

Resource Summary Report

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CAZy- Carbohydrate Active Enzyme

RRID:SCR_012909

Type: Tool

Proper Citation

CAZy- Carbohydrate Active Enzyme (RRID:SCR_012909)

Resource Information

URL: <http://www.cazy.org>

Proper Citation: CAZy- Carbohydrate Active Enzyme (RRID:SCR_012909)

Description: Database that describes the families of structurally-related catalytic and carbohydrate-binding modules (or functional domains) of enzymes that degrade, modify, or create glycosidic bonds. This specialist database is dedicated to the display and analysis of genomic, structural and biochemical information on Carbohydrate-Active Enzymes (CAZymes). CAZy data are accessible either by browsing sequence-based families or by browsing the content of genomes in carbohydrate-active enzymes. New genomes are added regularly shortly after they appear in the daily releases of GenBank. New families are created based on published evidence for the activity of at least one member of the family and all families are regularly updated, both in content and in description. An original aspect of the CAZy database is its attempt to cover all carbohydrate-active enzymes across organisms and across subfields of glycosciences. One can search for CAZY Family pages using the Protein Accession (Genpept Accession, Uniprot Accession or PDB ID), Cazy family name or EC number. In addition, genomes can be searched using the NCBI TaxID. This search can be complemented by Google-based searches on the CAZy site.

Abbreviations: CAZy

Synonyms: Carbohydrate-Active enZYme, Carbohydrate-Active enZYmes Database

Resource Type: database, data or information resource

Defining Citation: [PMID:24270786](#)

Keywords: carbohydrate, carbohydrate-binding, carbohydrate binding module, carbohydrate esterase, catalytic binding, glycosidic bond, glycosidic hydrolase, glycosyl transferase, polysaccharide lyase, enzyme class, enzyme, module, genome, virus, bio.tools, FASEB list

Resource Name: CAZy- Carbohydrate Active Enzyme

Resource ID: SCR_012909

Alternate IDs: r3d100012321, biotools:cazy, OMICS_01677, nif-0000-02642, SCR_012935

Alternate URLs: <https://bio.tools/cazy>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260808T190243+0000

Ratings and Alerts

No rating or validation information has been found for CAZy- Carbohydrate Active Enzyme.

No alerts have been found for CAZy- Carbohydrate Active Enzyme.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2435 mentions in open access literature.

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

Shi R, et al. (2026) The novel synbiotic (Lactiplantibacillus plantarum and galacto-oligosaccharides) ameliorates obesity-related metabolic dysfunction: Arginine as a key mediator signaling molecule. Journal of advanced research, 81, 111.

Zhuo JJ, et al. (2026) Biological Activities, Health Benefits and Synthesis of Equol and Its Derivatives: A Comprehensive Review. Food science & nutrition, 14(1), e71443.

Han H, et al. (2026) Whole-genome analysis and fermentation-metabolite profiling of a cellulolytic Arthrobacter sp. FMD isolated from forest musk-deer faeces. BMC microbiology, 26(1), 43.

Wang H-Q, et al. (2026) Structural and functional insights into Uly1040, an ulvan lyase from polysaccharide lyase family 40. Applied and environmental microbiology, 92(2), e0210125.

Kajiura H, et al. (2026) Protein-Derived Signal Peptides Induced by Agrobacterium Infection Promote the Secretion of Recombinant Proteins in Nicotiana benthamiana. Plant biotechnology journal, 24(1), 187.

- Sai ZP, et al. (2026) Green bioconversion of insoluble chitin: chitinase development pathways via multi-strategy synergy. *Bioresources and bioprocessing*, 13(1), 16.
- Castro-Amorim J, et al. (2026) Mechanism of Hyaluronic Acid Hydrolysis Catalyzed by Snake Venom Hyaluronidase. *Journal of chemical information and modeling*, 66(7), 4033.
- Tigabu A, et al. (2026) Broad-spectrum antibiotic treatment reshapes the gut microbiome, resistome, and colonization potential of opportunistic pathogens: a metagenomics study. *Gut pathogens*, 18(1).
- Kataoka R, et al. (2026) Effects of *Aspergillus oryzae*-derived rice-koji protein on the sake metabolome. *Applied and environmental microbiology*, 92(3), e0195525.
- Qian Y, et al. (2026) Metagenomic sequencing and binning reveal carbon cycling microorganisms and gene functions in park environments. *BMC microbiology*, 26(1).
- Fan C, et al. (2026) Fecal carbohydrate-degrading bacteria are associated with reduced incidence of lower gastrointestinal GVHD. *Blood advances*, 10(6), 1979.
- Wei C, et al. (2026) Lipid Metabolism and Membrane Remodeling Drive Sclerotium Formation in *Morchella eximia*: Insights from Integrated Transcriptomics and Metabolomics. *Journal of fungi (Basel, Switzerland)*, 12(2).
- Koníťíková R, et al. (2026) Molecular Insights into the Activation of a Fungal Copper Radical Oxidase by Peroxidases. *Chem & bio engineering*, 3(2), 199.
- Amir A, et al. (2026) Seasonal diet shifts alter the gut microbiome and resistome of captive geriatric giant pandas (*Ailuropoda melanoleuca*). *BMC microbiology*, 26(1).
- Kajiura H, et al. (2026) N-Glycoengineering of insect cells for tri-antennary N-glycan biosynthesis. *Scientific reports*, 16(1).
- Ohnuma T, et al. (2026) MoChia1 is a GH18 reducing-end GlcNAc-releasing chitin oligosaccharide hydrolase from the rice blast fungus *Magnaporthe oryzae*. *The Journal of biological chemistry*, 302(6), 111462.
- Wang X, et al. (2026) *Niallia yueguangensis* sp. nov., a novel bacterium from maize rhizosphere in saline-alkaline soil enhancing plant salt tolerance. *BMC microbiology*, 26(1).
- Watanabe A, et al. (2026) Characterization of a novel bifunctional endo- α -1,4-glucanase/mannanase from *Aspergillus oryzae*. *Applied microbiology and biotechnology*, 110(1).
- Das R, et al. (2026) Microbial community structure, functional potential, probiotic signatures, and MAG reconstruction of fermented bamboo shoots from Northeast India. *FEMS microbes*, 7, xtag032.
- Tingley JP, et al. (2026) Distribution of microbial carrageenan foraging pathways reveals a widespread latent trait within the ruminant intestinal microbiome. *Nature communications*, 17(1).