# **Resource Summary Report**

Generated by RRID on May 18, 2025

# **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

**Proper Citation:** Conserved Domain Database (RRID:SCR\_002077)

**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: database, data or information resource

**Defining Citation:** PMID:25414356, PMID:18984618

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

sequence, structure, amino acid, gold standard

**Funding:** 

Resource Name: Conserved Domain Database

Resource ID: SCR 002077

**Alternate IDs:** nif-0000-02647

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

**Record Creation Time:** 20220129T080211+0000

Record Last Update: 20250517T055517+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 297 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.

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.

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.

Xie J, et al. (2024) The C4 photosynthesis bifunctional enzymes, PDRPs, of maize are coopted 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).

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.

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

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.

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.

Liu Y, et al. (2024) Genome-Wide Analysis of Trehalose-6-Phosphate Phosphatase Gene Family and Their Expression Profiles in Response to Abiotic Stress in Groundnut. Plants (Basel, Switzerland), 13(8).

Xing Y, et al. (2024) Evolution and function analysis of auxin response factors reveal the molecular basis of the developed root system of Zygophyllum xanthoxylum. BMC plant biology, 24(1), 81.

Gokulanathan A, et al. (2024) Glucose influence cold tolerance in the fall armyworm, Spodoptera frugiperda via trehalase gene expression. Scientific reports, 14(1), 27334.

Li X, et al. (2024) Genome-wide identification of the wall-associated kinase gene family and their expression patterns under various abiotic stresses in soybean (Glycine max (L.) Merr). Frontiers in plant science, 15, 1511681.

Nassar M, et al. (2023) The survival of Amblyomma sculptum ticks upon blood-feeding depends on the expression of an inhibitor of apoptosis protein. Parasites & vectors, 16(1), 96.

Germon A, et al. (2023) Protein disulfide isomerase A3 activity promotes extracellular accumulation of proteins relevant to basal breast cancer outcomes in human MDA-MB-A231 breast cancer cells. American journal of physiology. Cell physiology, 324(1), C113.

Sun Y, et al. (2023) The Space Environment Activates Capsular Polysaccharide Production in Lacticaseibacillus rhamnosus Probio-M9 by Mutating the wze (ywqD) Gene. Microbiology spectrum, 11(2), e0467722.

Tripathi S, et al. (2023) Defining the condensate landscape of fusion oncoproteins. Nature communications, 14(1), 6008.

Farhan Y, et al. (2023) Genetic mutations linked to field-evolved Cry1Fa-resistance in the European corn borer, Ostrinia nubilalis. Scientific reports, 13(1), 8081.