

Resource Summary Report

Generated by [dkNET](#) on Apr 27, 2025

Conserved Domains Search

RRID:SCR_018729

Type: Tool

Proper Citation

Conserved Domains Search (RRID:SCR_018729)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>

Proper Citation: Conserved Domains Search (RRID:SCR_018729)

Description: Web tool for conserved domains searching within protein or coding nucleotide sequence.

Synonyms: CD-search

Resource Type: service resource, data or information resource, web service, data access protocol, software resource

Keywords: Conserved domain, protein, coding nucleotide sequence, domain search, domain, nucleotide sequence

Funding:

Availability: Free, Freely available

Resource Name: Conserved Domains Search

Resource ID: SCR_018729

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250426T060729+0000

Ratings and Alerts

No rating or validation information has been found for Conserved Domains Search.

No alerts have been found for Conserved Domains Search.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1067 mentions in open access literature.

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

Yan XC, et al. (2025) Single-cell transcriptomic profiling of maize cell heterogeneity and systemic immune responses against *Puccinia polysora* Underw. *Plant biotechnology journal*, 23(2), 549.

Lan P, et al. (2025) Molecular and biological characterization of infectious full-length cDNA clones of two viruses in *Paris yunnanensis*, including a novel potyvirus. *Scientific reports*, 15(1), 473.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (*Oryza sativa* L.) and their expression profiles in response to phytohormones. *PLoS one*, 20(1), e0317008.

Purnama PR, et al. (2025) Uncovering genetic determinants of antioxidant properties in Thai landrace rice through genome-wide association analysis. *Scientific reports*, 15(1), 1443.

Tian Z, et al. (2025) Genome-wide identification and analysis of the NF-Y transcription factor family reveal its potential roles in tobacco (*Nicotiana tabacum* L.). *Plant signaling & behavior*, 20(1), 2451700.

Bende G, et al. (2025) The *Neosartorya* (*Aspergillus*) *fischeri* antifungal protein NFAP2 has low potential to trigger resistance development in *Candida albicans* in vitro. *Microbiology spectrum*, 13(1), e0127324.

Liu X, et al. (2025) Comparative analysis of HKTs in six poplar species and functional characterization of PyHKTs in stress-affected tissues. *BMC genomics*, 26(1), 18.

Yang T, et al. (2025) Genome-Wide Study of Plant-Specific PLATZ Transcription Factors and Functional Analysis of OsPLATZ1 in Regulating Caryopsis Development of Rice (*Oryza sativa* L.). *Plants* (Basel, Switzerland), 14(2).

Poonsiri T, et al. (2025) SidF, a dual substrate N5-acetyl-N5-hydroxy-L-ornithine transacetylase involved in *Aspergillus fumigatus* siderophore biosynthesis. *Journal of*

structural biology: X, 11, 100119.

Xu Z, et al. (2025) An orphan viral genome with unclear evolutionary status sheds light on a distinct lineage of flavi-like viruses infecting plants. *Virus evolution*, 11(1), veaf001.

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (*Lobesia botrana*). *Viruses*, 17(1).

Yu L, et al. (2025) Unraveling TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR Transcription Factors in Safflower: A Blueprint for Stress Resilience and Metabolic Regulation. *Molecules* (Basel, Switzerland), 30(2).

Liu C, et al. (2025) Decarboxylase mediated oxalic acid metabolism is important to antioxidation and detoxification rather than pathogenicity in *Magnaporthe oryzae*. *Virulence*, 16(1), 2444690.

Ou C, et al. (2025) Functional Characterization of the PoWHY1 Gene from *Platycladus orientalis* and Its Role in Abiotic Stress Tolerance in Transgenic *Arabidopsis thaliana*. *Plants* (Basel, Switzerland), 14(2).

Li J, et al. (2025) Genome-Wide Identification and Expression Analysis of bHLH-MYC Family Genes from Mustard That May Be Important in Trichome Formation. *Plants* (Basel, Switzerland), 14(2).

Chen Y, et al. (2025) Genomic, Evolutionary, and Pathogenic Characterization of a New Polorovirus in Traditional Chinese Medicine *Viola philippica*. *Viruses*, 17(1).

Zhang J, et al. (2025) Genome-wide identification of the Sec14 gene family and the response to salt and drought stress in soybean (*Glycine max*). *BMC genomics*, 26(1), 73.

Huang R, et al. (2025) The Identification of Auxin Response Factors and Expression Analyses of Different Floral Development Stages in Roses. *Genes*, 16(1).

Wang H, et al. (2025) In Silico Exploration of Staphylococcal Cassette Chromosome mec (SCCmec) Evolution Based on Phylogenetic Relationship of ccrAB/C. *Microorganisms*, 13(1).

Song L, et al. (2025) Wheat Leaf Rust Effector Pt48115 Localized in the Chloroplasts and Suppressed Wheat Immunity. *Journal of fungi* (Basel, Switzerland), 11(1).