

Resource Summary Report

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Batch Web CD-Search Tool

RRID:SCR_018756

Type: Tool

Proper Citation

Batch Web CD-Search Tool (RRID:SCR_018756)

Resource Information

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

Proper Citation: Batch Web CD-Search Tool (RRID:SCR_018756)

Description: Web tool for detection of structural and functional domains in protein sequences. Allows computation and download of conserved domain annotation for large sets of protein queries. Allows to view results graphically. Shows domain footprints, alignment details, and conserved features on any individual query sequence.

Synonyms: NCBI Batch CD Search Tool, Batch conserved domain search, Conserved Domain Search service, CD-search

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

Defining Citation: [PMID:15215404](#)

Keywords: Functional domain detection, protein sequence, protein sequence domain, functional domain, protein, nucleotide sequence, conserved domain search, bio.tools

Funding: NIH Intramural Research Program

Availability: Free, Freely available

Resource Name: Batch Web CD-Search Tool

Resource ID: SCR_018756

Alternate IDs: biotools:cd-search

Alternate URLs: <https://bio.tools/cd-search>

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260919T195358+0000

Ratings and Alerts

No rating or validation information has been found for Batch Web CD-Search Tool.

No alerts have been found for Batch Web CD-Search Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 838 mentions in open access literature.

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

Wei Y, et al. (2026) The identification of gibberellin 2-oxidase gene family in cotton and functional analysis. BMC plant biology, 26(1).

Liu Q, et al. (2026) Single-cell and spatial transcriptomics define 20E-driven developmental reprogramming in silkworm wing disc. Nature communications, 17(1).

Iqbal M, et al. (2026) MdBBX47, a B-box transcription factor directly and indirectly regulates ALA-induced anthocyanin accumulation in apple. BMC plant biology, 26(1).

Zhang D, et al. (2026) Genome-Wide Identification of the CCCH Gene Family and Functional Exploration of MdC3H49 Under Drought Stress Response in Apple (*Malus domestica*). Plants (Basel, Switzerland), 15(8).

Zhang Z, et al. (2026) Bioinformatics analysis of the KEA gene family in rice. Open life sciences, 21(1), 20251230.

Liu J, et al. (2026) Transcriptome-based identification of the WRKY gene family in *Polygala tenuifolia* Willd. and their response to cold stress. BMC plant biology, 26(1).

Du C, et al. (2026) Genome-wide identification and expression pattern analysis of the COBRA-like gene family of *Triticum aestivum* (L.) under drought and heat stresses. BMC plant biology, 26(1).

Wang H, et al. (2026) Genome-wide analysis of flax bZIP genes using a T2T genome reveals abiotic stress roles. iScience, 29(2), 114671.

Chen D, et al. (2026) Genome-wide identification, evolutionary diversification and developmental expression of the Sox gene family in three brachyuran crabs. BMC genomics, 27(1).

Wang D, et al. (2026) Genome-wide identification and stress-responsive expression analysis of the Actin-Depolymerizing Factor (ADF) gene family in *Avena sativa* L. BMC plant biology, 26(1).

Xue H, et al. (2026) Genome-wide identification and expression analysis under selenium stress of glutaredoxin system genes in *Cardamine hupingshanensis*. *BMC plant biology*, 26(1).

Zhu X, et al. (2026) Comparative genomics of light harvesting chlorophyll a/b binding protein (LHC) family in green jujube (*Ziziphus mauritiana*) reveal the effect of domestication based on haplotype-resolved genome. *BMC plant biology*, 26(1).

Cerruti GV, et al. (2026) Genome-wide analysis of the R2R3-MYB family reveals potential regulators of lignin and tricin metabolism in the model grass *Setaria viridis*. *Molecular genetics and genomics* : MGG, 301(1), 38.

Wu Y, et al. (2026) Genome-wide identification and salt stress response analysis of the WD40 protein family in *Populus yunnanensis*. *BMC genomics*, 27(1), 207.

Li Y, et al. (2026) Regulation of Pollen Viability, Pollen Tube Growth and Seed Development in Maize by Application of Cysteine Protease ZmPCP. *Plants (Basel, Switzerland)*, 15(5).

Martínez-Flores I, et al. (2026) Comparative genomics of methicillin-resistant and -susceptible *Staphylococcus aureus* from Mexico City hospitals. *Microbiology spectrum*, 14(4), e0314025.

He L, et al. (2026) Pan-Genome Analysis of the Fructokinase Gene Family Reveals a Light-Regulated SiPhyC-SiFRK4 Module Controlling Carbon Partitioning in Foxtail Millet. *Plants (Basel, Switzerland)*, 15(6).

Guo Z, et al. (2026) Genome-wide identification and functional characterization of the ABF gene family in maize reveals ZmABF8 as a key regulator of drought tolerance. *Frontiers in plant science*, 17, 1849922.

Basharat S, et al. (2026) Bioinformatic analysis, expression analysis, and subcellular localization of GeBP transcriptional regulator family in response to abiotic stress in *Brassica napus*. *Frontiers in plant science*, 17, 1858194.

Yan J, et al. (2026) Weak Phd2-Hif-1? Affinity Coupled with High Basal Expression Is Predicted to Enhance HIF Pathway Flexibility in Nile Tilapia (*Oreochromis niloticus*). *Animals : an open access journal from MDPI*, 16(10).