

Resource Summary Report

Generated by [dkNET](#) on May 21, 2025

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: data or information resource, database

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

Funding:

Resource Name: CAZy- Carbohydrate Active Enzyme

Resource ID: SCR_012909

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

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250521T061440+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 1902 mentions in open access literature.

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

Forsberg Z, et al. (2025) A modular enzyme with combined hemicellulose-removing and LPMO activity increases cellulose accessibility in softwood. The FEBS journal, 292(1), 75.

Espinheira RP, et al. (2025) Discovery and Characterization of Mannan-Specialized GH5 Endo-1,4-?-mannanases: a Strategy for Açaí (Euterpe oleracea Mart.) Seeds Upgrading. Journal of agricultural and food chemistry, 73(1), 625.

Bao Z, et al. (2025) Microbiome dynamics and functional profiles in deep-sea wood-fall micro-ecosystem: insights into drive pattern of community assembly, biogeochemical processes, and lignocellulose degradation. Applied and environmental microbiology, 91(1), e0216524.

Rüttiger AS, et al. (2025) The global RNA-binding protein RbpB is a regulator of polysaccharide utilization in Bacteroides thetaiotaomicron. Nature communications, 16(1), 208.

Schwartz LA, et al. (2025) Carbohydrate Deacetylase Unique to Gut Microbe *Bacteroides* Reveals Atypical Structure. *Biochemistry*, 64(1), 180.

Payne PE, et al. (2025) Uncovering novel functions of the enigmatic, abundant, and active *Anaerolineae* in a salt marsh ecosystem. *mSystems*, 10(1), e0116224.

Marjamaa K, et al. (2025) LPMO-Catalyzed Oxidation of Cellulosic Fibers with Controlled Addition of a Reductant and H₂O₂. *ACS sustainable chemistry & engineering*, 13(1), 220.

Theobald S, et al. (2025) Comparative genomics of *Aspergillus nidulans* and section *Nidulantes*. *Current research in microbial sciences*, 8, 100342.

Trudeau ED, et al. (2025) Origins of xyloglucan-degrading enzymes in fungi. *The New phytologist*, 245(2), 458.

Plouhinec L, et al. (2025) Unlocking soybean meal pectin recalcitrance using a multi-enzyme cocktail approach. *Scientific reports*, 15(1), 1716.

Yang Y, et al. (2025) A Chromosome-Scale Genome of *Trametes versicolor* and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene Biosynthesis. *Journal of fungi (Basel, Switzerland)*, 11(1).

Dai W, et al. (2025) Metagenomic Insights into Pigeon Gut Microbiota Characteristics and Antibiotic-Resistant Genes. *Biology*, 14(1).

Vuillemin M, et al. (2025) Discovery of Lacto-N-Biosidases and a Novel N-Acetylactosaminidase Activity in the CAZy Family GH20: Functional Diversity and Structural Insights. *Chembiochem : a European journal of chemical biology*, 26(2), e202400710.

Monteiro R, et al. (2025) Molecular properties of the RmlT wall teichoic acid rhamnosyltransferase that modulates virulence in *Listeria monocytogenes*. *Nature communications*, 16(1), 24.

Lombard V, et al. (2025) CAZac: an activity descriptor for carbohydrate-active enzymes. *Nucleic acids research*, 53(D1), D625.

Nakazawa Y, et al. (2025) Structure and function of a β -1,2-galactosidase from *Bacteroides xylanisolvens*, an intestinal bacterium. *Communications biology*, 8(1), 66.

Mokshina N, et al. (2025) A Fresh Look at Celery Collenchyma and Parenchyma Cell Walls Through a Combination of Biochemical, Histochemical, and Transcriptomic Analyses. *International journal of molecular sciences*, 26(2).

Guo L, et al. (2025) Mining versatile feruloyl esterases: phylogenetic classification, structural features, and deep learning model. *Bioresources and bioprocessing*, 12(1), 7.

Jin Z, et al. (2024) Dapagliflozin ameliorates diabetes-induced spermatogenic dysfunction by modulating the adenosine metabolism along the gut microbiota-testis axis. *Scientific reports*,

14(1), 641.

Netherway T, et al. (2024) Pervasive associations between dark septate endophytic fungi with tree root and soil microbiomes across Europe. *Nature communications*, 15(1), 159.