

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

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: 20260905T133115+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 358 mentions in open access literature.

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

Liu Q, et al. (2026) Genome-wide characterisation and expression analysis of PLATZ gene family of *Eucalyptus grandis* under arbuscular mycorrhizal symbiosis. *Frontiers in plant science*, 17, 1727363.

Li X, et al. (2026) Functional Analysis of GhEXLB2 in Regulating Cotton Resistance to Verticillium Wilt. *Plants* (Basel, Switzerland), 15(11).

Tang Y, et al. (2026) Identification and Expression Analysis of the ??-1,3-Glucanase Gene Family in the Mycoparasitic *Alternaria alternata* KMR13 from Rose Powdery Mildew. *Microorganisms*, 14(6).

Lou Y, et al. (2026) Blood feeding-induced transcriptomic changes in the hard tick *Ixodes persulcatus*. *Frontiers in insect science*, 6, 1669026.

Li Y, et al. (2026) Analysis of BpbHLH Gene Family Responsive to MeJA Signalling in *Betula platyphylla* Suk. and Functional Mechanisms of BpbHLH42/44 in Genetic Improvement and Triterpenoid Biosynthesis. *Plant biotechnology journal*, 24(6), 4342.

Bai Y, et al. (2025) Genome-Wide Identification and Characterization of Heat Shock Proteins in the Stored-Product Pest *Rhyzopertha dominica* (Fabricius): Phylogenetic, Structural, and Stress-Induced Expression Analyses. *Insects*, 16(2).

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.

Sun C, et al. (2025) The PAP Gene Family in Cotton: Impact of Genome-Wide Identification on Fiber Secondary Wall Synthesis. *International journal of molecular sciences*, 26(9).

Semper C, et al. (2025) Global survey of secondary metabolism in *Aspergillus niger* via activation of specific transcription factors. *PNAS nexus*, 4(8), pgaf249.

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.

An P, et al. (2025) Genome-Wide Identification and Analysis of bZIP Transcription Factor Gene Family in Broomcorn Millet (*Panicum miliaceum* L.). *Genes*, 16(7).

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.

Zhu X, et al. (2025) Genome-Wide Characterization of the MDS Gene Family in *Gossypium* Reveals GhMDS11 as a Key Mediator of Cold Stress Response. *International journal of molecular sciences*, 26(20).

Guo X, et al. (2025) Genome-Wide Identification and Expression Analysis of Amino Acid/Auxin Permease (AAP) Genes in Grapes (*Vitis vinifera* L.) Under Abiotic Stress and During Development. *Plants (Basel, Switzerland)*, 14(1).

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.

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.

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.

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.