

Resource Summary Report

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Conserved Domain Database

RRID:SCR_002077

Type: Tool

Proper Citation

Conserved Domain Database (RRID:SCR_002077)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/cdd>

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Description: Database of annotations of functional units in proteins including multiple sequence alignment models for ancient domains and full-length proteins. This collection of models includes 3D structures that display the sequence/structure/function relationships in proteins. It also includes alignments of the domains to known three-dimensional protein structures in the MMDB database. The source databases are Pfam, Smart, and COG. Users can identify amino acids in protein sequences with the resources available as well as view single sequences embedded within multiple sequence alignments.

Abbreviations: CDD

Synonyms: Conserved Domains Database, Conserved Domains

Resource Type: data or information resource, database

Defining Citation: [PMID:25414356](#), [PMID:18984618](#)

Keywords: protein, amino acid sequence, nucleic acid, 3d structure, annotation, function, sequence, structure, amino acid, gold standard

Resource Name: Conserved Domain Database

Resource ID: SCR_002077

Alternate IDs: nif-0000-02647, r3d100010653

Alternate URLs: <http://www.ncbi.nlm.nih.gov/sites/entrez?db=cdd>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260804T043138+0000

Ratings and Alerts

No rating or validation information has been found for Conserved Domain Database.

No alerts have been found for Conserved Domain Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 306 mentions in open access literature.

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

Zhang J, et al. (2025) Eucalyptus grandis WRKY genes provide insight into the role of arbuscular mycorrhizal symbiosis in defense against Ralstonia solanacearum. Frontiers in plant science, 16, 1510196.

Li H, et al. (2025) A rare dominant allele DYSOC1 determines seed coat color and improves seed oil content in Brassica napus. Science advances, 11(1), eads7620.

Wang Y, et al. (2025) Genome-wide characterization of the UDP-glycosyltransferases (UGT) family and functional analysis of VcUGT160 involved in dihydrozeatin glycosylation during blueberry fruits development. BMC genomics, 26(1), 1044.

Li L, et al. (2025) Genome-wide identification of CDPKs in jujube and expression profile analysis in response to multiple biological processes. Frontiers in plant science, 16, 1593446.

Yang J, et al. (2025) Physiological response of safflower to water deficit and genome-wide identification of its NAC transcription factor family. Scientific reports, 15(1), 31257.

Kong X, et al. (2025) Transcriptional regulation of miR528-PPO module by miR156 targeted SPLs orchestrates chilling response in banana. Molecular horticulture, 5(1), 2.

Kurowska M, et al. (2025) Functional analysis of HvSNAC1 in stomatal dynamics and drought adaptation. Journal of applied genetics, 66(4), 817.

Shah IH, et al. (2025) Comprehensive characterization and expression profiling of sucrose phosphate synthase (SPS) and sucrose synthase (SUS) family in Cucumis melo under the application of nitrogen and potassium. BMC plant biology, 25(1), 285.

Zhang X, et al. (2025) Promoting cytidine biosynthesis by modulating pyrimidine metabolism and carbon metabolic regulatory networks in Bacillus subtilis. Microbial cell factories, 24(1), 103.

Tang Y, et al. (2025) The biocontrol effects and mechanisms of mycoparasitic Alternaria alternata against Chinese rose powdery mildew. Frontiers in microbiology, 16, 1598458.

Granda Farias A, et al. (2025) Phenotypic screens for SIRPA expression reveal RAB21 as a general regulator of macrophage surface identity. *Cell reports*, 44(7), 115921.

Xie J, et al. (2024) The C4 photosynthesis bifunctional enzymes, PDRPs, of maize are co-opted to cytoplasmic viral replication complexes to promote infection of a prevalent potyvirus sugarcane mosaic virus. *Plant biotechnology journal*, 22(7), 1812.

Ji Z, et al. (2024) Genome-Wide Identification and Expression Analysis of BrBASS Genes in *Brassica rapa* Reveals Their Potential Roles in Abiotic Stress Tolerance. *Current issues in molecular biology*, 46(7), 6646.

Ma L, et al. (2024) Genome-wide analysis of AP2/ERF transcription factors that regulate fruit development of Chinese prickly ash. *BMC plant biology*, 24(1), 565.

Yang Y, et al. (2024) Genome-Wide Identification and Expression Analysis Unveil the Involvement of the Cold Shock Protein (CSP) Gene Family in Cotton Hypothermia Stress. *Plants (Basel, Switzerland)*, 13(5).

Chen S, et al. (2024) Genome-Wide Analysis of Nuclear factor-YC Genes in the Tea Plant (*Camellia sinensis*) and Functional Identification of CsNF-YC6. *International journal of molecular sciences*, 25(2).

Sheikh S, et al. (2024) The *Acrasis kona* genome and developmental transcriptomes reveal deep origins of eukaryotic multicellular pathways. *Nature communications*, 15(1), 10197.

Chen X, et al. (2024) Discovery of bifunctional diterpene cyclases/synthases in bacteria supports a bacterial origin for the plant terpene synthase gene family. *Horticulture research*, 11(10), uhae221.

Li S, et al. (2024) Genome-wide identification of B-box zinc finger (BBX) gene family in *Medicago sativa* and their roles in abiotic stress responses. *BMC genomics*, 25(1), 110.

Zhang X, et al. (2024) Genome-Wide Analyses of MADS-Box Genes Reveal Their Involvement in Seed Development and Oil Accumulation of Tea-Oil Tree (*Camellia oleifera*). *International journal of genomics*, 2024, 3375173.