

Resource Summary Report

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[GlycReSoft](#)

RRID:SCR_012122

Type: Tool

Proper Citation

GlycReSoft (RRID:SCR_012122)

Resource Information

URL: <https://code.google.com/p/glycresoft/>

Proper Citation: GlycReSoft (RRID:SCR_012122)

Description: A software package for automated recognition of glycans from LC/MS data.

Resource Type: software resource

Defining Citation: [PMID:23049804](#)

Keywords: software package

Availability: GNU General Public License

Resource Name: GlycReSoft

Resource ID: SCR_012122

Alternate IDs: OMICS_05674

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260808T185957+0000

Ratings and Alerts

No rating or validation information has been found for GlycReSoft.

No alerts have been found for GlycReSoft.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Balbisi M, et al. (2026) Distinct Proteomic and Glycosylation Signatures Differentiate A549 Tumor and BEAS-2B Nontumor Cell Line-Derived Small Extracellular Vesicles. *Molecular & cellular proteomics : MCP*, 25(3), 101524.

Tursumamat N, et al. (2026) High-sensitive glycomics using seGRAP-mass spectrometry uncovers a conserved N-glycome in single human oocytes. *Nature communications*, 17(1).

Lopandi Z, et al. (2025) Hybrid Adjuvant-Allergen H1sD2 Proteoforms Enhance Innate Immunity Activation via Distinct N-Glycosylation Profiles. *Cells*, 14(24).

Sugár SN, et al. (2025) Glycoproteomics Analysis of Triple Wild-Type Lung Adenocarcinoma Tissue Samples. *Journal of proteome research*, 24(5), 2419.

Andrade-Silva D, et al. (2025) N-Glycoproteomic Portraits of Bothrops Snake Venoms Reveal Evolutionarily Conserved and Divergent Phenotypes. *Journal of proteome research*, 24(12), 5948.

Chen G, et al. (2025) Structure-function relationship of the GH168 fucanase reveals an unusual enzyme recognition mechanism for sulfated polysaccharide. *Nature communications*, 16(1), 9216.

Klein J, et al. (2024) Expanding N-glycopeptide identifications by modeling fragmentation, elution, and glycome connectivity. *Nature communications*, 15(1), 6168.

Wojtkiewicz M, et al. (2024) Multinozzle Emitter for Improved Negative Mode Analysis of Reduced Native N-Glycans by Microflow Porous Graphitized Carbon Liquid Chromatography Mass Spectrometry. *Analytical chemistry*, 96(15), 5746.

Marie AL, et al. (2023) Highly-sensitive label-free deep profiling of N-glycans released from biomedically-relevant samples. *Nature communications*, 14(1), 1618.

Cavallero GJ, et al. (2022) O-Glycoproteomic analysis of engineered heavily glycosylated fusion proteins using nanoHILIC-MS. *Analytical and bioanalytical chemistry*, 414(27), 7855.

Chang D, et al. (2022) Improving Statistical Certainty of Glycosylation Similarity between Influenza A Virus Variants Using Data-Independent Acquisition Mass Spectrometry. *Molecular & cellular proteomics : MCP*, 21(11), 100412.

Sethi MK, et al. (2022) In-Depth Matrisome and Glycoproteomic Analysis of Human Brain Glioblastoma Versus Control Tissue. *Molecular & cellular proteomics : MCP*, 21(4), 100216.

Chang D, et al. (2021) Data-independent acquisition mass spectrometry for site-specific glycoproteomics characterization of SARS-CoV-2 spike protein. *Analytical and*

bioanalytical chemistry, 413(29), 7305.

Pan L, et al. (2021) In vitro fermentation and isolation of heparin-degrading bacteria from human gut microbiota. *Anaerobe*, 68, 102289.

Lang Y, et al. (2021) Comparison of Different Labeling Techniques for the LC-MS Profiling of Human Milk Oligosaccharides. *Frontiers in chemistry*, 9, 691299.

Cao S, et al. (2021) Cloning, Heterologous Expression, and Characterization of a ??-Carrageenase From Marine Bacterium *Wenyingzhuangia funcanilytica*: A Specific Enzyme for the Hybrid Carrageenan-Furcellaran. *Frontiers in microbiology*, 12, 697218.

Hackett WE, et al. (2021) The Need for Community Standards to Enable Accurate Comparison of Glycoproteomics Algorithm Performance. *Molecules (Basel, Switzerland)*, 26(16).

Li L, et al. (2020) Multi-task learning sparse group lasso: a method for quantifying antigenicity of influenza A(H1N1) virus using mutations and variations in glycosylation of Hemagglutinin. *BMC bioinformatics*, 21(1), 182.

Chang D, et al. (2020) Measuring Site-specific Glycosylation Similarity between Influenza a Virus Variants with Statistical Certainty. *Molecular & cellular proteomics : MCP*, 19(9), 1533.

Chen J, et al. (2019) Comparison of Low-Molecular-Weight Heparins Prepared From Ovine Heparins With Enoxaparin. *Clinical and applied thrombosis/hemostasis : official journal of the International Academy of Clinical and Applied Thrombosis/Hemostasis*, 25, 1076029619840701.