

Resource Summary Report

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PLACE- A Database of Plant Cis-acting Regulatory DNA Elements

RRID:SCR_013428

Type: Tool

Proper Citation

PLACE- A Database of Plant Cis-acting Regulatory DNA Elements (RRID:SCR_013428)

Resource Information

URL: <http://www.dna.affrc.go.jp/PLACE/>

Proper Citation: PLACE- A Database of Plant Cis-acting Regulatory DNA Elements (RRID:SCR_013428)

Description: A database of motifs found in plant cis-acting regulatory DNA elements, all from previously published reports. It covers vascular plants only. In addition to the motifs originally reported, their variations in other genes or in other plant species reported later are also compiled. The PLACE database also contains a brief description of each motif and relevant literature with PubMed ID numbers. DDBJ/EMBL/GenBank nucleotide sequence databases accession numbers will be also included. Note: As of January 2007, PLACE is no longer updated or maintained.

Abbreviations: PLACE

Resource Type: data or information resource, database

Defining Citation: [PMID:9847208](#)

Keywords: motif, cis-acting regulatory dna element, FASEB list

Availability: Free, Acknowledgement requested

Resource Name: PLACE- A Database of Plant Cis-acting Regulatory DNA Elements

Resource ID: SCR_013428

Alternate IDs: nif-0000-03296, OMICS_00557

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260729T044329+0000

Ratings and Alerts

No rating or validation information has been found for PLACE- A Database of Plant Cis-acting Regulatory DNA Elements.

No alerts have been found for PLACE- A Database of Plant Cis-acting Regulatory DNA Elements.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 329 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Liu S, et al. (2025) A novel transcription factor OsMYB73 affects grain size and chalkiness by regulating endosperm storage substances' accumulation-mediated auxin biosynthesis signalling pathway in rice. *Plant biotechnology journal*, 23(4), 1021.

Jiang R, et al. (2025) FaMYB63 and FvWYRK75 Activate FvPR10.14 Boosting Strawberry Immunity Against Powdery Mildew. *Molecular plant pathology*, 26(12), e70186.

Amirkhosravi A, et al. (2025) Ectopic expression of wax ester synthase under a wood-specific promoter enhances cell wall production and wood hydrophobicity. *Biotechnology for biofuels and bioproducts*, 18(1), 66.

Gou C, et al. (2025) Genome wide identification of Dof transcription factors in Carmine radish reveals RsDof33 role in cadmium stress and anthocyanin biosynthesis. *Scientific reports*, 15(1), 4766.

Zhang Y, et al. (2024) Genome-wide identification and expression analysis of ARF gene family in embryonic development of Korean pine (*Pinus koraiensis*). *BMC plant biology*, 24(1), 267.

Fu W, et al. (2024) Genome-wide identification and expression analysis of Ubiquitin-specific protease gene family in maize (*Zea mays* L.). *BMC plant biology*, 24(1), 404.

Kazakova E, et al. (2024) Radiation Hormesis in Barley Manifests as Changes in Growth Dynamics Coordinated with the Expression of PM19L-like, CML31-like, and AOS2-like. *International journal of molecular sciences*, 25(2).

Ma B, et al. (2024) RtNAC055 promotes drought tolerance via a stomatal closure pathway linked to methyl jasmonate/hydrogen peroxide signaling in *Reaumuria trigyna*. *Horticulture research*, 11(2), uhae001.

Lv J, et al. (2024) MdARF3 switches the lateral root elongation to regulate dwarfing in apple plants. *Horticulture research*, 11(4), uhae051.

Wu R, et al. (2024) The DBB Family in *Populus trichocarpa*: Identification, Characterization, Evolution and Expression Profiles. *Molecules* (Basel, Switzerland), 29(8).

Ahmed B, et al. (2023) Genome-wide investigation of SnRK2 gene family in two jute species: *Corchorus olitorius* and *Corchorus capsularis*. *Journal, genetic engineering & biotechnology*, 21(1), 5.

Wu R, et al. (2023) The G2-Like gene family in *Populus trichocarpa*: identification, evolution and expression profiles. *BMC genomic data*, 24(1), 37.

Wang Y, et al. (2023) Two B-box proteins, PavBBX6/9, positively regulate light-induced anthocyanin accumulation in sweet cherry. *Plant physiology*, 192(3), 2030.

Allen PJ, et al. (2023) MYB-bHLH-TTG1 in a Multi-tiered Pathway Regulates Arabidopsis Seed Coat Mucilage Biosynthesis Genes Including PECTIN METHYLESTERASE INHIBITOR14 Required for Homogalacturonan Demethylesterification. *Plant & cell physiology*, 64(8), 906.

Nawade B, et al. (2022) Longer Duration of Active Oil Biosynthesis during Seed Development Is Crucial for High Oil Yield-Lessons from Genome-Wide In Silico Mining and RNA-Seq Validation in Sesame. *Plants* (Basel, Switzerland), 11(21).

Chen S, et al. (2022) Characterization of two constitutive promoters RPS28 and EIF1 for studying soybean growth, development, and symbiotic nodule development. *aBIOTECH*, 3(2), 99.

Aslam MM, et al. (2022) Identification and expression analysis of phosphate transporter (PHT) gene family in *Lupinus albus* cluster root under phosphorus stress. *International journal of biological macromolecules*, 205, 772.

Zhou X, et al. (2022) Genetic dissection of fatty acid components in the Chinese peanut (*Arachis hypogaea* L.) mini-core collection under multi-environments. *PloS one*, 17(12), e0279650.

Gao C, et al. (2022) Genome-wide analysis of metallothionein gene family in maize to reveal its role in development and stress resistance to heavy metal. *Biological research*, 55(1), 1.

Zhang J, et al. (2022) Genome-wide identification and expression profiling analysis of maize AP2/ERF superfamily genes reveal essential roles in abiotic stress tolerance. *BMC genomics*, 23(1), 125.