

# Tailored Glycoproteomic Methods For The Sequencing, Mapping and Identification of Cellular Glycoproteins

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## 摘要

Protein glycosylation is an important post-translational modification of proteins that has profound effects on structure and function. However, the complex and nontemplated nature of glycans has been a barrier to studying many of their basic features, especially on a proteome-wide scale. We introduce a glycoproteomic method, glycoprotein identification and glycan mapping (GIDmap), that tailors the isolation of specific glycoprotein subpopulations based on display of metabolically inserted alkynyl sugar probes that can be selectively manipulated using the bioorthogonal Cu(I)-catalyzed [3 + 2] azide-alkyne cycloaddition. This saccharide-selective glycoprotein immobilization allows for subsequent manipulation and analysis of peptides and glycopeptides by liquid chromatography-tandem mass spectrometry. The power of GIDmap was demonstrated by mapping over 200 N-linked glycosylation sites from glycoproteins isolated from prostate cancer cells treated with an alkynyl sugar derivative of N-acetylmannosamine.

## 技術優勢

GIDmap is a robust method that aids in inventorying glycoproteins and mapping glycosylation sites, in addition to providing specific information about saccharide content and glycan behavior.

## 應用範圍

Glycoprotein identification on a proteome-wide scale  
Biomarker discovery

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