Name_____**Rec. Section**_____ **TA**_____

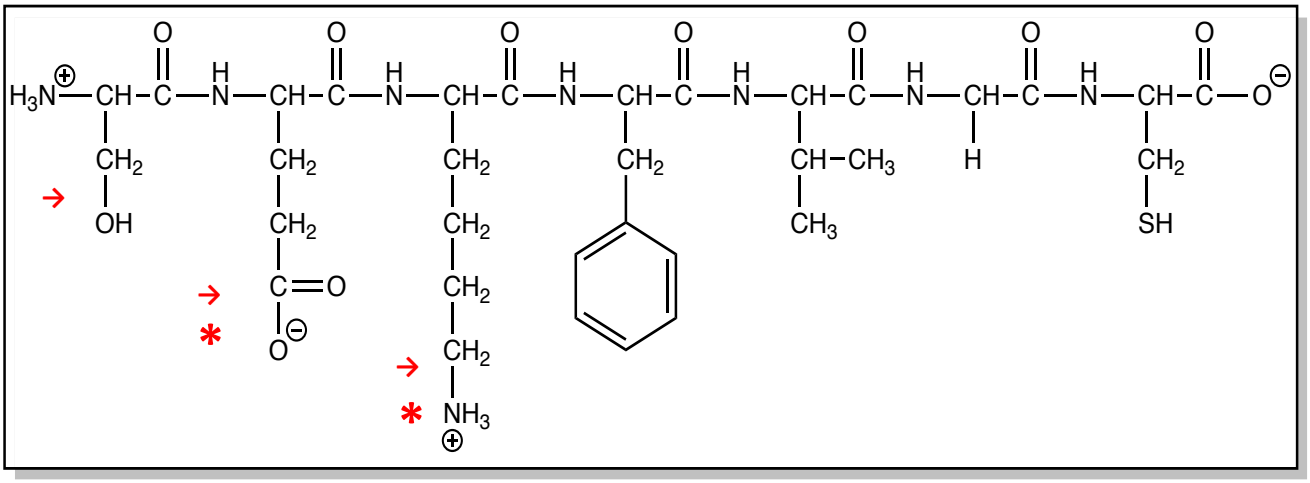
7.012 Fall 2018: Problem Set 1 Solutions

Due: Mon 9/17/2018

The solutions to these problems must be submitted electronically to your TA through the 7.012 Stellar site. All submissions must be received before 9:50 AM on September 17, 2018. Check your file to ensure it was successfully submitted. Only the material that is received prior to the deadline will be graded, no additional material will be accepted after the deadline.

Question 1 (4.5 points)

Please answer the questions below. No explanation is required.



A.) What kind of a macromolecule is shown above?

Peptide (protein)

B.) Name all the monomeric units starting from the amino terminus of the molecule.

N- serine – glutamate – lysine – phenylalanine – valine – glycine – cysteine- C

C.) Which of the monomeric units would be more likely to be found in the core of a lipid bilayer?

Phenylalanine, valine, glycine

D.) Which level of structure is shown for this molecule: primary, secondary, tertiary or quaternary?

Primary

E.) Mark with an asterisk a side chain of a monomer that as drawn can participate in an electrostatic interaction.

Glutamate and lysine are marked

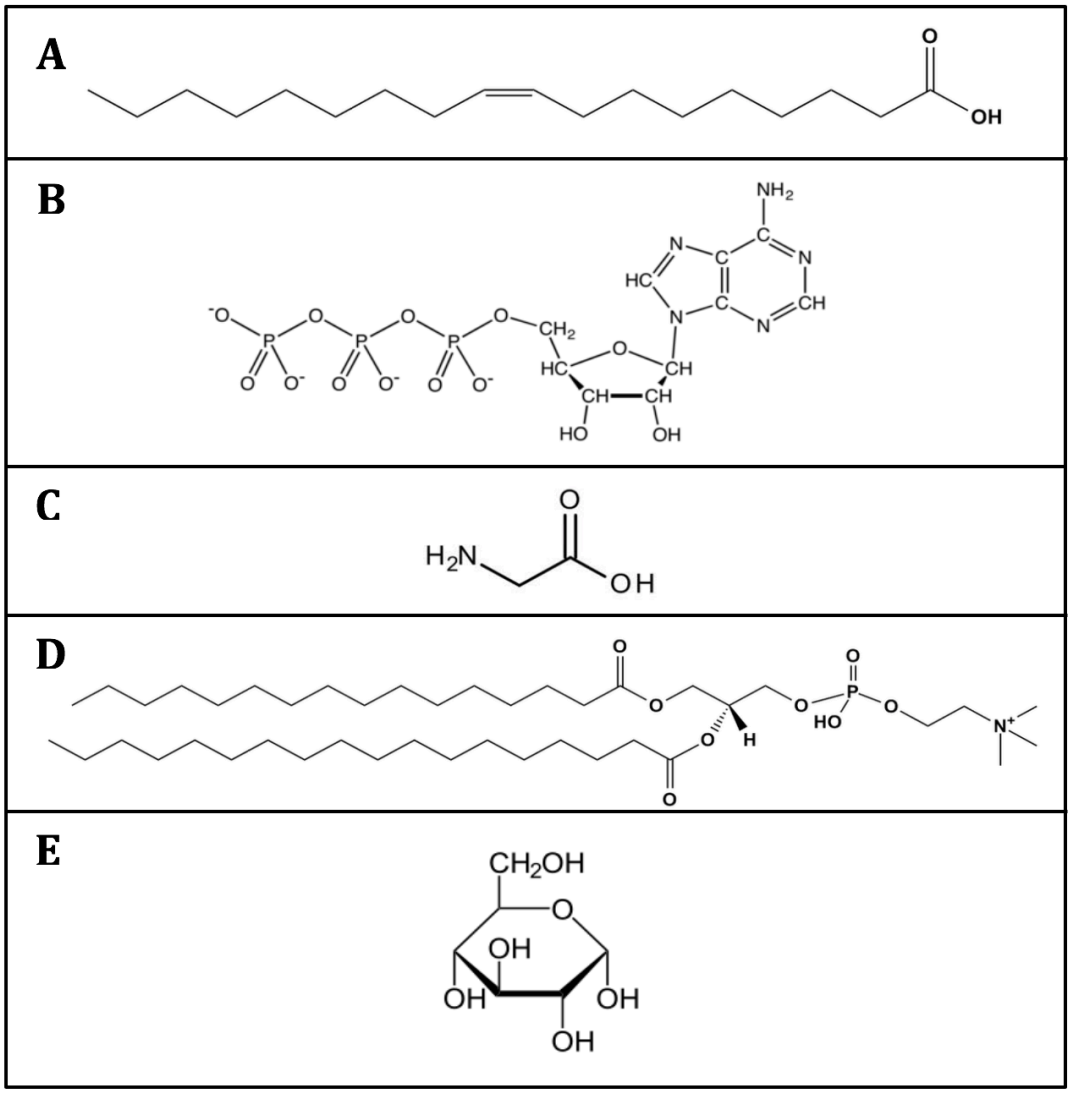
F.) Mark with an arrow a side chain of a monomer that can participate in a hydrogen bond.

Serine, glutamate, lysine are marked. In rare cases, S-H group can also participate in a hydrogen bond so no points off if cysteine is also marked.

G.) If the macromolecule was at pH=1, name the monomeric units whose side chains would have a different charge from the charge that is drawn (if any).

Glutamate

Question 2 (2 points)
Please answer the questions (i-vii) below. No explanation is required.



i.) Which molecule from above, if any, can be added to grow the macromolecule polymer shown in question 1?
C (the amino acid)

ii.) To which end of the macromolecule from question 1 would a new unit be added?
Carboxyl end

iii.) Which molecule from above if any is generated during glycolysis?
B (the ribonucleotide shown is ATP)

iv.) The polymers of which macromolecule(s) shown above if any are stabilized by hydrogen bonds?
B, C, E

v.) Which molecule forms a cell's lipid bilayer?
D

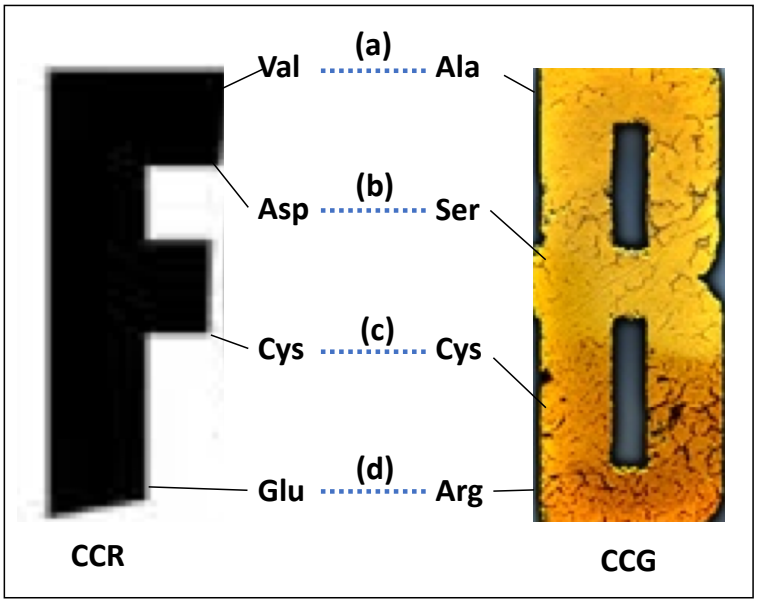
Question 2, continued

vi.) Which molecule from above, if any, is a building block for DNA?
none

vii.) Which molecule if any does not make a covalent bond to bring together its monomers for its biological function?
D

Question 3 (4 points)

Two bovine proteins Cortnite: Cattle Royale (CCR) and Clayerunknown's Cattlegrounds (CCG) interact at the amino acid residues shown in the diagram below. An amino acid structure chart can be found on the last page.



A.) For each interaction, indicate the strongest type of bond and/or interaction that the two residues can form in the table below and list the interactions (a – d) according to their strength 1 being the strongest and 4 being the weakest.

Interaction	Type of interaction (hydrogen bond, covalent bond, hydrophobic, electrostatic)	Strength of interaction (1 – 4)
a	*hydrophobic*	*4*
b	*hydrogen bond*	*3*
c	*covalent bond*	*1*
d	*electrostatic*	*2*

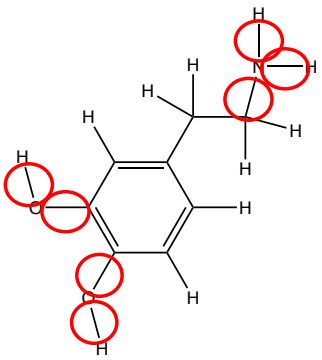
Question 3, continued

B.) The following mutations have been made in the CCR and CCG proteins. Predict whether the two proteins will still interact at this site, and if so, whether the change will lead to an interaction that is similar in strength, stronger or weaker.

Interaction	Mutation in CCR	Mutation in CCG	Type of interaction (hydrogen bond, covalent bond, hydrophobic interaction, electrostatic interaction, none)	Strength compared to original interaction (similar, stronger or weaker)
a	Val -> Thr	Ala -> Ser	*hydrogen bond*	*stronger*
b	Asp -> Ile	Ser -> Ala	*hydrophobic*	*weaker*
c	Cys -> Met	Cys -> Met	*hydrophobic or none*	*weaker*
d	Glu ->Gln	No change	*hydrogen bond*	*weaker*

Question 4 (3 points)

A.) Circle the polar bonds in the neurotransmitter dopamine below. Electronegativity values for the following atoms are: 2.20 for H, 2.55 for C, 3.04 for N, and 3.44 for O.

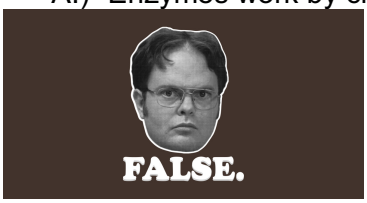


B.) The carbon–hydrogen bonds are nonpolar. Briefly explain why.

The carbon-hydrogen bonds are nonpolar because the electronegativity between the two atoms are close in value (less than 0.4).

Question 5 (3.5 points)
Label the following statement as True or False. Briefly explain your answer.

A.) Enzymes work by changing ΔG for the reaction to be more favorable.

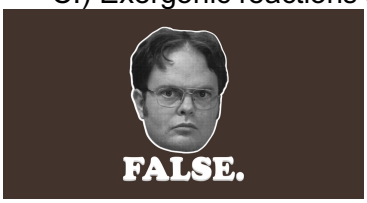


False. Enzymes speed up a reaction, lower the activation barrier but do not alter the thermodynamics. The ΔG is a value that is inherent to the reactant- and the product molecules.

B.) The magnitude of the activation energy barrier determines whether the reaction will be exergonic (spontaneous).

False. The sign of ΔG (whether ΔG is positive or negative) indicates whether a reaction is endergonic or exergonic. In other words, the difference between the free energy of reactants and the free of products determines whether a reaction will be exergonic or endergonic. The magnitude of the activation energy barrier determines the degree to which a catalyst can speed up a reaction

C.) Exergonic reactions are always fast.



False. Spontaneous reactions can be very slow. For example the activation energy is high for diamonds to turn into coal (and therefore the saying "diamonds are forever"). Thermodynamics do not imply kinetics.

D.) For an enzymatic reaction that has an equilibrium constant that is greater than one, ΔG° is always negative.

True. If K_{eq} is greater than zero, then ΔG° will be negative according to the equation: $\Delta G^\circ = -RT \ln K_{eq}$

Question 5, continued

E.) A reversible enzymatic reaction at equilibrium is still making product.

True. Reactions at equilibrium are still going, but there is no net change in the amount of product or the amount of reactant.

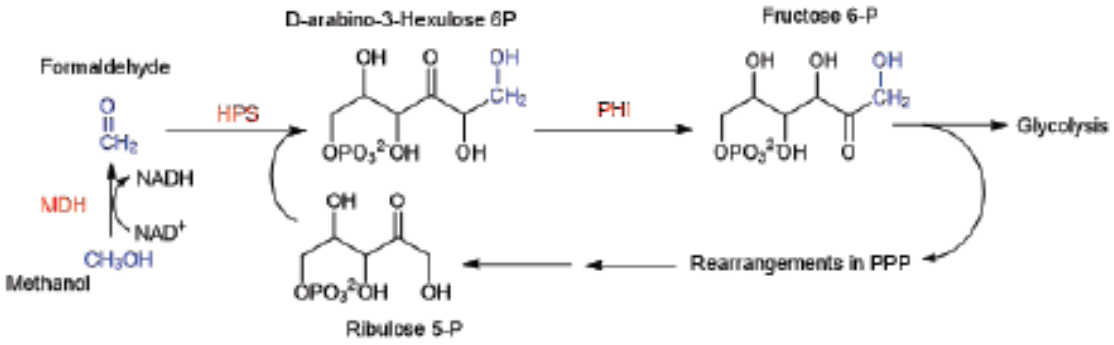
F.) An endergonic enzymatic reaction can be driven forward by coupling it to an exergonic reaction like the hydrolysis of ATP.

True. Favorable (spontaneous) reactions are often coupled to an unfavorable endergonic reaction to drive the unfavorable reaction forward.

G.) The direction of a reversible enzymatic reaction can be shifted by adding product.

True. $\Delta G = \Delta G° + RT \ln(\text{Products}/\text{Reactants})$. When product concentration increases, ΔG can change and become positive (making the reverse reaction spontaneous), and this change will shift the reaction toward reactants until equilibrium is achieved.

Question 6 (3 points)



Three enzymes: MDH, HPS, and PHI (shown in red in the diagram above) have been engineered into an organism that you have named "Methallica" in the hopes of providing the organism with the ability to grow on methanol by the pathway shown above. However, the pathway shown above does not appear to be working well as the organism does not appear to be growing well on methanol. Answer questions below to troubleshoot what the problem might be.

A.) Name a possible problem with step 1 (the MDH step) and a possible fix.

Some possible answers:

- *MDH may be too slow or may have low affinity for methanol. (Use a different MDH.)*
- *There may not be enough NAD+ or methanol. (Add some or add an enzyme that makes it.)*
- *Formaldehyde may build up and may be toxic to cells. (Substitute a different HPS so that formaldehyde doesn't build up.)*

B.) Name a possible problem with step 2 (the HPS step) and a possible fix.

Some possible answers.

- *HPS may be too slow or may have low affinity for ribulose 5-P. (Use a different HPS.)*
- *There may not be enough ribulose-5-P. (Add some or redirect pathway at branch to make more.)*

C.) You discover that adding more ribulose 5-P leads to a significant improvement in growth on methanol. This result may or may not change your thinking about the problem with your pathway design. Circle all possible problems with the designed pathway that are consistent with the ribulose 5-P finding.

Circle i.) There was too much flux toward glycolysis and not enough toward ribulose 5-P at the pathway branch point.
Circle ii.) The build-up of formaldehyde, which can be toxic, was limiting cell growth.
Circle iii.) The choice of HPS was not good; it had a low affinity for ribulose 5-P.
iv.) The pathway was subject to feedback inhibition by ribulose 5-P.
Circle v.) The pathway design should have included an enzyme to make additional ribulose 5-P.