



Details about GRable

GRable is a software to estimate site-specific glycan compositions of glycopeptides, using an MS1-based glycoproteomic method named “Glyco-RIDGE” (Glycan heterogeneity-based Relational Identification of Glycopeptide signals on Elution profile).

First, this method identifies glycopeptide signals based on the chromatographic properties of glycopeptides and mass differences due to the glycan heterogeneity. That is, glycopeptides having the same core peptide but different glycans elute within a narrow range of elution time, so glycopeptide signals with a similar elution time and mass differences corresponding to glycan units (e.g. Hex, HexNAc, and dHex) can be assigned as a cluster, without MS2 spectrum analyses. In parallel, core peptides present actually in the glycopeptide sample are identified by PNGase-mediated deglycosylation followed by LC/MS.

The mass value of glycopeptide is sum of those of core peptide and glycan. Glycan mass is presumable from the glycan compositions. Therefore, the combination of peptide and glycan is searchable from these three lists, i.e., the masses of glycopeptides, peptides, and glycans.

If you belong to an academic research institute, you can use the full version without functional limitations by concluding a joint research agreement between your organization and AIST. Please contact us: M-GRable-inquiry-ml[at]aist.go.jp (at=@).

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Glyco-RIDGE method

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Applications of the Glyco-RIDGE method

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