

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 Note: As of January 2007, PLACE is no longer updated or maintained.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: 20260811T043447+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 351 mentions in open access literature.

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

Liu J, et al. (2026) Genetic identification of Pid3-1 and its regulatory role in promoting blast resistance in rice. *G3* (Bethesda, Md.), 16(4).

Xiang L, et al. (2026) Cloning and Characterization of IbHQT1: A BAHD Acyltransferase Gene That Positively Regulates Chlorogenic Acid Biosynthesis in Sweet Potato. *Genes*, 17(2).

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 FvWYRKY75 Activate FvPR10.14 Boosting Strawberry Immunity Against Powdery Mildew. *Molecular plant pathology*, 26(12), e70186.

Zhang Y, et al. (2025) Genome-wide identification and characterization of GATA gene family involved in ovule development of Korean pine (*Pinus koraiensis*). *BMC plant biology*, 26(1), 113.

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.

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.

Wei Y, et al. (2025) Genome-Wide Characterization, Comparative Analysis, and Expression Profiling of SWEET Genes Family in Four Cymbidium Species (Orchidaceae). *International journal of molecular sciences*, 26(9).

Hamera S, et al. (2025) StACS3-mediated drought stress adaptation in potato involves interactions with StPP2C2 and St14-3-3 proteins. *Frontiers in plant science*, 16, 1671817.

Yu Q, et al. (2024) McWRKY43 Confers Cold Stress Tolerance in *Michelia crassipes* via Regulation of Flavonoid Biosynthesis. *International journal of molecular sciences*, 25(18).

Javed T, et al. (2024) Pathogenesis-Related 1 (PR1) Protein Family Genes Involved in Sugarcane Responses to *Ustilago scitaminea* Stress. *International journal of molecular sciences*, 25(12).

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.

Zhang H, et al. (2024) SgR1, Encoding a Leucine-Rich Repeat Containing Receptor-like Protein, Is a Major Aphid (*Schizaphis graminum*) Resistance Gene in Sorghum. *International journal of molecular sciences*, 26(1).

Fatahi B, et al. (2024) Deciphering the possible role of RNA-helicase genes mechanism in response to abiotic stresses in rapeseed (*Brassica napus* L.). *BMC plant biology*, 24(1), 206.

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.

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

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

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.