

Resource Summary Report

Generated by PRECISE-TBI on Aug 27, 2026

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: 20260821T194002+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 [PRECISE-TBI](#) .

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.

Pudlo NA, et al. (2026) Description of *Hoskinsella mucinilytica* gen. nov., sp. nov., a mucin-degrading isolate from human faeces, and reclassification of *Amedibacillus hominis* Abdugheni et al. 2023 as a later heterotypic synonym of *Eubacterium hominis* Liu et al. 2022 within the genus *Hoskinsella* gen. nov. *International journal of systematic and evolutionary microbiology*, 76(1).

Downing BE, et al. (2026) Genus-specific remodeling of carbon and energy metabolism facilitates acetoclastic methanogenesis in *Methanosarcina* spp. and *Methanotherix* spp. *Journal of bacteriology*, 208(2), e0044825.

Stead CE, et al. (2026) Exploring the biotechnological potential of terrestrial hot spring microbiomes for CO₂ utilisation. *Environmental microbiome*, 21(1).

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.

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

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

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

Zhou J, et al. (2026) *Clostridium zhoujianii* sp. nov., a novel gram-negative species isolated from bat feces and its genetic characteristics. *BMC microbiology*, 26(1).

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).

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

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).

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

Lee HG, et al. (2026) metaFun: An analysis pipeline for metagenomic big data with fast and unified functional searches. *Gut microbes*, 18(1), 2611544.

Al-Hasan BA, et al. (2026) Complete genome sequence and functional characterization of *Bacillus amyloliquefaciens* NJF-55: a sheep-derived probiotic candidate. *Scientific reports*, 16(1), 6408.

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*.

Sun C, et al. (2026) Root microbiome dynamics favor slow-growth strategies during *Pinus* seedling development. *ISME communications*, 6(1), ycag018.

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

Prasoodanan Pk V, et al. (2026) Unbinned contigs expand known diversity in the global microbiome. *Nature microbiology*, 11(5), 1437.