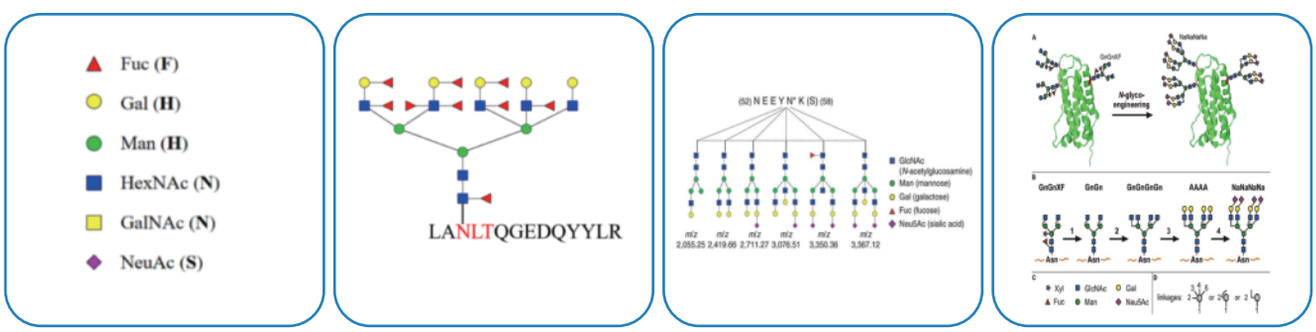
N-linked Intact Glycopeptides Proteomics Overview

Service Description

Glycosylation modification plays an important role in the formation of protein function and structure. Over half of the proteins present in living organisms undergo glycosylation modification. Glycosylated proteins are involved in various phenomena like cell adhesion, molecular recognition, and signal transduction. N-linked glycosylation is a prevalent and essential type of protein glycosylation modification. Precisely characterizing N-linked glycosylation is valuable for discovering disease biomarkers and potential therapeutic targets, as well as developing effective vaccines against various viruses.

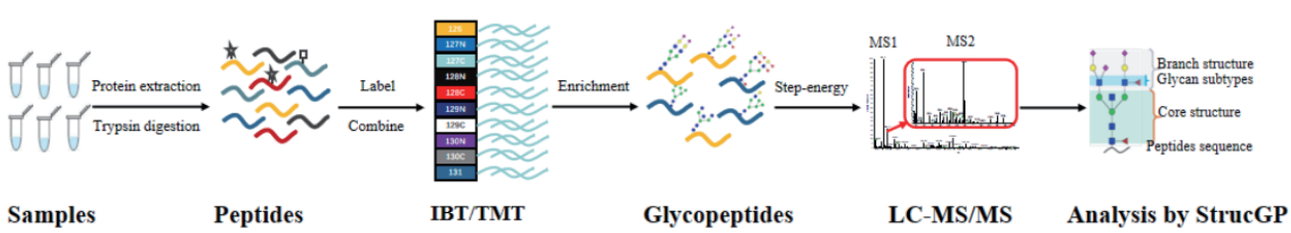
The structural analysis of site-specific glycans remains challenging due to the complexity of glycan structures and the heterogeneity of glycosylation. We provide an N-linked intact glycopeptide analysis to determine detailed N-glycan structures at the site-specific level by using the StrucGP[1], which was published in Nature Methods in 2021 and is the first software to distinguish different structure isoforms within the same glycan composition and identify new glycan structures. In addition, N-linked intact glycopeptides can be accurately quantified using isobaric label quantitative proteomics service.



Complex monosaccharide species	Complex glycan unchained structure	Multiple glycans at one glycosylation site	Multiple glycosylation sites at one protein

The complexity of glycan structures and the heterogeneity of glycosylation

Workflow



Advantages

Interprets precise glycan structures and identifies new/rare glycans without relying on glycan database.

Simultaneously obtains the glycan chain structure, glycosylation-modified peptide, and the relationship between the glycan chain and the glycosylation site.

Identifies over 5,000 glycopeptides for conventional full-spectrum identification and over 14000 for ultra-deep detection.

TMT (Tandem Mass Tags for Quantitation)/ IBT (Isobaric Tags for Quantitation) analysis can simultaneously compare 18 different samples.

Research Applications

Disease biomarker research

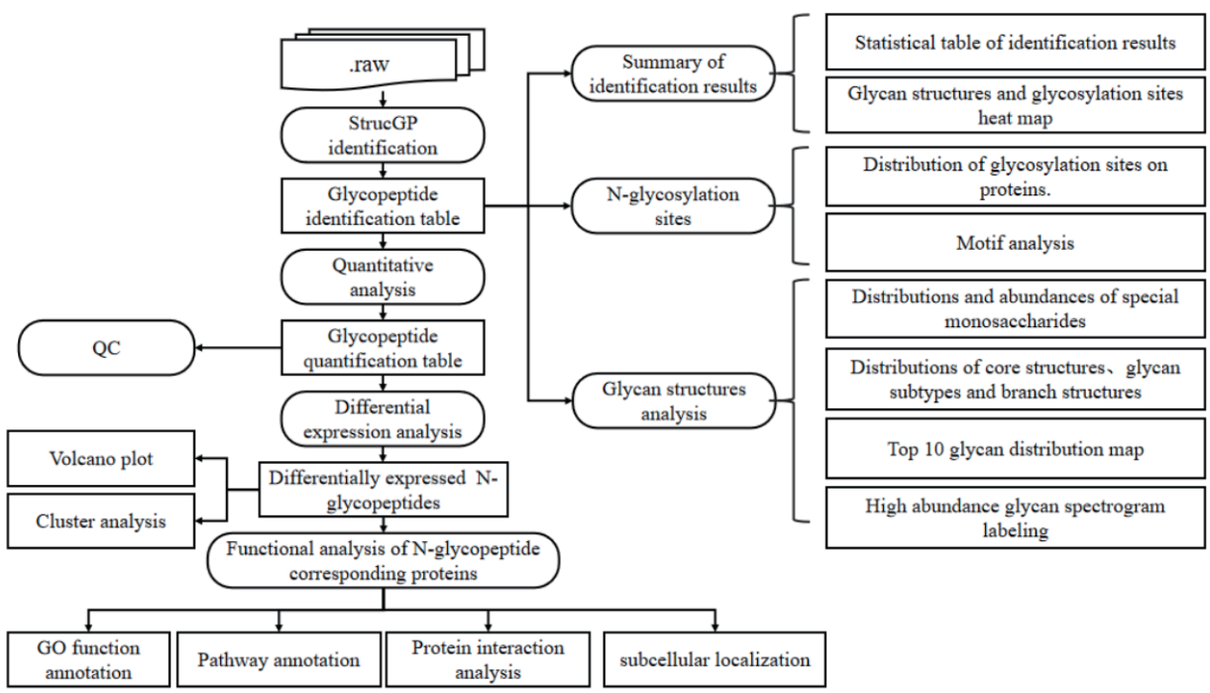
Molecular typing research

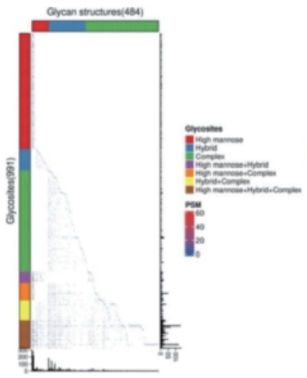
Molecular mechanism research

Growth and development research

Biologics characterization

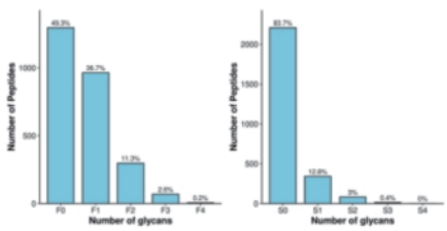
Results





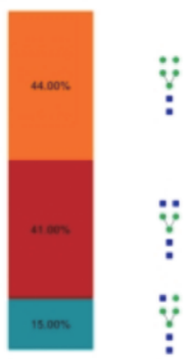
Glycan structures and glycosylation sites heat map

Identified glycan structures

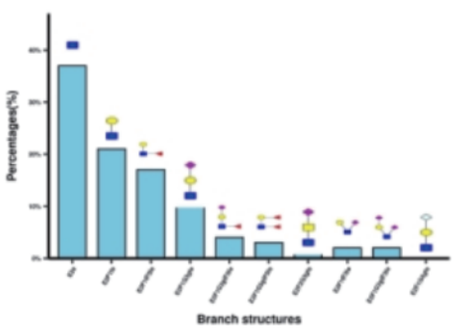


Distributions and abundances of special monosaccharides

Distributions of four core structures



Distributions of three glycan subtypes



Distributions and abundances of branch structures identified

General Sample Requirements

Sample Type		Sample Amount	
		Recommended	Minimum
Animal	Common animal tissues: animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc.	≥ 100 mg	≥ 50 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 100 mg	≥ 50 mg
Cell	Suspended cells, adherent cells	≥ $1x10^8$	≥ $5x10^7$
Protein Solution	Complex protein solution, protein powder	≥ 5 mg	≥ 3 mg
	Single protein (purified protein solution by IP, CO-IP, etc.)	30 μg	20 μg
Liquid	Serum and plasma	500 μL	300 μL
	Body fluid	2 mL	1 mL

Turn Around Time

Typical 4-5 weeks from sample QC acceptance to data report delivery

Reference

[1] StrucGP: de novo structural sequencing of site-specific N-glycan on glycoproteins using a modularization strategy. *Nat Methods*.2021

Request for Information or Quotation

Contact a BGI Genomics representative to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics.

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