

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: software resource, data access protocol, service 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: 20260801T190618+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 368 mentions in open access literature.

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

Lu SS, et al. (2025) Transcriptome and VcCADs gene family analyses reveal mechanisms of blight resistance in rabbiteye blueberry. *Frontiers in plant science*, 16, 1601658.

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.

Zhang T, et al. (2025) Regulation of Stomatal Responses to Pathogen and Drought Stress by the F-Box Protein AtSKIP5. *Molecular plant pathology*, 26(3), e70074.

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).

Gong F, et al. (2025) Genome-wide identification and expression analysis of the PYL gene family in response to salt, drought and cold stresses in *Solanum melongena* L. *BMC genomics*, 26(1), 1007.

Singh S, et al. (2025) A comprehensive analysis to speculate the role of trithorax genes in photoperiod-mediated tuberization in potato and comparison with storage root crops. *BMC plant biology*, 25(1), 1603.

Lou H, et al. (2025) Regulation and functional analysis of BvMBF1c in response to *Cercospora* leaf spot (CLS) stresses in sugar beet (*Beta vulgaris* L.). *BMC plant biology*, 25(1), 1574.

Wen J, et al. (2025) Dynamic transcriptomic features accompanying the onset of first flowering in roses. *BMC plant biology*, 26(1), 23.

Zhang Y, et al. (2025) LuCSD3 enhances salt stress tolerance in flax: genome-wide profiling and functional validation of the SOD gene family. *Frontiers in plant science*, 16, 1609085.

Jafri RA, et al. (2025) Changes in the Adenylate Kinase Activity are Proportional to the ADP/ATP Ratio Upon Resorption and Regeneration of *Chlamydomonas reinhardtii*

Flagella. Cell biochemistry and biophysics, 83(4), 5035.

Wang K, et al. (2025) Two novel trimethoprim resistance genes, *dfra50* and *dfra51*, identified in phage-plasmids. Antimicrobial agents and chemotherapy, 69(7), e0169524.

Sun X, et al. (2025) *Hamiltonella* symbionts benefit whitefly fertilization by regulating the maternal protein Tudor-mediated piRNA pathway. Proceedings of the National Academy of Sciences of the United States of America, 122(24), e2427053122.

Chen Y, et al. (2025) Genome-wide identification, characterization, and expression analysis of the *SOS1* gene family in the medicinal plant *Paeonia ostii* under salt stress. Frontiers in plant science, 16, 1614011.

Lin X, et al. (2025) Natural-selected plastics biodegradation species and enzymes in landfills. PNAS nexus, 4(3), pgaf066.

Wu N, et al. (2025) Genome-wide identification and expression analysis of soybean bHLH transcription factor and its molecular mechanism on grain protein synthesis. Frontiers in plant science, 16, 1481565.

Tian Y, et al. (2025) Genome-wide identification, phylogeny, and expression analysis of PEBP gene family in *Castanea mollissima*. Frontiers in genetics, 16, 1530910.

Penot-Raquin M, et al. (2025) Prevalence and environmental abundance of the TSET complex in cosmopolitan algal groups. iScience, 28(6), 112679.

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).

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.

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.