism of forkhead transcription factors binding to a novel palindromic DNA site. Nucleic acids research, 49(6), 3573.

Cheng H, et al. (2021) Gene Expression Correlation Analysis Reveals MYC-NAC Regulatory Network in Cotton Pigment Gland Development. International journal of molecular sciences, 22(9).

Zeng L, et al. (2021) Nuclear receptors NHR-49 and NHR-79 promote peroxisome proliferation to compensate for aldehyde dehydrogenase deficiency in C. elegans. PLoS genetics, 17(7), e1009635.

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.

Kaletsky R, et al. (2018) Transcriptome analysis of adult Caenorhabditis elegans cells reveals tissue-specific gene and isoform expression. PLoS genetics, 14(8), e1007559.

Cantalapiedra CP, et al. (2017) Large Differences in Gene Expression Responses to Drought and Heat Stress between Elite Barley Cultivar Scarlett and a Spanish Landrace. Frontiers in plant science, 8, 647.

Kelemen Z, et al. (2015) Analysis of the DNA-Binding Activities of the Arabidopsis R2R3-MYB Transcription Factor Family by One-Hybrid Experiments in Yeast. PloS one, 10(10), e0141044.