

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 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: service resource, data or information resource, data analysis service, database, 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: 20260729T044324+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 [dkNET](#) .

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

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

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

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

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

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.

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.

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

Maeke MD, et al. (2025) Extensive data mining uncovers novel diversity among members of the rare biosphere within the Thermoplasmatota. *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.

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

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

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

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.

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

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

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

Zhang Z, et al. (2025) Probiotic-induced enrichment of *Adlercreutzia equolifaciens* increases gut microbiome wellness index and maps to lower host blood glucose levels. *Gut microbes*, 17(1), 2520407.

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.