

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

Defining Citation: [PMID:15215404](https://pubmed.ncbi.nlm.nih.gov/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: 20250509T060306+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 306 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Chen B, et al. (2025) Functional analysis of key members affecting egg production in the transglutaminase gene family in chickens. *Poultry science*, 104(2), 104794.

Feng X, et al. (2025) Genome-Wide Analysis of bZIP Transcription Factors and Expression Patterns in Response to Salt and Drought Stress in *Vaccinium corymbosum*. *International journal of molecular sciences*, 26(2).

Zhang J, et al. (2025) Genome- and Transcriptome-Wide Characterization and Expression Analyses of bHLH Transcription Factor Family Reveal Their Relevance to Salt Stress Response in Tomato. *Plants (Basel, Switzerland)*, 14(2).

Tan ZW, et al. (2025) Genome-Wide Analysis of the APETALA2/Ethylene-Responsive Factor Gene Family in *Carthamus tinctorius* L. *Plant direct*, 9(1), e70032.

Rungsirivanich P, et al. (2025) Functional genomic insights into *Floricoccus penangensis* ML061-4 isolated from leaf surface of Assam tea. *Scientific reports*, 15(1), 2951.

Wang HW, et al. (2025) Identification, characterization, and expression of *Oryza sativa* tryptophan decarboxylase genes associated with fluroxypyr-meptyl metabolism. *The plant genome*, 18(1), e20547.

Wang Y, et al. (2025) Identification of the CaCRT gene family and function of CaCRT1 under low-temperature stress in pepper (*Capsicum annuum* L.). *Scientific reports*, 15(1), 90.

Sun T, et al. (2025) Re-Examination Characterization and Screening of Stripe Rust Resistance Gene of Wheat TaPR1 Gene Family Based on the Transcriptome in Xinchun 32. *International journal of molecular sciences*, 26(2).

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.

Rizwan HM, et al. (2025) The members of zinc finger-homeodomain (ZF-HD) transcription factors are associated with abiotic stresses in soybean: insights from genomics and expression analysis. *BMC plant biology*, 25(1), 56.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. *BMC plant biology*, 25(1), 57.

Yao PH, et al. (2025) Differential detoxification enzyme profiles in C-corn strain and R-rice strain of *Spodoptera frugiperda* by comparative genomic analysis: insights into host adaptation. *BMC genomics*, 26(1), 14.

Zhao X, et al. (2025) Genome-Wide Identification and Expression Analysis of PkNRT Gene Family in Korean Pine (*Pinus koraiensis*). *Plants (Basel, Switzerland)*, 14(2).

Yang X, et al. (2025) Genome-wide characterization of the MADS-box gene family in *Paeonia ostii* and expression analysis of genes related to floral organ development. *BMC genomics*, 26(1), 49.

Zhao L, et al. (2025) m6A demethylase CpALKBH regulates CpZap1 mRNA stability to modulate the development and virulence of chestnut blight fungus. *mBio*, 16(1), e0184424.

Zhao Y, et al. (2025) Genome-wide Characterization of the MBF1 Gene Family and Its Expression Pattern in Different Tissues and Under Stresses in *Medicago truncatula* and *Medicago sativa*. *International journal of molecular sciences*, 26(2).

Xiong Y, et al. (2025) Quantitative Trait Loci Identification and Candidate Genes Characterization for Indole-3-Carbinol Content in Seedlings of *Brassica napus*. *International journal of molecular sciences*, 26(2).

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).

Wu J, et al. (2025) Identification and functional characterization of AsWRKY9, a WRKY transcription factor modulating alliin biosynthesis in garlic (*Allium sativum* L.). *BMC biology*, 23(1), 14.

Wen J, et al. (2024) An integrated multi-omics approach reveals polymethoxylated flavonoid biosynthesis in *Citrus reticulata* cv. Chachiensis. *Nature communications*, 15(1), 3991.