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Southern Regional Research Center

CCRC Glyfinder-aided Studies of Cellulose

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COTTON FIBER

20 _U

CUTICLE

An elongated (30 mm) plant cell with excessive cellulose (95%)

COTTON CELLULOSE

Molecule is 10 µm long, 0.4 nm thick, 0.82 nm wide

PRIMARY



WINDING

nicrofibril crystallite

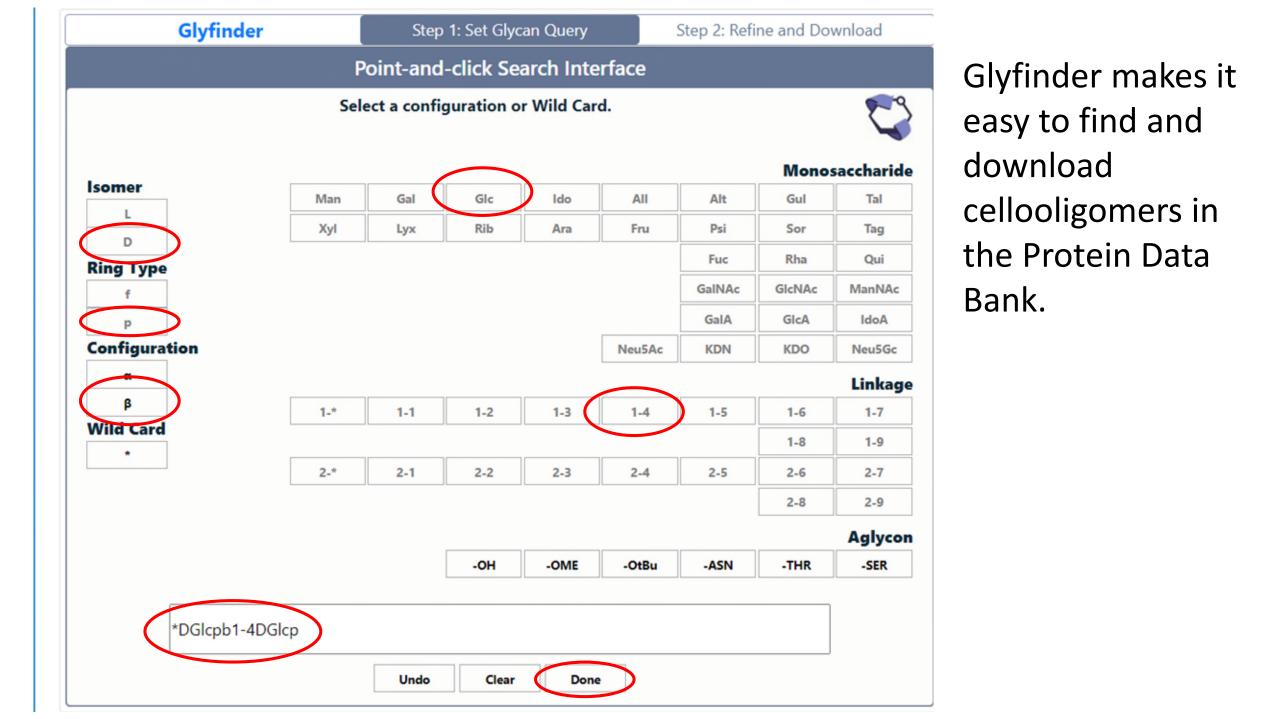
LUMEN

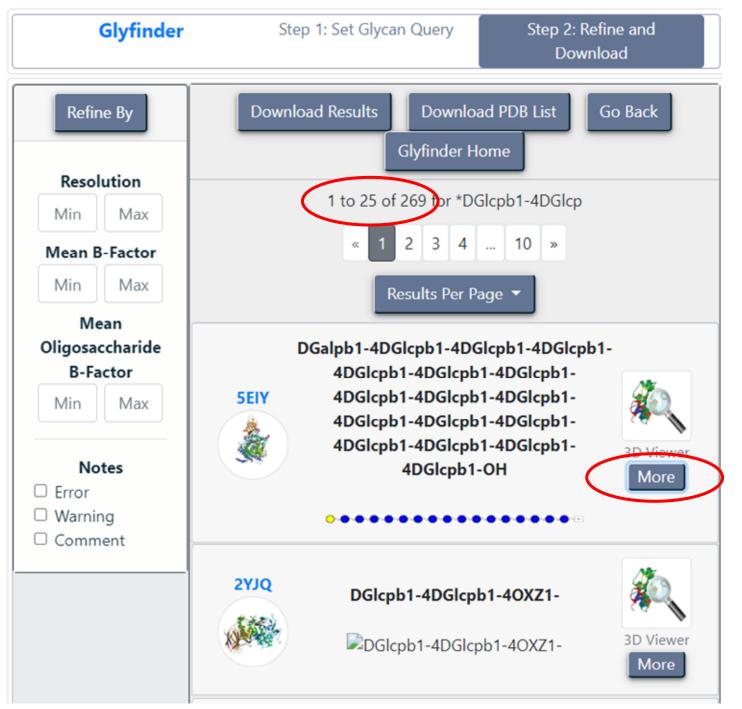
Short section of

Cotton fibers are complete cells. They are said to be composed of crystalline and amorphous regions. Many reactions occur in amorphous regions, yet they are not well understood.

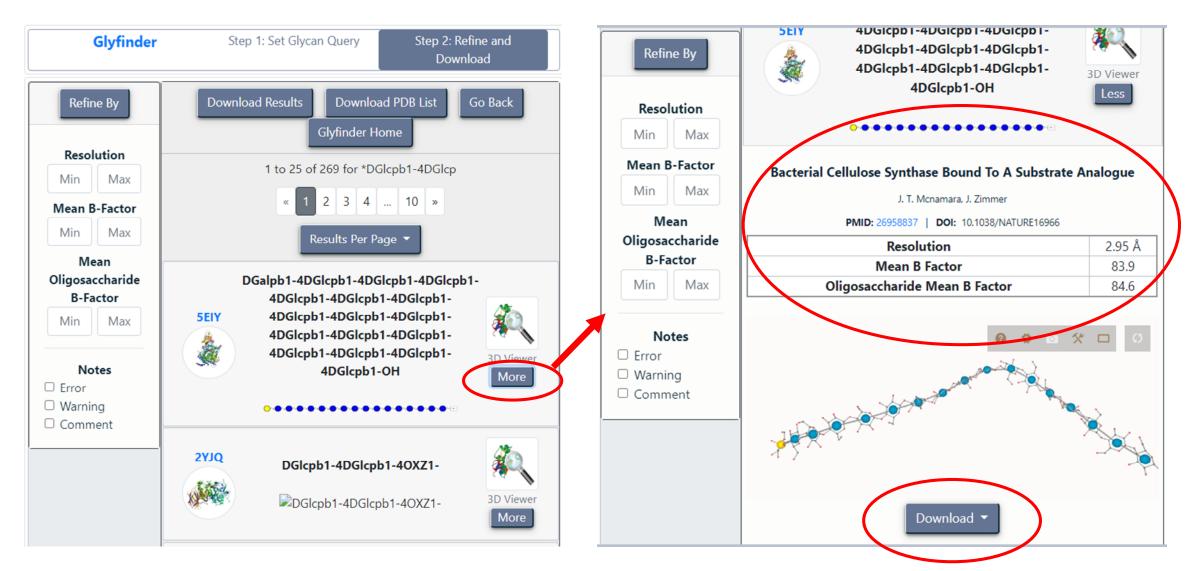
What shapes can cellulose molecules have?

Express shapes in ϕ, ψ



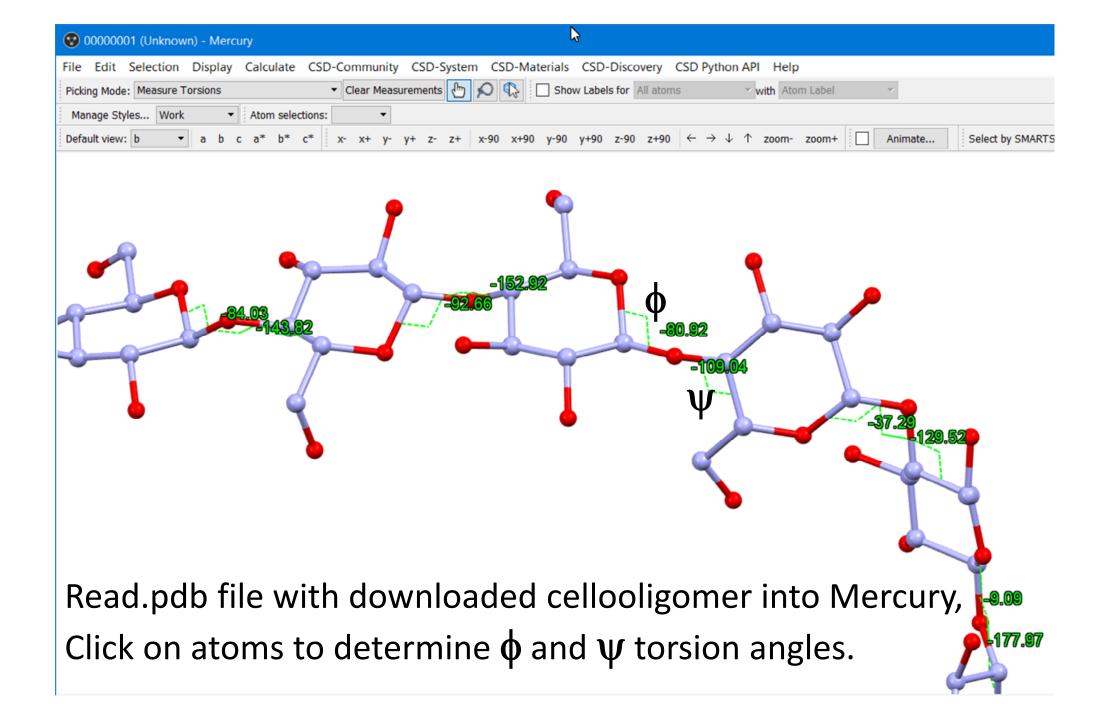


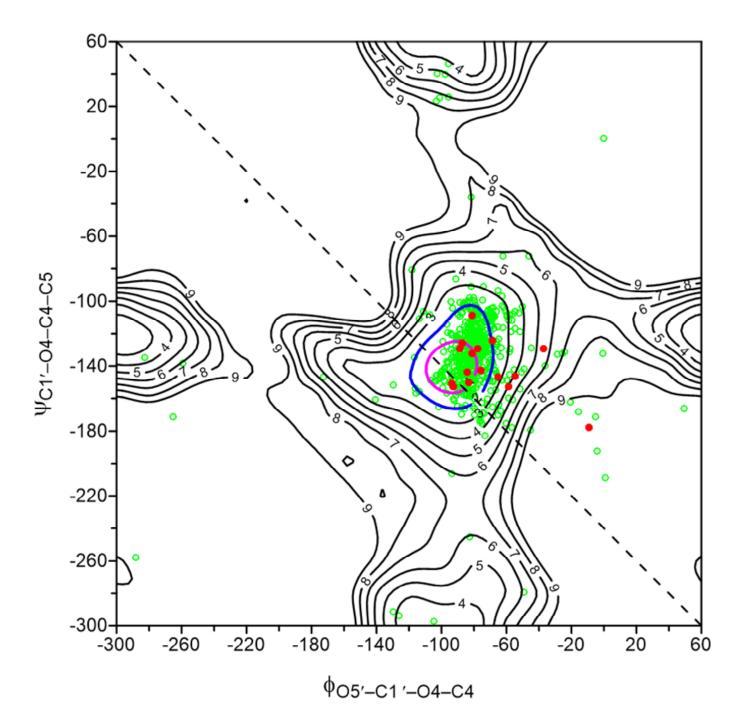
Almost instantly returns 269 oligomers that contain one or more cellobiose linkages, named by the complexing protein



5EIY looks like a great find, with 16 useful linkages

Take note of reference, data quality





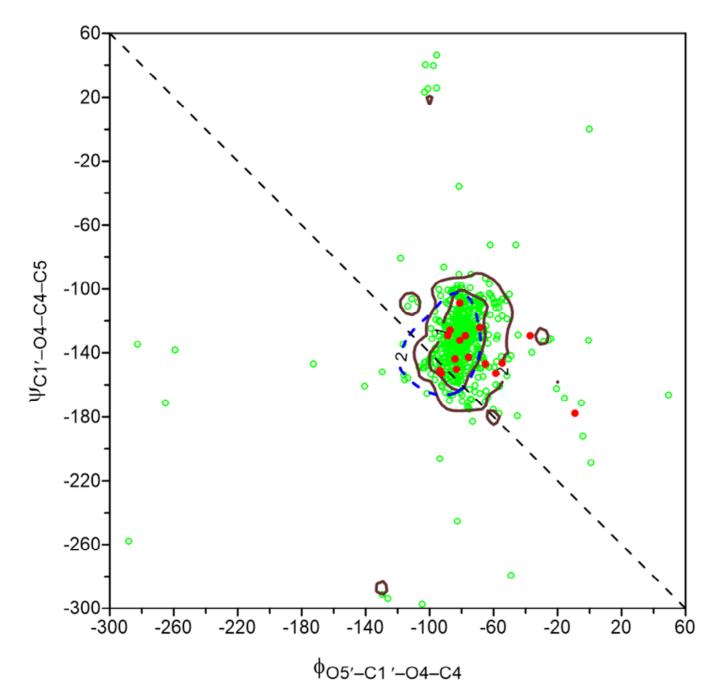
Ramachandran plot with Quantum Mechanics energies (SMD//B3LYP/6-31+G*).

Energy contours are in increments of 1 kcal/mol.

Dashed line shows 2-fold screw axis shapes favored by crystalline cellulose.

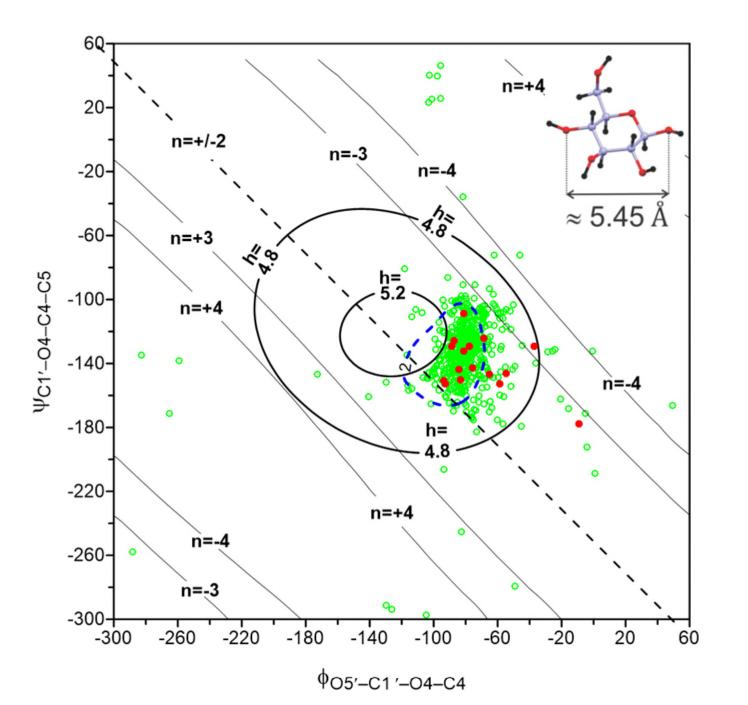
Green dots show PDB structures located by Glyfinder. Red dots are for the just-found 5EIY.

Only one CSD structure has an energy >2 kcal/mol.



An energy map can also be made from the frequency of the different values of ϕ and ψ . "Only" 559 values were available, with a maximum of 61 in a 10° x 10° cell, limiting the extent of contouring to 2 kcal/mol when temperature = 298 K.

The 2-kcal/mol contour from the DFT map is shown as a dashed blue line, with the 5EIY conformations as red dots.



The ϕ and ψ values can be converted to the helix parameters **n** and **h**.

n is the number of monomerunits per helix turn, and *h* isthe advance along the helixaxis per monomer.

Linkages in amorphous cellulose are likely to be those for 2- to left-handed 3-fold helices by both PDB analogy and DFT calculation.

Conclusions

- Glyfinder is valuable for locating oligomers with polysaccharide linkages of interest to agriculture (we have also looked at starch, xylan, lactose, and β -(1 \rightarrow 3)-glucan).
- Carbohydrate structures in the PDB roughly agree with our quantum mechanics studies, although structures from the Cambridge Crystal Structure Database agree much better.
- The high-energy conformations in the PDB deserve comment in the publications, although they are not discussed often.
- We look forward to the improvements mentioned by David Montgomery in Glyfinder to assist tabulating conformational attributes like φ and ψ.