Exam 1 Key

Thursday, September 29, 2016 10:29 AM

Name

This exam is schedule for 75 minutes and I anticipate it to take the full time allotted. You are free to leave if you finish.

Clearly circle the most appropriate answer(s).

1. The unfolding of which common biomolecule can be monitored by absorbance at 260 nm?

lipid bilayers polysaccharides proteins **DNA**

2. Circle all amino acids do **NOT** have an ionizable proton on the side chain?

Glutamine Lysine Cysteine Tyrosine Histidine **Tryptophan**

3. Which class of lipid is not typically found in biological membranes?

sphingolipid phosphoglyceride **triglyceride** cholesterol

4. Which is the most common carbon chain length for lipids in biological membranes?

10 14 **18** 22

5. Water has a _____ dielectric constant than hydrophobic solvents.

Lower **higher** similar

6. Cytosine is an example of a

Purine **Pyrimidine** Pyrole Indole

7. The most common tautomeric form of the purine and pyrimidine bases in nucleic acids is the:

amide keto ester **enol** none of the above

8. What is the common stereoisomeric form of amino acids in biological systems?

D-amino acids **L-amino acids**

9. DNA and RNA polymers are formed through _____ linkages.

glycosidic peptide disulfide **phosphodiester**

10. Phosphoglycerides commonly have unsaturated carbon chains attached at which position of the glycerol backbone.

1 **2** 3 no preference

11. Which carbon is the anomeric carbon in a 6 carbon ketose?

1 **2** 3 4 5 6

12. Mutation at which codon position is least likely to lead to a change in the amino acid sequence?

1 2 **3** 4

13. Which of the following provides the primary energy that stabilizes B-form DNA?

Pi stacking Ion pairing H-bonding Hydrophobic Effect

14. Increasing the concentration of which of the following would produce a more fluid membrane?

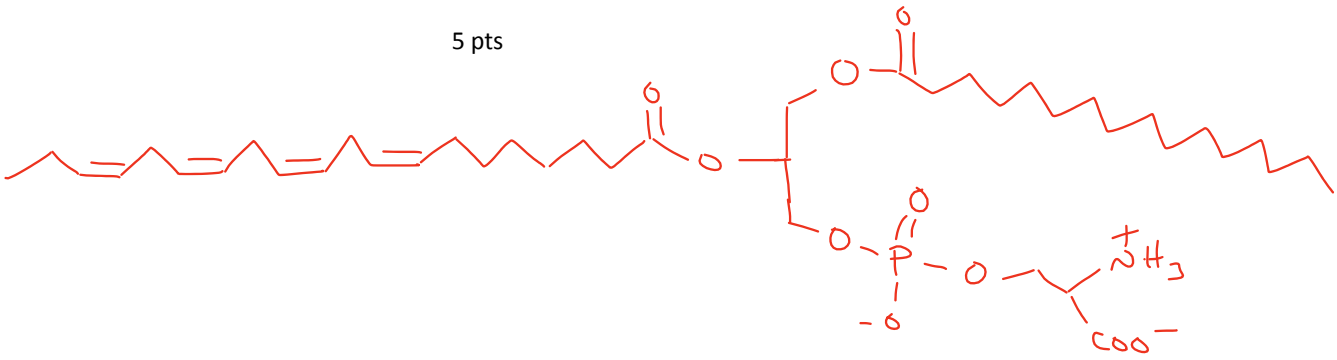
Polar head groups cholesterol trans fats 18:0 **18:2n-6**

15. Which amino acid has the most restricted Φ,Ψ angles?

proline alanine histidine isoleucine glycine

16. Sketch phosphatidylserine that contains 16:0 and 20:4n-3

5 pts



17. Describe the process of protein folding. Make sure to include the forces that stabilize each step and the role of entropy.
    a) amino acids in close proximity form H-bonds within the backbone leading to small regions of secondary structure. Energetically, there is little enthalpy or entropy that drives this.
    b) Extended secondary structures form through more H-bonding within the backbone. Again, there is not much energy that drives this.
    c) Secondary structures collapse together such that the nonpolar side chains cluster in the middle. There is a large entropic driving force that makes this a very favorable step because of the hydrophobic effect.
    d) Domains interact form the complete tertiary structure. This could be driven by any type of interaction, but they are commonly weak.
    e) Individual subunits come together to form the complete quaternary structure.

5 pts

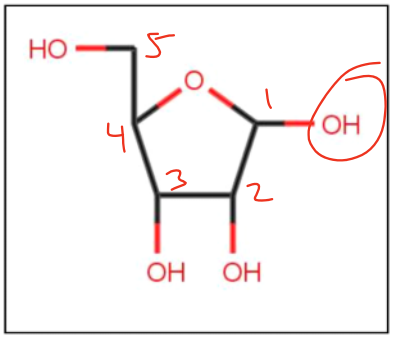
18. Ribose is shown as you may expect to see it in RNA.

a) Is this **D** or L ribose? 1 pt

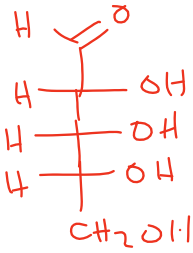
b) Label the carbons with the appropriate numbers. 1 pt

c) Clearly mark where the base is attached. 2 pt

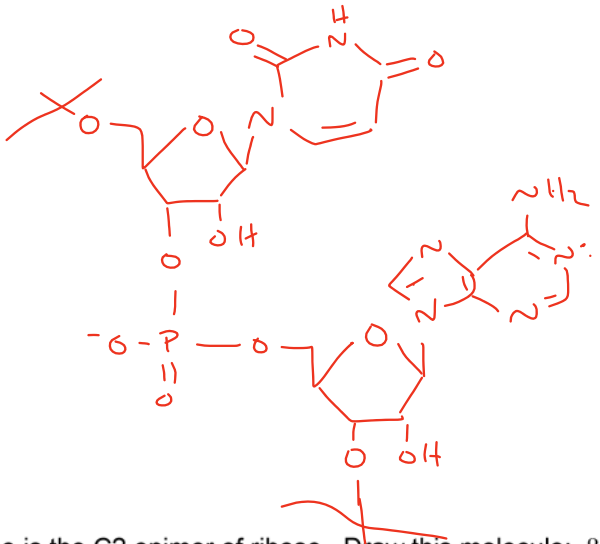
d) Ribose is drawn in a way that does not imply alpha or beta configuration. In RNA polymers, is ribose alpha or beta? **Beta** 1 pt



e) Show the linear form of ribose using a Fisher projection. 5 pts

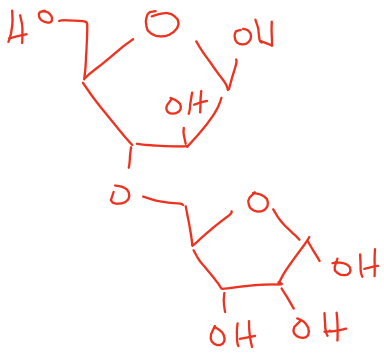


f) As a separate image, show the linkage between two ribose molecules that are part of an RNA polymer. The 5' ribose contains a uracil base and the 3' ribose contains an adenine base.



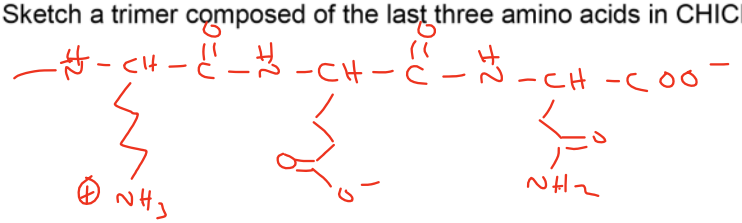
5 pts for backbone
5 points for base structure

g) Arabinose is the C2 epimer of ribose. Draw this molecule: β-D-arabinose (3→5) α-D-ribose.



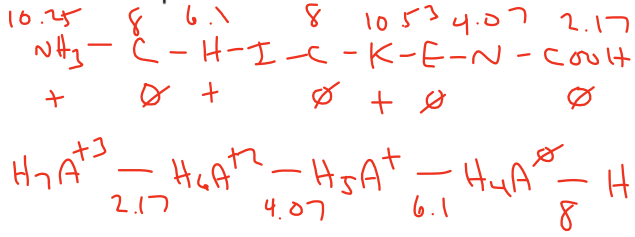
19. You isolated a small protein from a wild animal that may be responsible for a terminal illness in humans. After experimenting with this protein, you determine that the N-terminal domain is likely responsible for a toxic interaction with a critical metabolic enzyme. Sequencing by mass spectrometry shows that two important peptides are ELEPHANT and CHICKEN:

a) Sketch a trimer composed of the last three amino acids in CHICKEN.



b) What is the charge of ELEPHANT at pH 7.5? **-2**

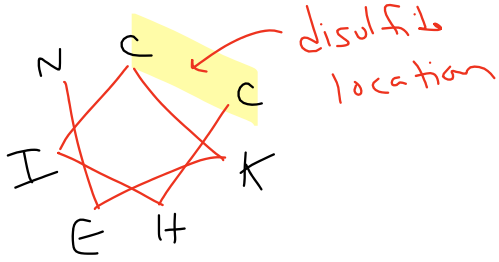
c) Calculate the pI of CHICKEN. Assume that the N and C termini are NOT part of a peptide bond.



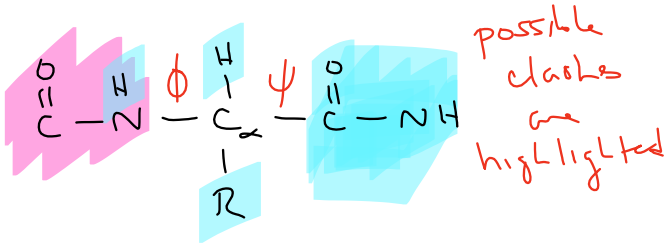
$pI = \frac{6.1 + 8}{2} = 7.05$

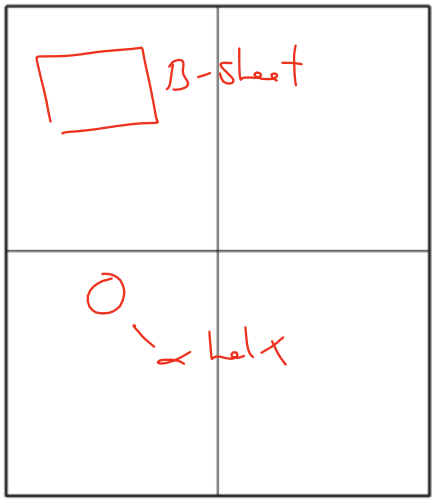
d) Which of these peptides cannot be part of a beta sheet? Justify your answer. ELEPHANT – it contains a proline in the middle of the sequence that will not support the formation of a beta sheet due to its inability to H-bond on the backbone nitrogen

e) CHICKEN forms an especially strong alpha helix that is very difficult to unfold. Justify this observation. Drawing out the heptad repeat, we see that the two cysteine residues are very near to each other. So close, in fact, that they are able to form a disulfide bridge with will make unfolding the helix very difficult.



20. Please describe the importance of ψ and ϕ angles in protein structure. In your discussion, make sure to include what these angles describe, common/restricted values and why they are restricted. Make sure that you include a sketch a biomolecule that supports your answer. Feel free to use the empty grid, but you'll want to include a title (what would you call this plot?) and label the axes appropriately. They are the torsion angles of the alpha carbon relative to the two peptide bond planes. As the peptide bond plane rotates, there are steric clashes that occur between atoms (backbone or sidechain) that prevent certain angle combinations (these are the restricted regions of the graph). Some angles are very favorable because they maximize the space that each atom gets – these are the angles found in common secondary structures.





Answer **two** of the following –use the back of this page if you need more space.

21. α helices and β sheets tend to form in the interior of globular proteins while irregular loops occur on the outside. Propose a reason for this observation. The loops have much more H-bonding potential because their backbones are not tied up in H-bonding to form the more common secondary structural elements.
22. 2D gel electrophoresis is a useful technique for protein biochemists but not for DNA or RNA biochemists. Why? 2D gels separate molecules based on size in one dimension and charge in the other directions. Since all DNA molecules have a negative charge (and very similar relative negative charges), they will not be effectively separated by their charge. Proteins, on the other hand, have distinct pI values that are dictated by the combination of amino acids. Consequently, they are very effectively separated by their charge.
23. Compare and contrast the experiments that are used to measure the melting temperatures of DNA vs. proteins. DNA is melted by increasing the temperature as the absorbance at 260nm is monitored. This is possible because of the hyperchromic effect, a physical phenomenon that makes pi stacked bases have a lower absorbance than unstacked bases). The resulting melting curve will have a sigmoidal shape indicating that the process is cooperative.

    Proteins, on the other hand, cannot be effectively monitored by the hyperchromic effect. Circular dichroism can be used – this technique monitors secondary structure – as the secondary structure collapses, the signal decreases. Overall, the shape of this will also indicate cooperativity; however, there may be multiple phases/transitions due to the presence of multiple domains or complex quaternary structure.

24. List three roles for sugars and three roles for lipids. You may not use energy production/storage of lipid bilayers as part of your answer.

Carbohydrates: cell walls in bacteria and plants, the lubricant in joints, the backbone of DNA/RNA
Lipids: steroid hormones, prostaglandin hormones, Vitamins, myelin sheathes, etc.