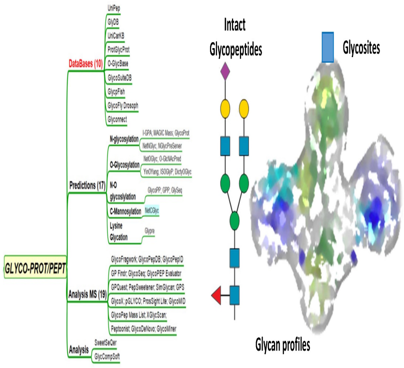
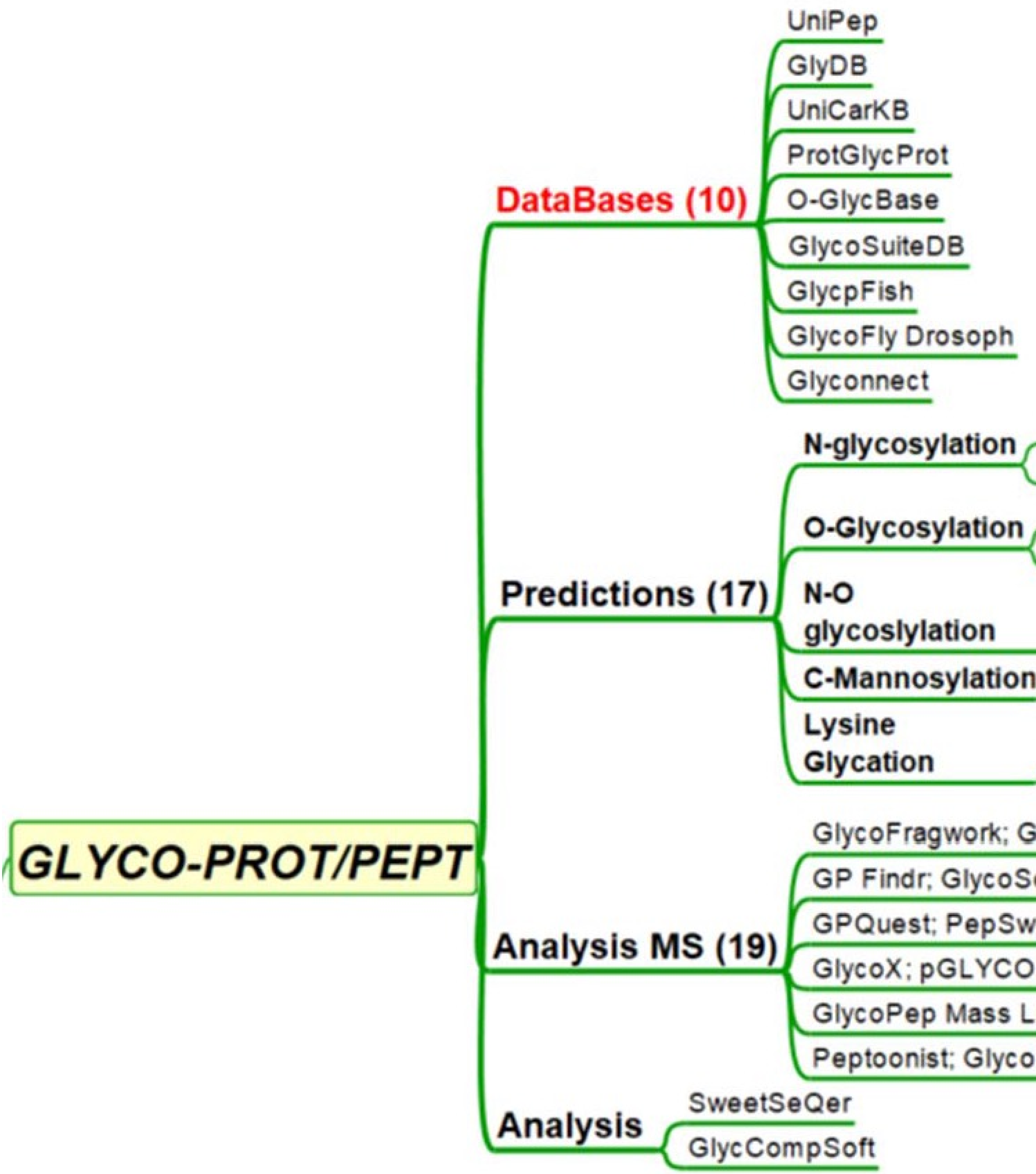


GlycoProteomics

Description


GLYCO-PROT/PEPT
DataBases (10)
UniPep
GlyDB
UniCarKB
ProtGlycProt
O-GlycBase
GlycoSuiteDB
GlycpFish
GlycoFly Drosoph
Glyconnect
Predictions (17)
N-glycosylation
O-Glycosylation
N-O glycoslylation
C-Mannosylation
Lysine Glycation
Analysis MS (19)
GlycoFragwork; G
GP Findr; GlycoS
GPQuest; PepSw
GlycoX; pGLYCO
GlycoPep Mass L
Peptoonist; Glyco
Analysis
SweetSeQer
GlycCompSoft

DATABASES

- **Glyconnect** https://glyconnect.expasy.org/ GlyConnect is a platform integrating sources of information to help characterise the molecular components of protein glycosylation
- **GlyDB** N-Glycan Structure Annotation of Glycopeptides Using a Linearized Glycan Structure Database
- **GlycoFish** http://betenbaugh.jhu.edu/GlycoFish A Database of Zebrafish N-linked Glycoproteins Identified Using SPEG Method Coupled with LC/MS
- **GlycoFly Drosoph** http://betenbaugh.jhu.edu/GlycoFly GlycoFly is a database for Drosophila N-linked glycoproteins identified using SPEG—MS techniques.
- **GlycoPAT** http://www. VirtualGlycome.org/glycopat GlycoProteomics Analysis Toolbox
- **GlyProt** http://www.glycosciences.de/glyprot/ GlyProt is a web-based tool that enables meaningful N-glycan conformations to be attached to all the spatially accessible potential N-glycosylation sites of a known three-dimensional (3D) protein structure.
- **GlycoSuiteDB** http://www.glycosuite.com GlycoSuiteDB is a relational database that curates information from the scientific literature on glyco-protein derived glycan structures
- **O-GlycBase** http://www.cbs.dtu.dk/databases/OGLYCBASE/ A database of glycoproteins with O-linked glycosylation sites
- **UniCarbKB** http://unicarbkb.org UniCarbKB : New database features for integrating glycan structure abundance, compositional glycoproteomics data, and disease associations
- **UniPep** http://www.unipep.org A database for human N-linked glycosites : a resource for biomarker discovery

PREDICTIONS

N-Glycosylation

- **I-GPA** Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation.
- **MAGIC** http://ms.iis.sinica.edu.tw/MAGIC-web/index.html. Identifies intact N-glycosylated peptides from a public protein database without requiring any prior information of proteins or glycans
- **NetNGlyc** http://www.cbs.dtu.dk/services/NtNGlyc/ The NetNglyc server predicts N-Glycosylation sites in human proteins using artificial neural networks that examine the sequence context of Asn-Xaa-Ser/Thr sequons
- **GlycoProt**

O-Glycosylation

- **DictyOGlyc** http://www.cbs.dtu.dk/services/DictyOGlyc/ The DictyOGlyc server produces neural network predictions for GlcNAc. O-glycosylation sites in *Dictyostelium discoideum* proteins.
- **ISOGlyP** isoglyp.utep.edu/ Provides isoform specific O-glycosylation prediction
- **NetOGlyc** www.cbs.dtu.dk/services/NetOGlyc/ The NetOglyc server produces neural network predictions of mucin type GalNAc O-glycosylation sites in mammalian proteins.
- **O-GlcNAcPred** http://121.42.167.206/OGlcPred/ A sensitive predictor to capture protein O-GlcNAcylation sites
- **YinOYang** www.cbs.dtu.dk/services/YinOYang/ The YinOYang WWW server produces neural

network predictions for O-ß-GlcNAc attachment sites in eukaryotic protein sequences.

N-O-Glycosylation

- **GlycoPP** http://crdd.osdd.net/raghava/glycopp/ GlycoPP is a webserver for predicting potential N- and O-glycosites in prokaryotic protein sequence(s)
- **GPP** http://comp.chem.nottingham.ac.uk/glyco/ Algorithmically prediction of N-linked and O-linked glycosylation.
- **GlySeq** http://www.glycosciences.de/tools/glyseq/Uses the PDB and SwissProt to perform statistical analysis of glycosylation site

C-Mannosylation

- **NetCGlyc** http://www.cbs.dtu.dk/services/NetCGlyc/ Prediction of mammalian C-mannosylation sites

Lysine Glycation

- **Glypre** http://www.cds.dtu.dk/databases/GlycateBase-1.0/ In Silico Prediction of Protein Glycation Sites by Fusing Multiple Features and Support Vector Machine

ANALYSIS

- **GlycCompSoft** http://www.heparin.rpi.edu Software for Automated Comparison of Low Molecular Weight Heparins Using Top-Down LC/MS Data
- **SweetSeQer** http://software.steenlab.org Simple de novo filtering and annotation of glycoconjugate mass spectra

ANALYSIS MS

- **GlycoDENovo** https://github.com/hongpengyu/GlycoDeNovoGlycoDeNovo provides an interpretation-graph which designates how to interpret each peak until the candidate topologies of precursor ion.
- **GlycoFragwork** http://darwin.informatics.indiana.edu/col/ A computational framework for identification of intact glycopeptides in complex samples
- **GP Finder** availabe from : cblebrilla@ucdavis.edu
- **GlycoMiner** http://www.szki.ttk.mta.hu/ms/glycominer/ A software tool to automatically identify tandem (MS/MS) spectra obtained in liquid chromatography/mass spectrometry
- **GlycoMID** http://proteomics.informatics.iupui.edu/software/glycomid/ A graph-based spectral alignment algorithm that can identify glycopeptides with multiple hydroxylysine O-glycosylation sites by tandem mass spectra.
- **GlycoPepDB** http://hexose.chem.ku.edu/sugar.php A Tool for Assigning Mass Spectrometry Data of N-Linked Glycopeptides on the Basis of Their Electron Transfer Dissociation Spectra
- **GlycoPEP Detector** http://glycopro.chem.ku.edu/ZZKHome.php. A Tool for Assigning Mass Spectrometry Data of N-Linked Glycopeptides on the Basis of Their Electron Transfer Dissociation Spectra
- **GlycoPEP Evaluator** https://desairegroup.ku.edu/research. GlycoPep Evaluator, generates

decoy glycopeptides de novo and enables accurate false discovery rate analysis for small data sets
- **GlycoPepID** http://www.hexose.chem.ku.edu/sugar.php
- **GlycoPep Mass List** MassList is an application that permits to compute theoretical glycopeptide masses while creating inclusion lists for targeted data acquisition on .
- **GPQuest** https://www.biomarkercenter.org/gpquest A Spectral Library Matching Algorithm for Site-Specific Assignment of Tandem Mass Spectra to Intact N-glycopeptides
- **GPS**http://edwardslab.bmcb.georgetown.edu/software/GlycoPeptideSearch.htmlTo explore site-specific N-glycosylation microheterogeneity of haptoglobin using glycopeptide CID tandem mass spectra and glycan database search.
- **GlycoSeq** https://github.com/dbaileychess/ GlycoSeq uses a heuristic iterated glycan sequencing algorithm that incorporates prior knowledge of the N-linked glycan synthetic pathway to achieve rapid glycan sequencing
- **GlycoX**To Determine Simultaneously the Glycosylation Sites and Oligosaccharide heterogeneity of Glycoproteins
- **pGLYCO** http://pfind.ict.ac.cn/software/pGlyco1505/ pGlyco is a software tool designed for the analysis of intact glycopeptides by using mass spectrometry.
- **Peptoonist** Peptoonist uses tandem mass spectrometry (MS/MS) to detect glycosylated peptides and single-MS to find the N-glycans present on each of these peptides
- **PepSweetener** EXPASY A Web?Based tool to support manual annotation of intact glycopeptide MS spectra
- **ProSIGHT Lite** http://www.prosightlite.northwestern.edu ProSight Lite : graphical software to analyze top?down mass spectrometry data
- **SimGlycan** http://www.premierbiosoft.com/glycan A predictive carbohydrate analysis tool for MS/MS data

Category

1. News