9. (1) False – *quaternary* 

- 1. (2) c
- 2. (2) b
- 3. (2) e
- 4. (2) b
- 5. (1) False a ketohexose
- 10. (1) False 11. (1) True 12. (4) d

7. (1) True

8. (1) True

- 6. (1) True
- 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  $\alpha$  or  $\beta$  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. phosphate4. glycerol
  - b. (2) D

c.

- c. (3) increase
- 22. a. (3) Ser: 13, His: 6, Asp: 4
  - b. (3) 3-7, 12-14



- 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:

$$pH = pKa + \log \frac{[A^-]}{[HA]}$$

13. (2) True 14. (2) False – *is* <u>proportional</u> 15. (2) True 16. (2) False 17. (2) True 18. (2) False  $\frac{[0^{-}]}{[0H]} = 10^{7-13} = 10^{-6} = \frac{1}{1,000,000}$   $\frac{[0H]}{[0^{-}]+[0H]} = \frac{1,000,000}{1,000,001} \approx 1$ 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:  $\frac{[0^{-}]}{[0H]} = 10^{7-4} = 10^3 = \frac{1,000}{1}$ Fraction of molecules with all three at pH 7

Fraction of molecules with all three at pH 7 (Ser +0 His +1 and Asp -1).

$$= 1 \times \frac{1}{11} \times \frac{1,000}{1,001} = 0.09$$

- e. (2) False *stabilize* <u>tertiary</u> 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

