1. (2) c  7. (1) True
2. (2) b  8. (1) True
3. (2) e  9. (1) False – *quaternary*
4. (2) b  10. (1) False
5. (1) False – *a ketohexose*  11. (1) False
6. (1) True  12. (4) d

13. (2) True
14. (2) False – *is proportional*
15. (2) True
16. (2) False
17. (2) True
18. (2) False
19. a. (2) True
b. (3) pH changes can lead to changes in protonation state and charge. Like charges on adjacent R-groups will destabilize *2°* structure.
20. a. (4pts) (1) C, G; (2) A, E, F, G
b. (4) Only sugar 2 is reducing, so all disaccharides will form via its anomeric carbon. Sugar 2 can adopt the α or β anomeric configuration before forming the glycosidic bond, and it can bond to carbon 2, 3, 4, or 6 of sugar 1. So there are 2 x 4 = 8 possible disaccharides.
21. a. (4) 1. linoleic acid, 2. glycerol, 3. phosphate 4. glycerol
c. (3) increase
22. a. (3) Ser: 13, His: 6, Asp: 4
b. (3) 3-7, 12-14
c. 

d. (4) There are three ways to get a zero charge state over Ser, His, and Asp at pH 7:
1. Ser: +0, His: +1, Asp: -1 (most likely)
2. Ser: +0, His: +0, Asp: +0 (minor)
3. Ser: -1, His: +1, Asp: +0 (very minor)
Because states 2 and 3 will not significantly contribute to the fraction with zero charge, we can ignore them. So we need calculate the fraction of chymotrypsin molecules in state 1:
Fraction of molecules with Ser +0 at pH 7:
\[ \frac{[O^-]}{[O]} = 10^{7-13} = 10^{-6} = \frac{1}{1,000,000} \]
\[ \frac{[OH]}{[O^-]+[OH]} = \frac{1,000,000}{1,000,001} \approx 1 \]
Fraction of molecules with His +1 at pH 7:
\[ \frac{[N]}{[NH^+] = 10^{7-6} = 10^1 = \frac{10}{1} \]
\[ \frac{[NH^+]}{[N]+[NH^+]} = \frac{1}{11} \]
Fraction of molecules with Asp -1 at pH 7:
\[ \frac{[O^-]}{[OH]} = 10^{7-4} = 10^3 = 1000 \]
\[ \frac{[O^-]}{[O^-]+[OH]} = \frac{1000}{1001} \]
Fraction of molecules with all three at pH 7 (Ser +0, His +1, and Asp -1):
\[ = 1 \times \frac{1}{11} \times \frac{1000}{1001} = 0.09 \]
e. (2) False – *stabilize tertiary structure*
f. (2) A
g. (3) The negative charge of Asp stabilizes the positive (protonated) state of His.
h. (4) Ser→Thr or Asp→Glu. Either substitution maintains the charge and functional group while only adding one methyl/methylene group. (No sub for His, because no other aa’s can form the same H-bond network and have pKa ~6.)
i. (3) A, C

23. a. (2) The most favorable dihedral angles for the peptide backbone
b. (2) Backbone conformations that are generally not allowed, due to steric clashes.
c. (2) The dihedral angles for each residue of chymotrypsin.
d. (3) c
24. (4) A, B, C
25. (3) one
26. (3) ex: