1. a. False – the carbonyl groups point toward the C-terminal end. (Consider the i→i-4 H-bonding pattern; the i-4 contributes the carbonyl oxygen to the hydrogen bond.)
   b. True
   c. False – keratin adopts an α-helical conformation, which *is* right-handed, but the collagen helix is left-handed.
   d. True
   e. False – the carbonyl and N-H groups of each β-strand alternate sides, so they don't all point in the same direction, and their individual bond dipoles cancel each other out.
   f. True – although the protein loses entropy on folding, the water gains more entropy as it is freed from interactions with the hydrophobic portions of the protein.
   g. False
   h. True
   i. False – water has no hydrophobic portion
   j. True
   k. False – some reducing sugars are too short to form a ring, like glyceraldehyde
   l. False – it is true that glycosaminoglycans are structural polysaccharides, but it is *peptido*glycan that provides stability to the bacterial cell wall.
   m. False – polypeptides and polysaccharides are completely different molecules and adopt different conformations.

2. A non-covalent, weak electrostatic interaction formed between a hydrogen that is covalently bonded to an electronegative atom and another electronegative atom

3. a. Having hydrophobic and hydrophilic parts
   b. Both 1 & 2
   c. Yes *(because the sequences are similar)*

4. a. H-bond
   b. Ion pair (salt bridge)
   c. Hydrophobic (or van der Waals)
   d. van der Waals
   e. H-bond or van der Waals

5. a. *assuming D-glucose only:* carbon 1 (C1) is needed in each bond (to be glycosidic bond); it can bond to C1 of the other glucose (α-α, β-β, or α-β) or to one of the 4 other C's with a hydroxyl group (C2, C3, C4, C6), making 4 different disaccharides with an α-bond, and 4 with a β-bond.
   Total = 3+4+4 = 11 different D-Glc−D-Glc disaccharides
   assuming D & L: from above, 11 D-only, and similarly 11 L-only; between D & L: for C1-C1 there are four possibilities 4: αD↔αL, αD↔βL, βD↔αL, βD↔βL; for C1-other C, there are 4 kinds of αD→L, 4 of βD→L, 4 of αL→D, 4 of βL→D.
   Total = 11+11+(5×4) = 42 different disaccharides of glucose
   b. *assuming L only*: 20 × 20 = 400 dipeptides
   assuming D & L: 400 D-only, 400 L-only, 400 D-L, 400 L-D = 4 × 400 = 1600 dipeptides
   c. Polysaccharide: fewer monosaccharides than amino acids, but many more ways to connect them

6. a. Asn
   b. Phe, Tyr, or Trp
   c. So far the sequence is: ___-(Phe/Tyr/Trp)-___-Asn

   The left titration curve shows 3 ionizable groups, with pKa's at 3, 8, and 12.5 (the pH's at the half-equivalent points). 3 and 8 correspond to the C- and N-termini, and 12.5 is the pKa of the Arg side-chain. If this titration curve came from the N-terminal half of the original tetrapeptide, the first half of the tetrapeptide sequence must be either Arg-Phe or Arg-Trp. (Arg-Tyr is not possible because Tyr would have given an additional buffering zone centered at pH 10.5.) Or this titration curve could have come from the C-terminal half of the tetrapeptide, which would mean the latter part of the sequence is Arg-Asn.

   The right titration curve also shows 3 ionizable groups, with pKa's at 3, 8, and 10.5, corresponding to C-term, N-term, and Tyr or Lys side chain. If this curve came from the N-term of the tetrapeptide, there are several possibilities for the sequence. If it contains Tyr, this must only be in the second position, because otherwise chymotrypsin would also have cut between amino acids 1 and 2. In that case the sequence would be (Ala/Gly/Ile/Leu/Met/Asn/Pro/Gln/Val)-Tyr. The amino acids that can occupy the first position are both non-ionizable (because there is no additional buffering range in the titration) and non-aromatic (because there is no additional cleavage by chymotrypsin). If the pKa 10.5 aa is instead Lys, the sequence must be either Lys-Phe or Lys-Trp.

   Or, this right titration curve could correspond to the C-term of the tetrapeptide, and then the sequence would have to be Lys-Asn (because if it were Tyr-Asn, chymotrypsin would have cut this bond).

   Combining all of these, the sequence could be:
   Arg-(Phe/Trp)-Lys-Asn *or*
   Lys-(Phe/Trp)-Arg-Asn *or*
   (Ala/Gly/Ile/Leu/Met/Asn/Pro/Gln/Val)-Tyr-Arg-Asn

7. The switching of anomeric configurations in a cyclic sugar.

8. In order for a cyclic sugar to mutarotate, it must open to its linear form. Likewise, in order for a sugar to be reducing, it must access its linear form, which contains the aldehyde or ketone. So cyclic, reducing sugars are also mutarotatory. And mutarotatory sugars are reducing. These sugars form hemiacetals or hemiketals in their cyclic form (from aldehydes or ketones, in the linear form). Sugars that have acetal or ketal groups have formed a glycosidic bond. These functional groups cannot convert directly to aldehydes or ketones, and so sugars (that is, monosaccharides) with these groups are non-reducing and are also not mutarotatory. (A polysaccharide will have many monosaccharide residues that are non-reducing and non-mutarotatory, but may have one monosaccharide residue that is reducing, making the entire polymer capable of acting as a reducing agent.)

9. e. *explanation:*
   a. is false, because a reducing sugar becomes oxidized in the presence of Cu^{2+}.
   b. is false, because some reducing sugars are too short to form rings
   c. is false; although a polysaccharide can have reducing and non-reducing ends, as a whole it will be either reducing or non-reducing (not both)
   d. is false; the monosaccharide on the right has its anomeric carbon (lower right) in the hemiacetal form

10. a. sugar alcohols (or polyols)
    b. It depends on which carbon is selected as carbon 1, since both ends of the molecule have equal priority. If the left-hand carbon is C1, the molecule is D; if the right-hand carbon is C1, the molecule is L.
    c. D-glucose; sorbitol is reduced at carbon 1 (from aldehyde to alcohol)
    d. glycerol

11. glycogen: A. branched, B. granular, C. helical, F. highly hydrated, G. loose intermolecular packing, I. limited hydrogen bonding (within/between glycogen chains), K. flexible, L. rings in chair conformation

    amylose: B. granular, C. helical, F. highly hydrated, G. loose intermolecular packing, I. limited hydrogen bonding (between chains of amylose & amylopectin), K. flexible, L. rings in chair conformation

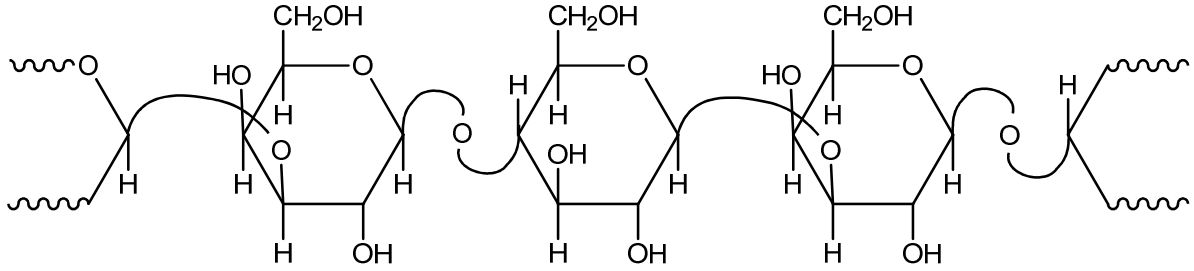
    amylopectin: A. branched, B. granular, C. helical, F. highly hydrated, G. loose intermolecular packing, I. limited hydrogen bonding (within/between amylopectin chains), K. flexible, L. rings in chair conformation

    cellulose: D. extended, E. fibrous, H. extensive hydrogen bonding (within and between cellulose chains), J. rigid, L. rings in chair conformation

    chitin: D. extended, E. fibrous, H. extensive hydrogen bonding (within and between chitin chains), J. rigid, L. rings in chair conformation

    heparin: C. helical, D. extended, F. highly hydrated, (under some interpretations: G. loose intermolecular packing, and I. limited hydrogen bonding (within/between heparin chains)), K. flexible, L. rings in chair conformation

12. a.



    b. structural or protective

13. b. Branched polysaccharides will have *at most* one *reducing* end, but will have *multiple* non-reducing ends.

14. a. B. hydrogen bonds between backbone atoms (the H-bonds form between β-strands, and are parallel to the length of the fibril)
    b. The researchers had expected to see hydrogen bonds between side chain atoms, because most of the side chainsare polar (or have many hydrogen-bonding groups).