

Resource Summary Report

Generated by ASWG on Aug 2, 2026

dbCAN

RRID:SCR_013208

Type: Tool

Proper Citation

dbCAN (RRID:SCR_013208)

Resource Information

URL: <http://csbl.bmb.uga.edu/dbCAN/>

Proper Citation: dbCAN (RRID:SCR_013208)

Description: A web server and DataBase for automated Carbohydrate-active enzyme ANnotation, funded by the BioEnergy Science Center of the DOE., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: dbCAN

Resource Type: data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

Keywords: FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: dbCAN

Resource ID: SCR_013208

Alternate IDs: OMICS_01678

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260801T190456+0000

Ratings and Alerts

No rating or validation information has been found for dbCAN.

No alerts have been found for dbCAN.

Data and Source Information

Usage and Citation Metrics

We found 723 mentions in open access literature.

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

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Liu W, et al. (2025) RDBSB: a database for catalytic bioparts with experimental evidence. *Nucleic acids research*, 53(D1), D709.

Yue H, et al. (2025) Enzyme Repertoires and Genomic Insights into *Lycium barbarum* Pectin Polysaccharide Biosynthesis. *Genomics, proteomics & bioinformatics*, 22(6).

Xiang X, et al. (2025) Chinese soy-based microbiome and associated microbial risks: a metagenomic investigation. *NPJ biofilms and microbiomes*, 11(1), 136.

Peng X, et al. (2025) Expanded genetic and functional diversity of oceanic fungi. *Microbiome*, 13(1), 179.

Miao Y, et al. (2025) A novel decomposer-exploiter interaction framework of plant residue microbial decomposition. *Genome biology*, 26(1), 20.

Viver T, et al. (2025) Comparative metagenomics indicates metabolic niche differentiation of benthic and planktonic Woeseiaceae. *Environmental microbiome*, 20(1), 74.

Guo K, et al. (2025) Organic matter degradation by oceanic fungi differs between polar and non-polar waters. *Nature communications*, 16(1), 7589.

Teune M, et al. (2025) Biochemical Characterization of Multimodular Xylanolytic Carbohydrate Esterases from the Marine Bacterium *Flavimarina* sp. Hel_I_48. *Chembiochem : a European journal of chemical biology*, 26(13), e202500058.

González-Serrano F, et al. (2025) Amphibian skin bacteria contain a wide repertoire of genes linked to their antifungal capacities. *World journal of microbiology & biotechnology*, 41(3), 78.

Nguyen TT, et al. (2025) In silico and in vitro analyses reveal the potential use of *Streptomyces parvulus* VNUA74 as bioagent for sustainable banana production. *Scientific reports*, 15(1), 7049.

Maeke MD, et al. (2025) Extensive data mining uncovers novel diversity among members of the rare biosphere within the Thermoplasmata. *Microbiome*, 13(1), 155.

Petersen C, et al. (2025) The Interaction Between the Nematode *Caenorhabditis elegans* and Its Coexisting Fungal Microbiome Member *Barnettozyma californica*. *Environmental microbiology reports*, 17(4), e70177.

Rhein-Knudsen N, et al. (2025) Identification and Characterization of a New Thermophilic α -Carrageenan Sulfatase. *Journal of agricultural and food chemistry*, 73(3), 2044.

Berkhout MD, et al. (2025) Milk and mucin glycans orchestrate a synthetic infant gut microbiota structure. *FEMS microbiology ecology*, 101(8).

Li B, et al. (2025) Comparative macrogenomics reveal plateau adaptation of gut microbiome in cervids. *BMC biology*, 23(1), 154.

Bhattacharjee D, et al. (2025) Diversity and prevalence of *Anaerostipes* in the human gut microbiota. *bioRxiv : the preprint server for biology*.

Hou L, et al. (2025) Microbial metabolism in laboratory reared marine snow as revealed by a multi-omics approach. *Microbiome*, 13(1), 114.

Lind AL, et al. (2025) Contiguous and complete assemblies of *Blastocystis* gut microbiome-associated protists reveal evolutionary diversification to host ecology. *Genome research*, 35(6), 1377.

Hirooka Y, et al. (2025) α -Characterisation of the genome and secretome of *Phytophthora cryptogea* and *P. erythrosetica*. *IMA fungus*, 16, e156195.