

CASPER – a tool for calculating NMR chemical shifts of oligo- and polysaccharides ↵
<http://www.casper.organ.su.se/casper/>

Glycan Builder – a software library and set of tools to allow for the rapid drawing of glycan structures with support for all of the most common symbolic notation formats↵
<http://www.unicarbk.org/builder>

GlycoDomainViewer – an online resource to study site glycosylation with respect to protein context and conservation↵
<http://glycodomain.glycomics.ku.dk/>

GlyMAP – an online resource mapping out the variational landscape of glyco-active enzymes ↵
<http://glymap.glycomics.ku.dk/>

GlycoMod – an online tool to predict oligosaccharide structures on proteins from experimentally determined masses↵
<http://web.expasy.org/glycomod/>

GlycoMiner/GlycoPattern – software tools designed to detect, characterize and perform relative quantitation of N-glycopeptides based on LC-MS runs↵
<http://www.szki.ttk.mta.hu/ms/glycominer/>

Glycosciences.de – a collection of databases and bioinformatics tools for glycobiology and glycomics↵
<http://glycosciences.de/index.php>

MonosaccharideDB – a comprehensive reference source for monosaccharide notation↵
<http://www.monosaccharidedb.org/start.action>

NetOGlyc – next generation prediction of O-glycosylation sites on proteins↵
<http://www.cbs.dtu.dk/services/NetOGlyc/>

SweetUnityMol – software to display 3-D structures of carbohydrates, polysaccharides and glycoconjugates↵
<http://sourceforge.net/projects/unitymol/files/>

CAZY – Carbohydrate Active Enzymes – describes the families of structurally-related catalytic and carbohydrate binding modules (or functional domains) of enzymes that degrade, modify or create glycosidic bonds↵
<http://www.cazy.org/>

Glycan Library – a list of approximately 830 lipid-linked sequence-defined glycan probes derived from diverse natural sources or chemically synthesised↵
<https://glycosciences.med.ic.ac.uk/glycanLibraryIndex.html>

GlycoBase 3.2 – a database of over 650 N- and O- linked glycan structures HPLC, UPLC, exoglycosidase sequencing and mass spectrometry (MALDI-MS, ESI-MS, ESI-MS/MS, LC-

MS, LC-ESI-MS/MS) data↵

https://glycobase.nibr.ie/glycobase/show_nibr.action

Glyco3D – a portal of 3D structures of mono, di, oligo and polysaccharides and carbohydrate recognizing proteins (lectin, monoclonal antibodies, glycosyltransferases and glycosaminoglycan binding proteins)↵

<http://glyco3d.cermav.cnrs.fr/home.php>

GlyGen : Computational and Informatics Resources for Glycoscience↵

GlyGen is a data integration and dissemination project for carbohydrate and glycoconjugate related data. GlyGen retrieves information from multiple international data sources and integrates and harmonizes this data. The GlyGen web portal allows exploration of this data and execution of unique searches that cannot be performed using any of the integrated databases in isolation. GlyGen also provides machine-readable APIs and a SPARQL endpoint to access the integrated data.↵

<https://www.glygen.org/>

GlyMAP – an online resource mapping out the variational landscape of glyco-active enzymes↵

<http://glymap.glycomics.ku.dk/>

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UniProtKB – the universal protein sequence database with information on glycosylated proteins↵

<http://www.uniprot.org/>

UniCarbKB↵

UniCarbKB is a curated and annotated glycan database which curates information from the scientific literature on glycoprotein derived glycan structures. It includes data previously available from GlycoSuiteDB.↵

<http://www.unicarbk.org/>

UniCarbDB↵

UniCarbDB is a platform for presenting glycan structures and fragment data characterised by LC-MS/MS strategies. The database is annotated with high-quality datasets and is designed to extend and reinforce those standards and ontologies developed by existing glycomics databases.↵

<http://unicarb-db.biomedicine.gu.se/>

SugarBindDB↵

SugarBindDB provides a collection of known carbohydrate sequences to which pathogenic organisms specifically adhere via lectins or adhesins. The data were compiled through an exhaustive search of literature published over the past 30 years by glycobiologists, microbiologists, and medical histologists.↵

<http://sugarbind.expasy.org/>

EXPASy

This section of the ExPASy server gathers a toolbox for processing data as well as simulating, predicting or visualising information, relative to glycans, glycoproteins and glycan-binding proteins.

<http://www.expasy.org/glycomics>