

Resource Summary Report

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Glycosylation Pathways Database

RRID:SCR_013486

Type: Tool

Proper Citation

Glycosylation Pathways Database (RRID:SCR_013486)

Resource Information

URL: <http://web.mit.edu/glycomics/gt/gtdb.shtml>

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Description: A pathway-based graphical interface for navigating the glycoenzyme database. The goal of the project is to define the paradigms by which carbohydrate binding proteins function in cellular communication. These pages are divided into six categories: -Glycosphingolipid: Sub-categories are Isogloboseries, Globoseries, Neo-lactoseries, Lactoseries and Ganglioseries - N-linked: Sub-categories are High-mannose, Hybrid and Complex -Mucin -Terminal Core 1 -Other O-linked -Terminal All: Includes all potential terminal structures for each glycan category

Synonyms: GTDB

Resource Type: data or information resource, database

Keywords: binding, carbohydrate, glycoenzyme, glycosylation, pathway, protein

Funding: NIGMS

Resource Name: Glycosylation Pathways Database

Resource ID: SCR_013486

Alternate IDs: nif-0000-20850

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260806T054601+0000

Ratings and Alerts

No rating or validation information has been found for Glycosylation Pathways Database.

No alerts have been found for Glycosylation Pathways Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 683 mentions in open access literature.

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

Farias FM, et al. (2026) Streptocyclin BTW is a novel member of a diverse family of circular bacteriocins in the genus *Streptococcus*. *Molecular nutrition & food research*, 70(1), e70290.

Li Z, et al. (2026) Phylogenetic and functional characterization of Asgard primases. *Molecular biology and evolution*, 43(1).

Kimbrel JA, et al. (2026) High-quality *Acinetobacter* genomes recovered from combat wounds via metagenomic sequencing resemble cultured isolate genomes. *Microbiology spectrum*, 14(1), e0187625.

Song LCT, et al. (2026) Identification of proteins influencing CRISPR-associated transposases for enhanced genome editing. *Science advances*, 12(1), eaea1429.

Song W, et al. (2026) Distinct patterns of microbial association across deep-sea corals from the Western Pacific Magellan Seamounts. *Microbiology spectrum*, 14(1), e0209325.

Häggglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Boukhchtaber DC, et al. (2025) Discovering Hidden Archaeal and Bacterial Lipid Producers in a Euxinic Marine System. *Environmental microbiology*, 27(3), e70054.

Bao Z, et al. (2025) MultiTax-human: an extensive and high-resolution human-related full-length 16S rRNA reference database and taxonomy. *Microbiology spectrum*, 13(2), e0131224.

Maghini DG, et al. (2025) Expanding the human gut microbiome atlas of Africa. *Nature*, 638(8051), 718.

Low SJ, et al. (2025) PathoGD: an integrative genomics approach to primer and guide RNA design for CRISPR-based diagnostics. *Communications biology*, 8(1), 147.

Santos CA, et al. (2025) A metagenomic 'dark matter' enzyme catalyses oxidative cellulose conversion. *Nature*, 639(8056), 1076.

Chen N, et al. (2025) Novel Gene Clusters for Secondary Metabolite Synthesis in Mesophotic Sponge-Associated Bacteria. *Microbial biotechnology*, 18(2), e70107.

Zeng Z, et al. (2025) Oxidative adaptations in prokaryotes imply the oxygenic photosynthesis before crown-group Cyanobacteria. *PNAS nexus*, 4(2), pgaf035.

Jiang Q, et al. (2025) Cold seeps are potential hotspots of deep-sea nitrogen loss driven by microorganisms across 21 phyla. *Nature communications*, 16(1), 1646.

Priest T, et al. (2025) Seasonal recurrence and modular assembly of an Arctic pelagic marine microbiome. *Nature communications*, 16(1), 1326.

Liu Y, et al. (2025) Timescale and genetic linkage explain the variable impact of defense systems on horizontal gene transfer. *Genome research*, 35(2), 268.

Castelli M, et al. (2025) Hepatinotholaceae (Alphaproteobacteria) are Distinct From Holosporales and Independently Evolved to Associate With Ecdysozoa. *Environmental microbiology*, 27(1), e70028.

Lao HY, et al. (2025) *Scrofinimicrobium appendicitidis* sp. nov., isolated from a patient with ruptured appendicitis. *International journal of systematic and evolutionary microbiology*, 75(1).

Miebach J, et al. (2025) Importance, structure, cultivability, and resilience of the bacterial microbiota during infection of laboratory-grown *Haematococcus* spp. by the blastocladial pathogen *Paraphysoderma sedebokerense*: evidence for a domesticated microbiota and its potential for biocontrol. *FEMS microbiology ecology*, 101(2).

Calderón-Osorno M, et al. (2025) The influence of depth on the global deep-sea plasmidome. *Scientific reports*, 15(1), 2959.