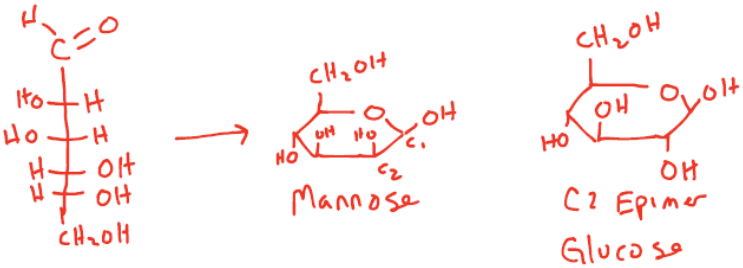
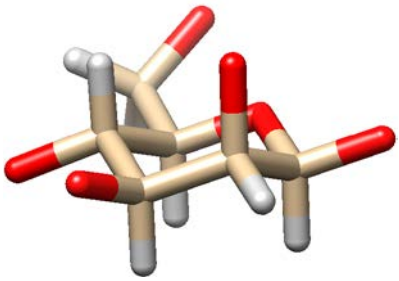
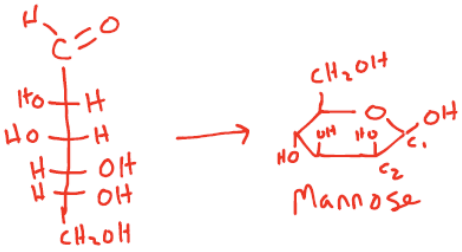
Problem Set 5 (**Due Sept 18th**)

1. Draw the Hawthorn projection (ring form) of Mannose and its C2 epimer. What is the common name of this epimer?





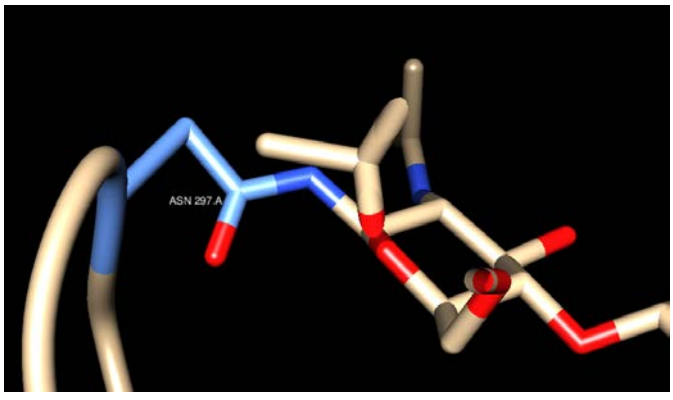
2. Examine the sugar shown here.
   a. Is this an **aldose** or ketose? Pentose or **hexose**?
   b. Label each carbon (C1, C2, etc)
   c. From the image, how can you be sure that it's an epimer of glucose? Only one OH is in the axial plane. Remember Glucose has ALL equatorial configuration.
   d. Which sugar is it? C2 epimer, so mannose.
   e. Draw the sugar using a Hawthorn projection and a Fisher projection.



3. Sucrose is a common disaccharide. What is the full name of this sugar?α-D-glucose-(1,2)-β–D-fructose

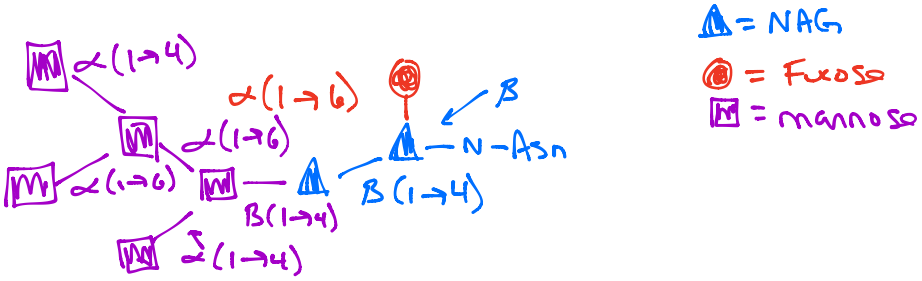
4. What is meant by the term reducing sugar? It has a free anomeric carbon that is formed from a aldose (so semialdehyde) Which of the common disaccharides discussed in class are not reducing sugars? Justify your answer. Sucrose because both anomeric carbons are tied up in the glycosidic bond. What experiment can you do to determine if a disaccharide is reducing? The tollens test, which produces solid Ag if there is a reducing end.

5. Using Chimera or another 3D molecule viewer, open pdbID 4B7I (the last letter is eye, not el).
   a. Verify that this is an N-linked oligosaccharide. What is the residue number of the glycosylated Asn? Asn297

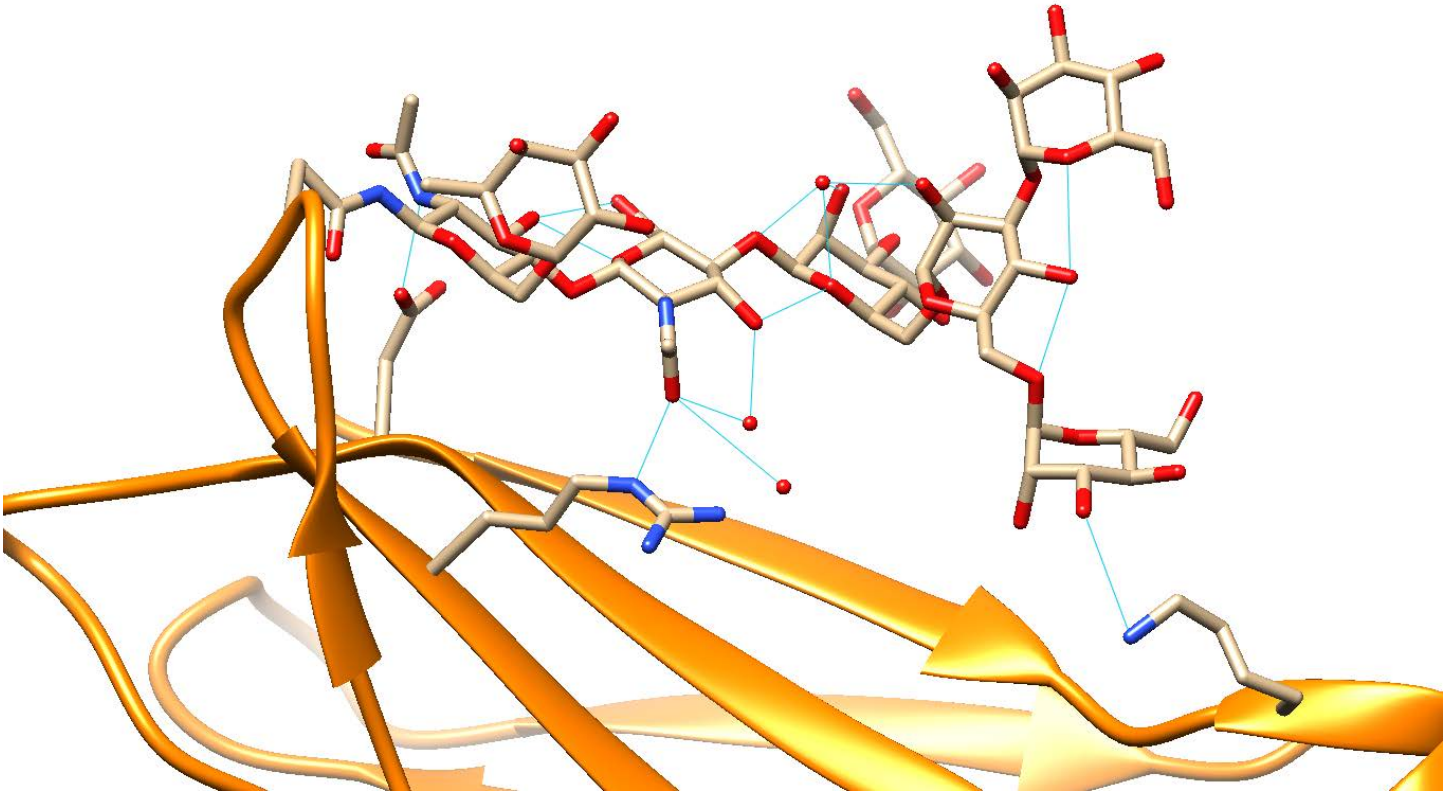


b. Does the protein follow the correct amino acid pattern for glycosyl transferase specificity? Be specific – you book discusses three invariable features of N-linked sugars. Yes. The requirement is Ser/Thr-X-Asn. Two amino acids away from the Asn is a Threonine

c. Using a sketch like seen in Figure 8.19, map the sugars. For each glyosidic bond, determine the linkage (e.g. α(1→4)). Hint: To determine the α/β orientation, you can set the focus to each sugar and observe if the anomeric carbon orientation is axial (α) or equatorial (β).



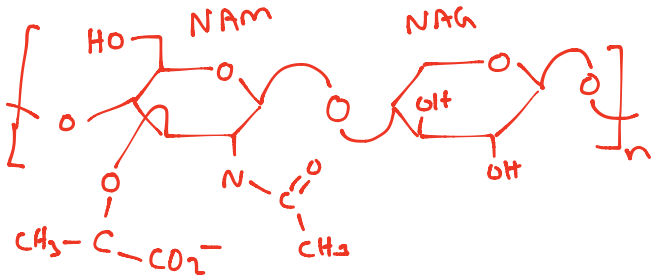
d. Are there any H-bonds between the oligosaccharide and amino acid side chains?



e. Draw this oligosaccharide using a Hawthorn projection. Make sure to show the linkage to Asn.

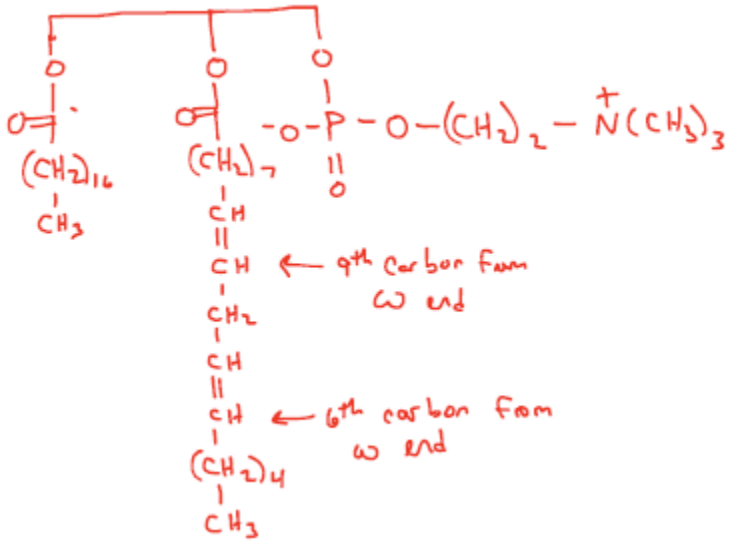
6. Discuss the differences between starch and cellulose. Make sure to consider the 3D structure of the polymers and how each interacts with other polymers. Amylose is a polymer of α-1,4 linked glucose while cellulose is a polymer of β-1,4 linked glucose. The beta configuration enables nice linear polymers that can readily H-bond with adjacent polymers; this makes very strong IMF in cellulose. Amylose, on the other hand, does not form linear polymers. Instead, they tend to coil up into helical structures; these are not able to form the strong inter-polymer interactions that cellulose can.

7. Bacterial cell walls are made from repeating patterns of two modified sugars. Draw these sugars as they would look in a cell wall. Discuss how linear polymers are connected in a cell wall.



Peptide linked to NAM & crosslinked

8. Draw a lipid containing stearic acid, linoleic acid and phosphatidylcholine. Recall that there are common positions on the glycerol backbone for each of these classes of molecules. Identify which regions of this molecule will occur on the surface of a lipid bilayer.



9. Why are triglycerides not common components of biological membranes? What is their function? They have 3 fatty acid chains esterified on a glycerol backbone. Consequently, there is not a polar head group and can therefore not be part of a membrane. These molecules function for fat storage.

10. Describe two trends in membrane fluidity. Increasing the % unsaturated fatty acids increases membrane fluidity. Increasing the temperature increases membrane fluidity. Increasing the carbon chain length decreases membrane fluidity. Etc. How does cholesterol influence membrane fluidity? It rigidifies membranes, so it decreases fluidity.

11. The structure of the photosynthetic reaction center from *Rps. viridis* has been determined (pdbID 1PRC). Please download this structure and use an appropriate program to show how this protein is embedded in a membrane. A good place to start would be to color all polar and ionic amino acids one color and the non-polar amino acids another color. You can select types by Select→Residue → amino acid category.