

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: 20260912T200212+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 859 mentions in open access literature.

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

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.

Jourdain L, et al. (2026) Environmental selection constrains metabolic network architecture despite taxonomic turnover in anaerobic digestion communities. *The ISME journal*, 20(1).

Nguyen TT, et al. (2026) Arctic deep-sea hydrothermal microbiomes as a natural niche for novel antimicrobial peptides. *BMC microbiology*, 26(1).

Tow WK, et al. (2026) Metagenomic insights into urolithin formation from rambutan rind extract by rat faecal-derived microbiome. *Applied microbiology and biotechnology*, 110(1).

Giacomini JJ, et al. (2026) Spatial ecology of the *Capnocytophaga* genus in the human oral cavity. *Microbiology spectrum*, 14(6), e0362625.

Liu Z, et al. (2026) Dietary regulation on gut resistome linked with microbial amino acid metabolism in pigs. *Animal microbiome*, 8(1).

Quiles-Perez CJ, et al. (2026) Anaerobic riboflavin degradation by human gut *Lachnospiraceae*. *bioRxiv : the preprint server for biology*.

Midani FS, et al. (2026) Infant gut microbiomes contribute to metabolic states that impact brain function. *bioRxiv : the preprint server for biology*.

Lu Z, et al. (2026) Tick-vectored mobilization of antibiotic resistance genes: transboundary dissemination across wildlife-livestock-vector-environment interfaces. *NPJ biofilms and microbiomes*, 12(1).

Jihnaoui N, et al. (2026) *Bradyrhizobium cedriense* sp. nov., a novel rhizobial species isolated from *Acacia saligna* nodules grown in polluted soils in Tunisia. *International journal of systematic and evolutionary microbiology*, 76(4).

Leroy M, et al. (2026) Microbiome and plasmidome shifts drive carbon, nitrogen, and greenhouse gas dynamics within transitioning permafrost. *Environmental microbiome*, 21(1).

Ma C, et al. (2026) Systematic evaluation of TCGA tumor microbiota reveals context-dependent reliability. *mSystems*, 11(5), e0018026.

Liu J, et al. (2026) Comprehensive profiling of antibiotic resistance, virulence genes, and mobile genetic elements in the gut microbiome of Tibetan antelopes. *mSystems*, 11(2), e0144325.

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

Bowerman KL, et al. (2026) A molecular inventory of the faecal microbiomes of 23 marsupial species. *Microbial genomics*, 12(1).

Brown JL, et al. (2026) Bacterial Community Composition and Functional Potential of the Kleptoplastic Sea Slug *Elysia papillosa*. *Biomolecules*, 16(6).

Peng X, et al. (2026) A 5.3-million-year-old deep-sea whale necropolis in the Diamantina Zone. *Nature*, 654(8120), 978.

Kim DD, et al. (2026) Metagenomic strain tracking reveals patterns of bacterial spread and the impact of water chlorination. *medRxiv : the preprint server for health sciences*.

Bi D, et al. (2026) Integrating ANI and phylogenies for re-evaluation of *Fusobacterium* taxonomy and disease associations. *Nature communications*, 17(1).

Korchagina MV, et al. (2026) Genome-resolved metagenomic survey of 500 samples from 56 hot springs across the Western US. *Scientific data*, 13(1).