

Bioinformatics Demo Session

Demo Schedule & Location

Kalia Tower: Level 2 - Kahlili Suite

Monday 17th of November 2:30 pm - 4:00pm
 &
Tuesday 18th of November 3:45 pm - 5:45pm

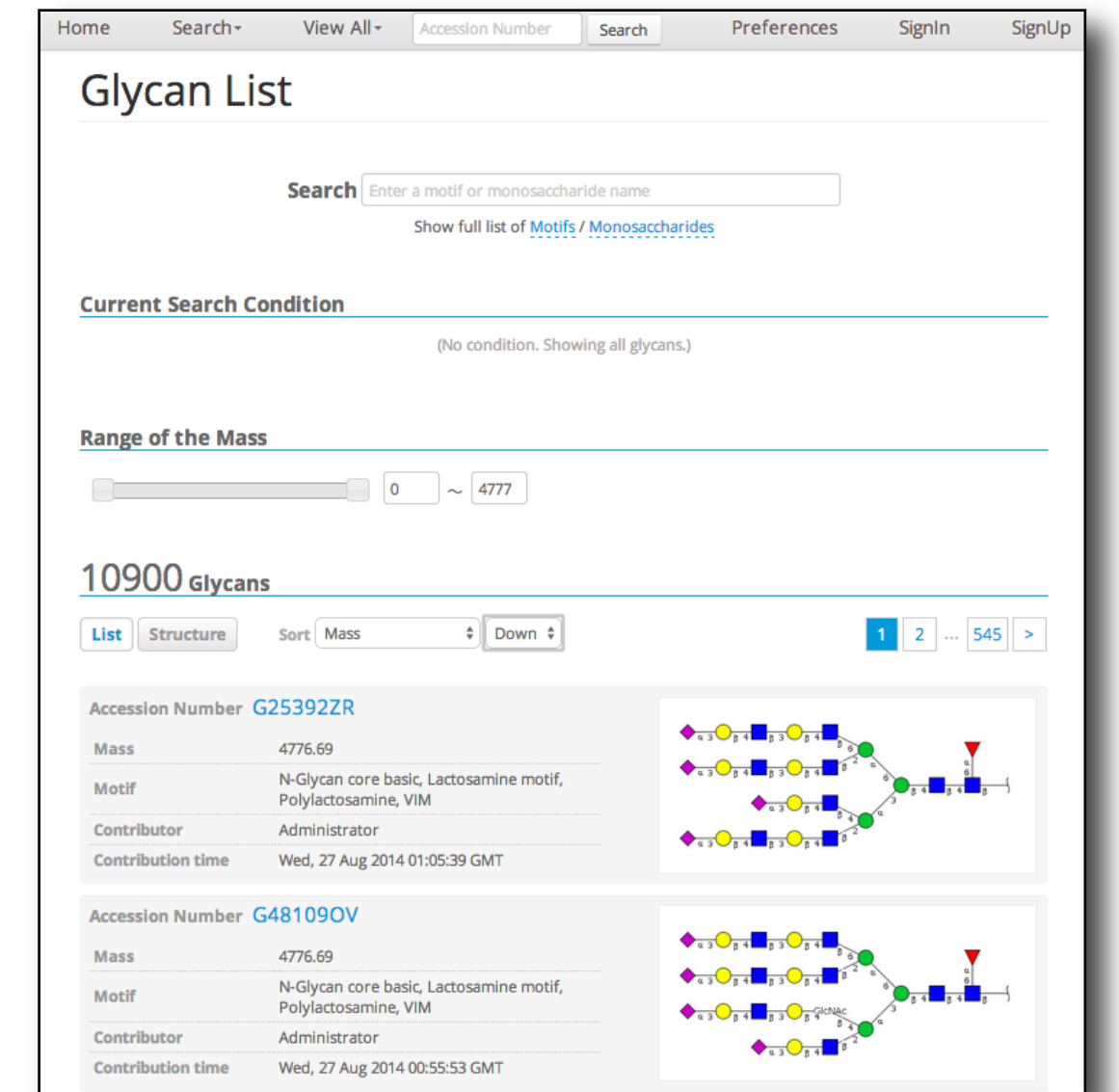
- GlyTouCan (Kiyoko Aoki-Kinoshita)
- UniCarbKB (Matthew Campbell)
- GlycoProtDB (Toshi Shikanai)
- GRITS toolbox (René Ranzinger)
- GNAT and GlycoPAT (Sriram Neelamegham)
- Glycam (Rob Woods)
- RINGS (Kiyoko Aoki-Kinoshita)

GlyTouCan

<http://glytoucan.org>

GlyTouCan is an international glycan structure repository, serving as a GenBank for glycan structures. This repository is a freely available, uncurated registry for glycan structures that assigns globally unique accession numbers to any glycan independent of the level of information provided by the experimental method used to identify the structure(s). Any glycan structure, ranging in resolution from monosaccharide composition to fully defined structures can be registered as long as there are no inconsistencies in the structure.

Talk in Session IX



UniCarbKB

Promoting the creation of online information storage and search platform for glycomics and glycobiology research. The demo session will cover:

UniCarbKB: building a glycoproteomics platform

UniCarbKB provides access to a curated database of information on the glycan structures of glycoproteins including global and site-specific attachment information

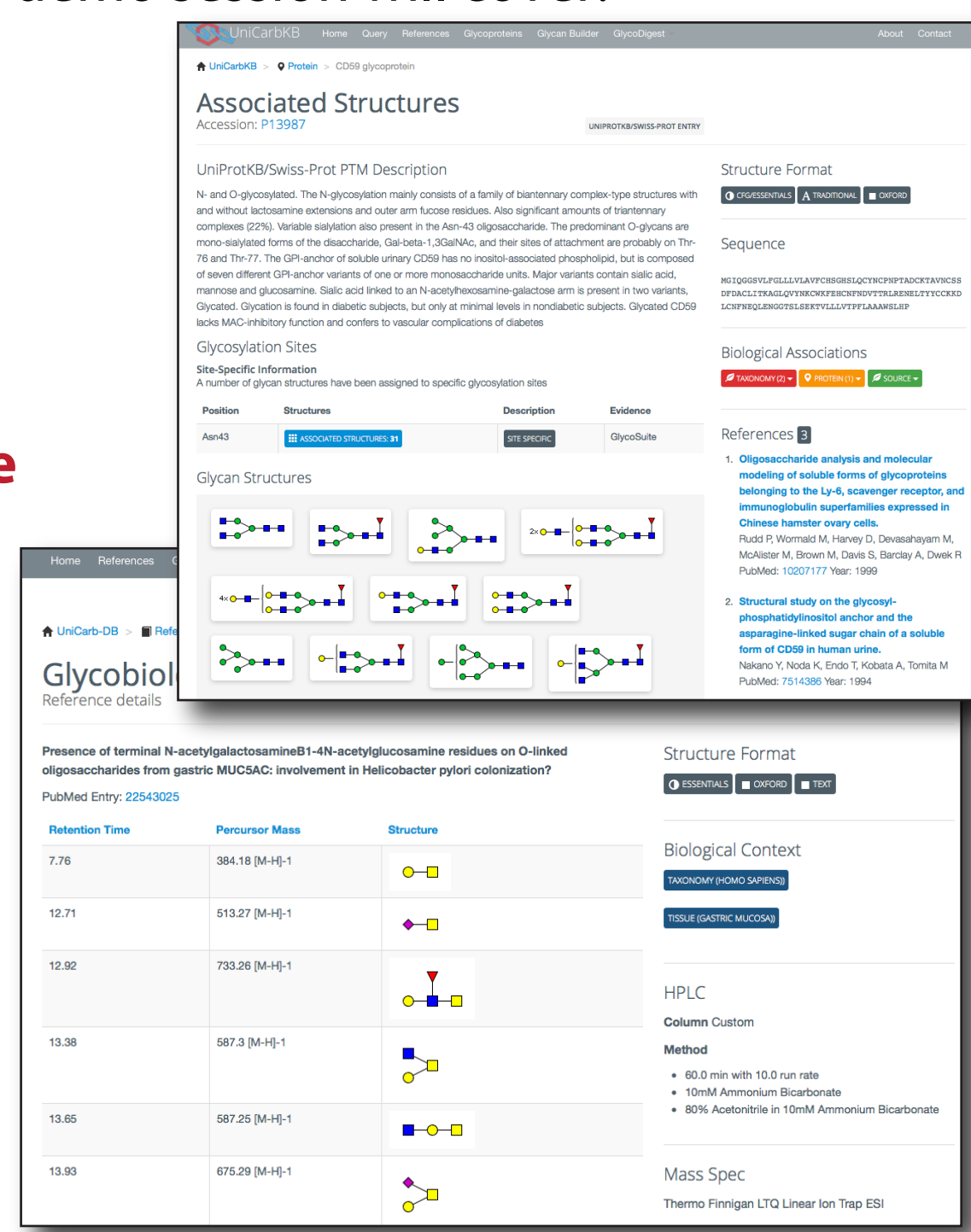
UniCarb-DB: an experimental LC-MS/MS database

Stemming from the success of EUROCarbDB, UniCarb-DB is a platform for storing and searching high-quality MS datasets

GlycoDigest: a tool for exoglycosidase digestions

Sequencing oligosaccharides by exoglycosidases is a powerful tool to determine the structure of complex glycans. This tool allows the targeted design of glycosidases to help guide glycan analysis

Poster 328

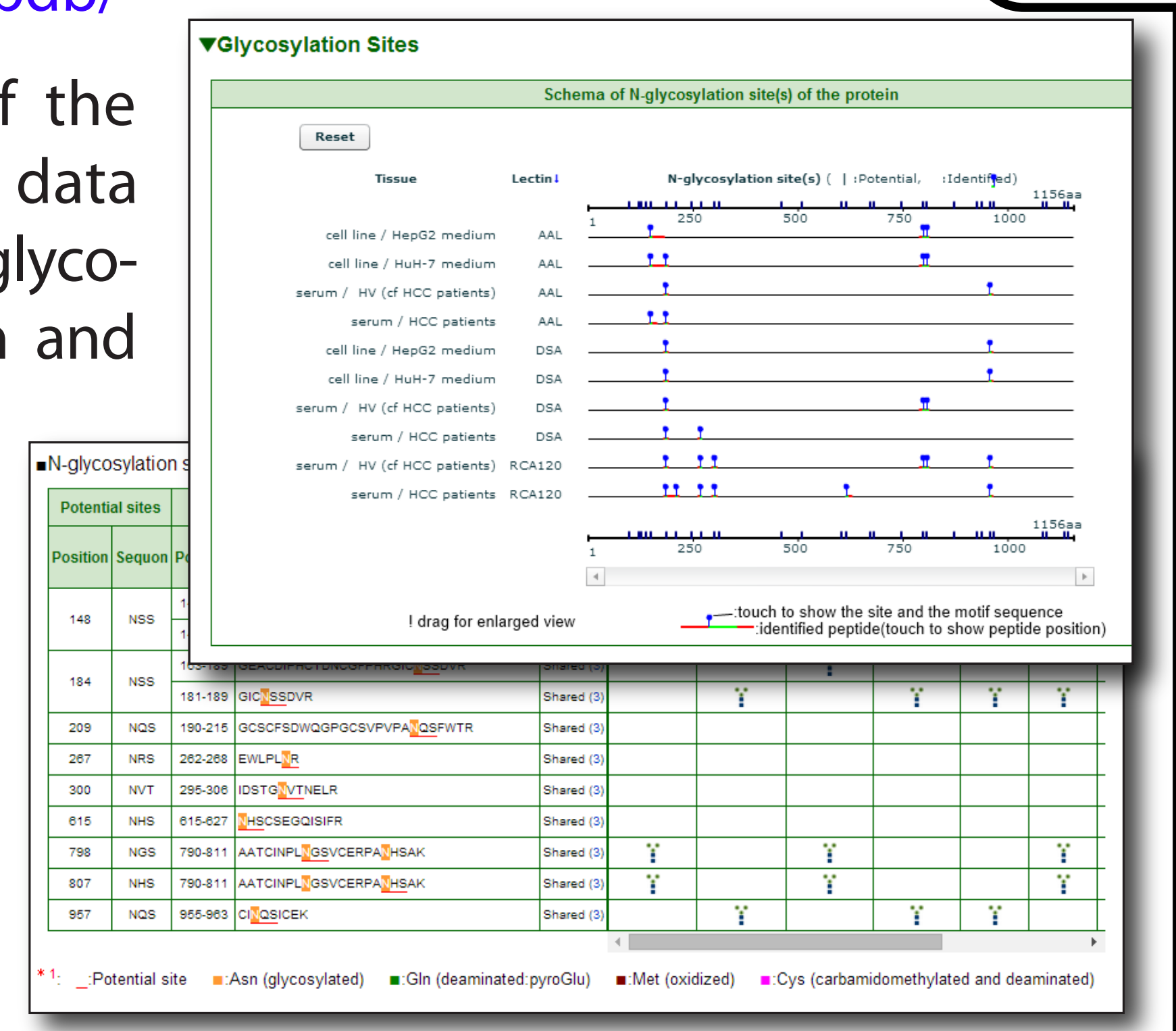


GlycoProtDB

<http://jcgdb.jp/rcmg/gpdb/>

GlycoProtDB consists of the experimentally-proven data of glycosylation sites for glycoproteins in mice, human and C. elegans. The data has been accumulated using the IGOT method. The database can be searched by gene ID, gene name, and gene description (protein name) as query.

Poster 325

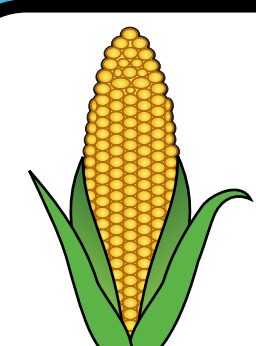


GRITS toolbox

<http://www.grits-toolbox.org>

GRITS toolbox is a freely available software suite for the annotation and interpretation of free glycan MS data. The software allows the processing of high-throughput MS data containing hundreds or even thousands of MS/MS spectra. GRITS toolbox also allows for the side-by-side comparison of glycans from different samples.

Poster 300



Tools for Systems Glycobiology

<http://sourceforge.net/projects/gnatmatlab/>

1. GlycoPAT: Analysis of high-throughput LC-MSⁿ glycoproteomics data

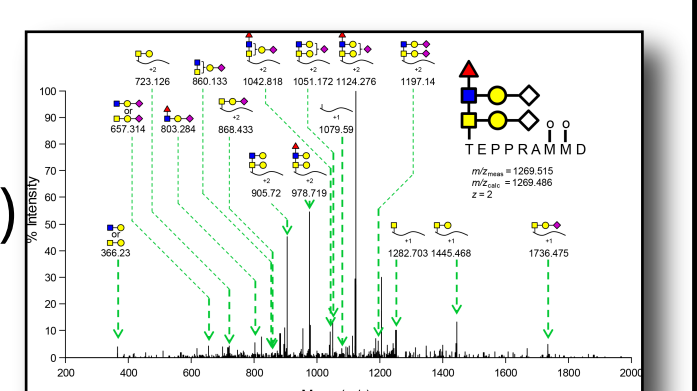
Input

Tandem-MS data (text or mzXML)

Open source/Free!
 SmallGlyPep nomenclature
 User friendly GUIs
 Parallel computing capable

Output

Spectra scoring (Xcorr, Pvalue etc.)
 False Discovery Rate



2. GNAT: Construction & simulation of glycosylation reaction networks

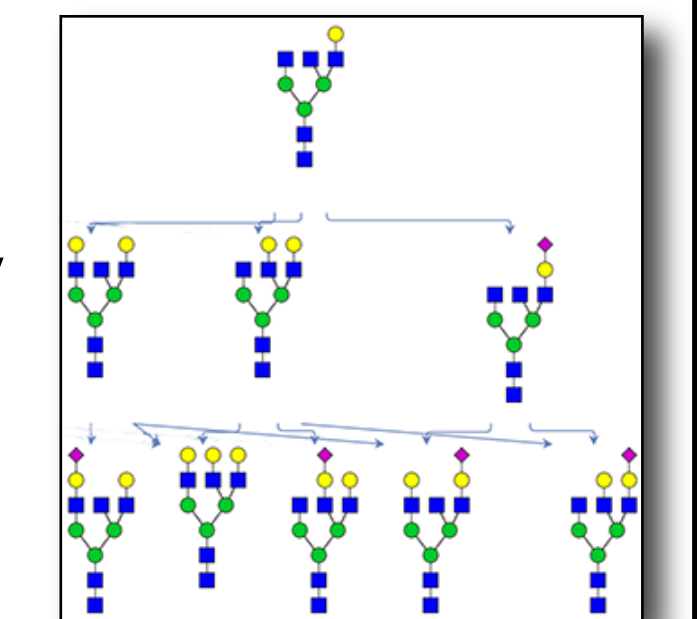
Input

Partial glycan list from Glycomics profiling or other experiments

Open source
 Network visualization
 Database query
 The enzyme class
 Integration with SBML file

Output

Full glycosylation network/pathway with simulation capability



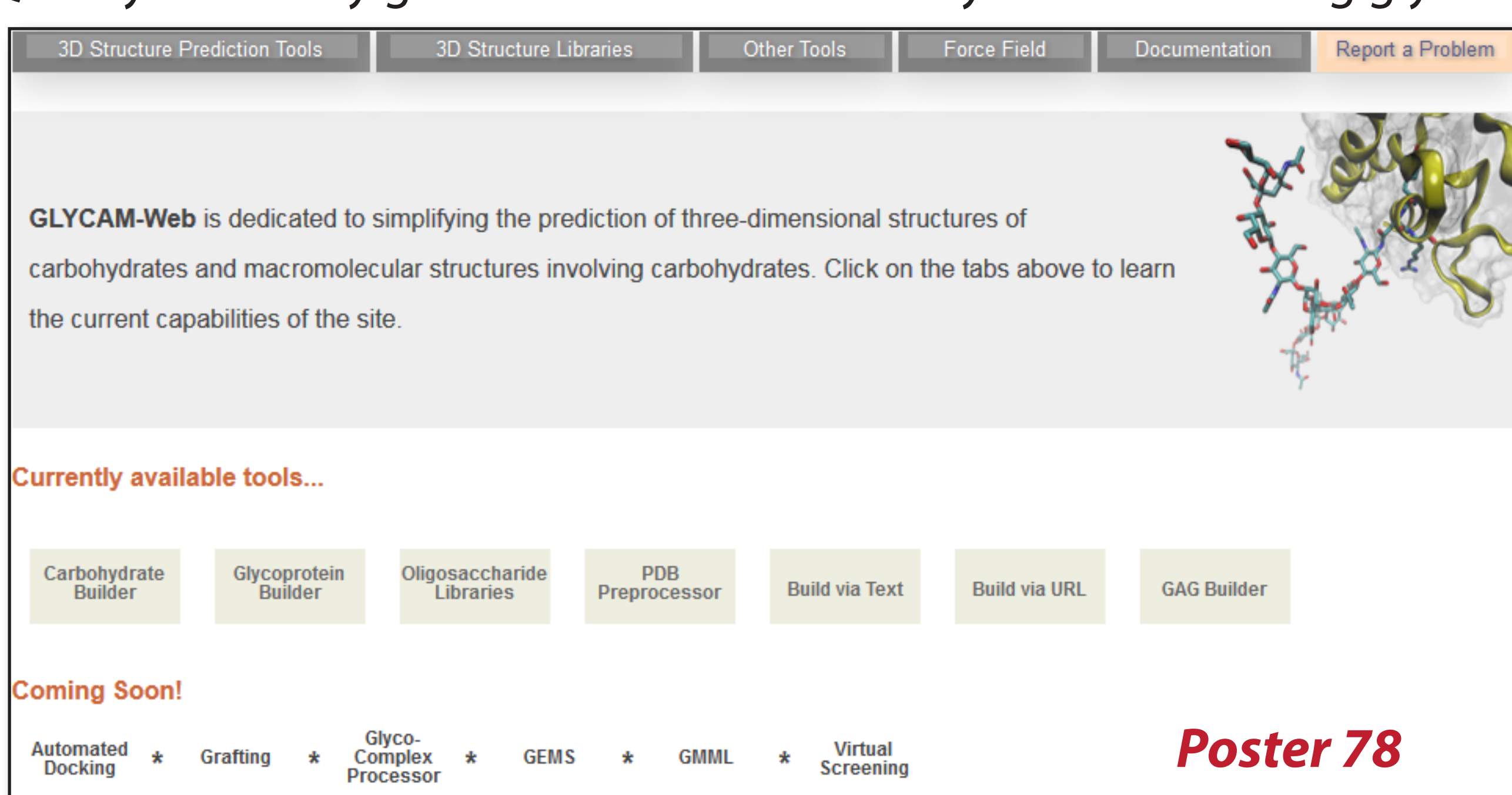
Poster 323



GLYCAM-Web

<http://glycam.org>

Quickly and easily generate 3D structures of systems containing glycans.



Poster 78



RINGS

<http://www.rings.t.soka.ac.jp>

RINGS is a freely-available web resource providing numerous tools and utilities to aid glycomics analyses. Utilities can convert glycan structure data between various sequence formats such as GlycoCT and LinearCode. Tools include data mining software such as:

- Glycan Miner Tool**, for mining glycan array or glycan MS data
- MCAW**, for visualizing glycan structure alignments
- Glycan Kernel Tool**, for finding distinguishing glycan structure patterns between two different glycan data sets
- Glycome Atlas**, for visualizing glycan profiles of various human and mouse tissues
- GPP**, for analyzing N-glycan biosynthesis pathways.

Poster 317

