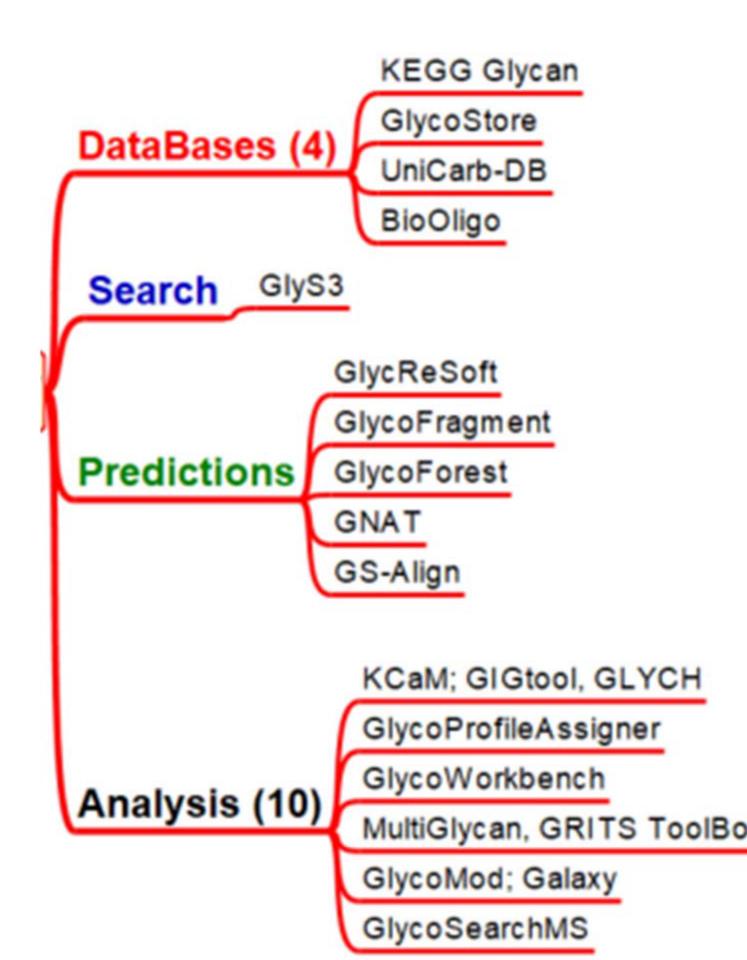


# Glycans

# Description



#### **DATABASES**

- BioOligo <a href="http://glyco3d.cermav.cnrs.fr/search.php?type=bioligo">http://glyco3d.cermav.cnrs.fr/search.php?type=bioligo</a> As part of the suite of interlinked Databases of 3D Structures of Glycan, BioOligo. contains representations, 3D structures and NMR spectra of most occurring glycans
- **GlycoStore** <a href="http://www.glycostore.org">http://www.glycostore.org</a> Provides a centralised resource that combines glycan structure information with chromatographic separation and electrophoretic data.
- KEGG Glycan <a href="https://www.genome.jp/kegg/glycan/">https://www.genome.jp/kegg/glycan/</a> The KEGG GLYCAN structure database is a collection of experimentally determined glycan structures. It contains all unique structures taken from CarbBank, structures entered from recent publications, and structures present in KEGG pathways
- UniCarb-DB <a href="http://unicarb-db.expasy.org/">http://unicarb-db.expasy.org/</a> UniCarb-DB is a structural and mass spectrometric database used in glycomics. UniCarb-DB provides over 1000 LC-MS/MS spectra for N- and O-linked glycans released from glycoproteins that were manually annotated.

#### **SEARCH**

GlyS3 <a href="https://glycoproteome.expasy.org/substructuresearch/">https://glycoproteome.expasy.org/substructuresearch/</a> GlyS3 matches any substructure such as glycan determinants to a large collection of structures recorded in GlyConnect and SugarBindDB.

### **PREDICTIONS**

- **GS Align** <a href="http://www.glycanstructure.org/gsalign">http://www.glycanstructure.org/gsalign</a> A computational method for glycan structure alignment and similarity measurement. GS-align generates possible alignments between two glycan structures
- **GlycoFragment**http://www.glycosciences.de/tools/GlycoFragments/manual.pdf A web tool to support the interpretation of mass spectra of complex carbohydrates.
- **GlycoForest** <a href="https://glycoforest.expasy.org/index.html">https://glycoforest.expasy.org/index.html</a> Glycoforest is a partial de-novo algorithm for sequencing glycan structures based on MS/MS spectra.
- GNAT <a href="http://gnatmatlab.sourceforge.net/">http://gnatmatlab.sourceforge.net/</a> Glycosylation Network Analysis Toolbox contains a variety of classes to describe glycans and glycosylation reaction networks. It also provides various methods to manipulate these classes
- **GlyReSoft** <a href="https://github.com/GlycReSoft2">https://github.com/GlycReSoft2</a> GlyReSoft is a modular software tool for assigning site specific glycosylation from bottom-up mass spectrometry data sets.

### **ANALYSIS**

- Galaxy <a href="http://www.glycoanalysis.info/galaxy2/manual/User\_Manual.pdf">http://www.glycoanalysis.info/galaxy2/manual/User\_Manual.pdf</a> Provides a useful method for an analytical procedure for N-glycan structures. Galaxy is a 2D/3D mapping method developed for the structural determination of asparagine-linked oligosaccharides (N-glycans) in glycoproteins.
- GIGTool <a href="https://www.genome.jp/tools/kcam/">https://www.genome.jp/tools/kcam/</a> GIG Tool is an application that extracts (i) precursor masses, (ii) oxonium ions and glycan fragments from tandem (liquid chromatography (LC)–MS/MS) mass spectra for glycan identification, and (iii) reporter ions from quaternary amine containing isobaric tag for glycan (QUANTITY) isobaric tags.
- GLYCH GLYCH (GLYcan CHaraterization) is package for glycan characterization using MS/MS.

- **GlycoMod** <a href="https://web.expasy.org/glycomod/">https://web.expasy.org/glycomod/</a> GlycoMod is a tool that can predict the possible oligosaccharide structures that occur on proteins from their experimentally determined masses
- **GlycoProfileAssigner** <a href="http://glycananalyzer.neb.com">http://glycananalyzer.neb.com</a> Automated structural assignment with error estimation for glycan LC data
- GlycoSearchMS <a href="http://www.glycosciences.de/database/start.php?action=form\_ms\_search">http://www.glycosciences.de/database/start.php?action=form\_ms\_search</a>
  GlycoSearchMS takes a list of mass spectra peak values as input and searches for matches with the calculated fragments of SweetDB structures.
- **GlycoWorkbench** <a href="https://glycoworkbench.software.informer.com/2.1/">https://glycoworkbench.software.informer.com/2.1/</a> A suite of software tools designed for the rapid drawing of glycan structures and for assisting the process of structure determination from mass spectrometry data.
- GRITS ToolBox <u>www.grits-toolbox.org/</u> GRITS Toolbox combines the analytical power of glycan permethylation with glycopeptide analysis, preserving site-specific information for comprehensive glycoprotein analysis
- KCaM<a href="https://www.genome.jp/tools/kcam/">https://www.genome.jp/tools/kcam/</a> KEGG Carbohydrate Matcher s a tool for the analysis of carbohydrate sugar chains, or glycans. It consists of a web-based graphical user interface that allows users to enter glycans easily with the mouse
- **MultiGlycan** <a href="https://bio.tools/MultiGlycan">https://bio.tools/MultiGlycan</a> To help user to gather glycan profile information from LC-MS Spectra. It also reports quantity of specific glycan composition

## Category

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