Name MATTHEW FENG Rec. Section 27 TA ANNA

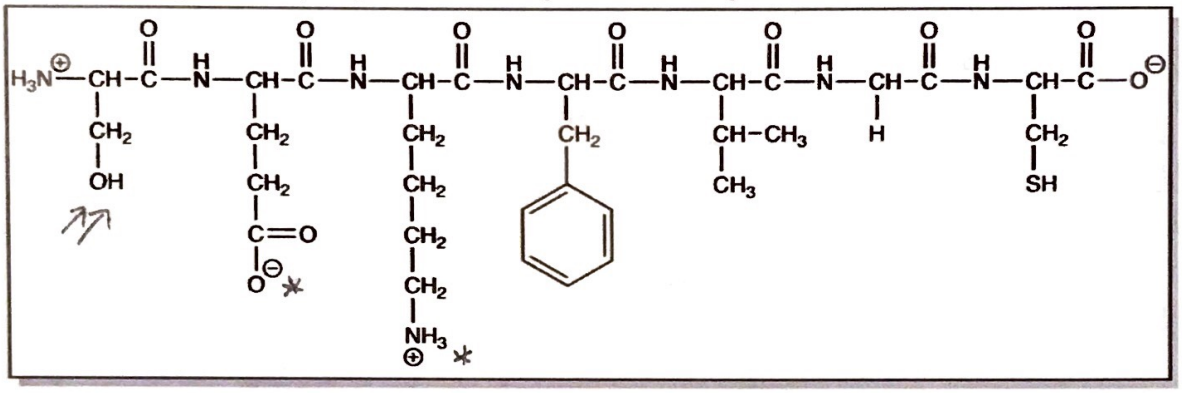
7.012 Fall 2018: Problem Set 1

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 (A-G) below. No explanation is required.



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

PROTEIN

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

SERINE, GLUTAMIC ACID, LYSINE, PHENYLALANINE, VALINE, GLYCINE, CYSTEINE

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.

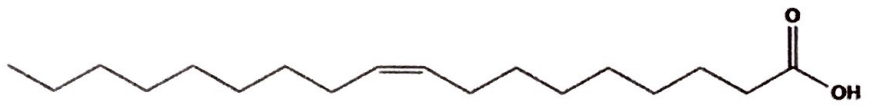
F.) Mark with a double arrow a side chain of a monomer that can participate in a hydrogen bond.

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).

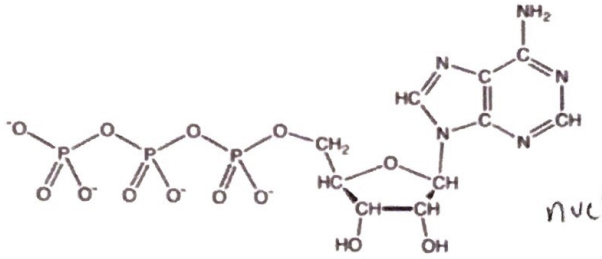
GLUTAMIC ACID

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

A

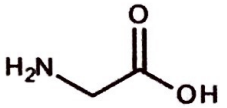


B



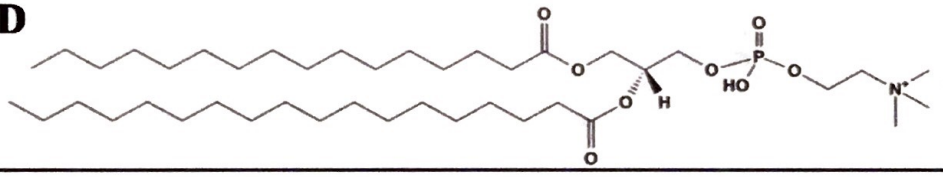
nucleic acid

C

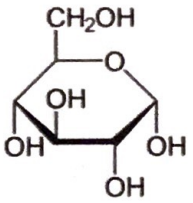


amino acid

D



E



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

C

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

The O^- side (right end). [c terminus]

iii.) Which molecule(s) from above, if any, is generated during glycolysis?

E

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

B, C, E

v.) Which molecule(s), if any, forms a cell's lipid bilayer?

A, D

Question 2, continued

vi.) Which molecule(s) from above, if any, is a building block for DNA?

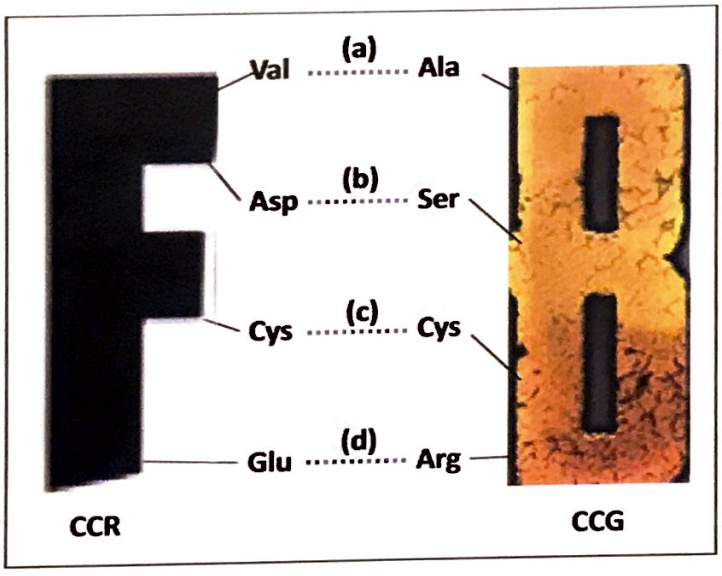
B

vii.) Which molecule(s) from above, if any, does not make a covalent bond to bring together its monomers for its biological function?

All use covalent bonds to connect monomers.

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 rank 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/c small side chains
b	hydrogen bond	3
c	covalent bond	1
d	electrostatic	2

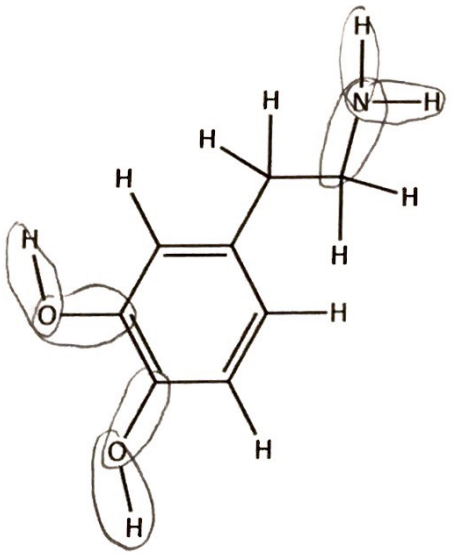
Question 3, continued

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	covalent bond	same
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.

$$|\chi_C - \chi_H| = |2.55 - 2.20| = 0.35 < 0.4.$$

By definition, we define C-H as nonpolar, since $|\Delta\chi| < 0.4$.

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 work by lowering activation energy barrier E_A, to improve reaction rate.

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

FALSE. E_A determines reaction rate. Spontaneity is determined by ΔG.

C.) Exergonic reactions are always fast.

FALSE. If E_A is large, the rate can be slow.

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

$\Delta G^\circ = -RT \ln K$

TRUE. lnK will be positive and so ΔG will be $< \emptyset$.

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

TRUE. Equilibrium is a dynamic equilibrium, so both product & reactants are being formed.

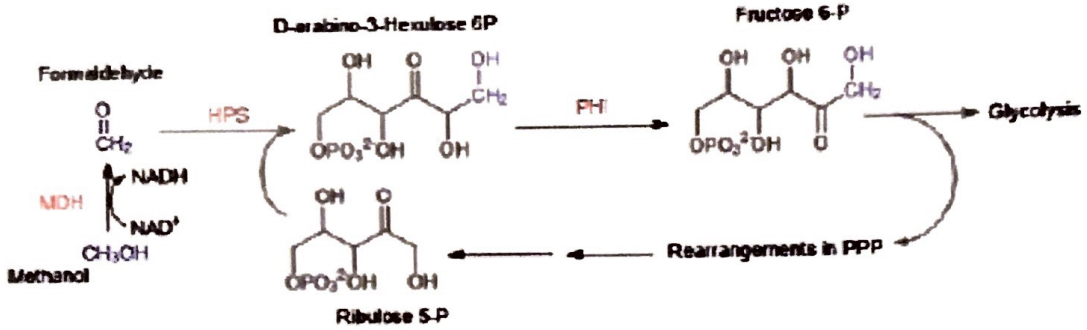
F.) An endergonic enzymatic reaction can be driven forward by coupling it to an exergonic reaction like the hydrolysis of ATP.

TRUE. The exergonic rxn can provide free energy for the endergonic rxn.

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

TRUE. By Le Chatlier's principle, the direction will shift to the left in order to create equilibrium.

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 name Methallica, in the hopes of providing the organism with the ability to grow on methanol by the pathway shown. However, the pathway shown above does not appear to be working well as the organism does not appear to be growing well on methanol. Troubleshoot what the problem might be.

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

The supply of NAD^+ is quickly exhausted b/c there is no reaction to turn NADH waste back into NAD^+.

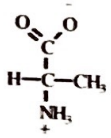
B.) Name a possible problem with step 2 (the HPS step) and a possible fix.

Without the formation of formaldehyde due to a problem w/ step 1, step 2 cannot proceed. Add formaldehyde to drive the rxn.

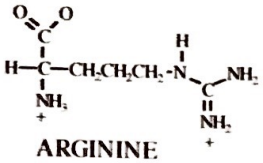
C.) You discover that adding more ribulose 5-P leads to a significant improvement in growth on methanol. This result may or may not change your thinking about the problem with your pathway design. Circle all possible problems with the designed pathway that are consistent with the ribulose 5-P finding.

i.) There was too much flux toward glycolysis and not enough toward ribulose 5-P at the pathway branch point
ii.) The build-up of formaldehyde, which can be toxic, was limiting cell growth
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
v.) The pathway design should have included an enzyme to make additional ribulose 5-P

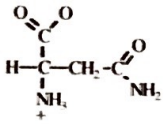
Amino Acid Structures at pH 7



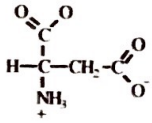
ALANINE
(ala)



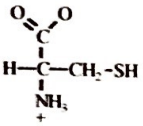
ARGININE
(arg)



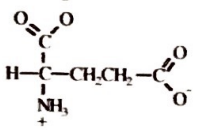
ASPARAGINE
(asN)



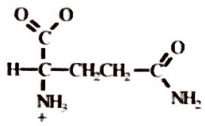
ASPARTIC ACID
(asp)



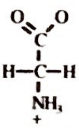
CYSTEINE
(cys)



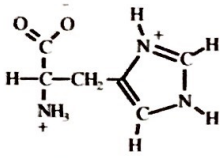
GLUTAMIC ACID
(glu)



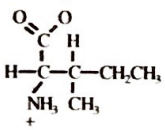
GLUTAMINE
(glN)



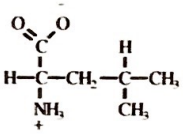
GLYCINE
(gly)



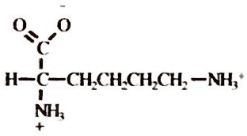
HISTIDINE
(his)



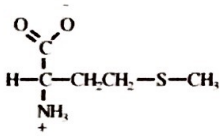
ISOLEUCINE
(ile)



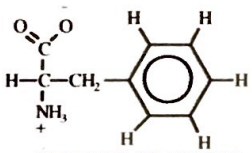
LEUCINE
(leu)



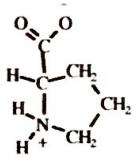
LYSINE
(lys)



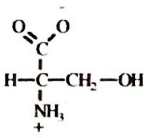
METHIONINE
(met)



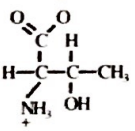
PHENYLALANINE
(phe)



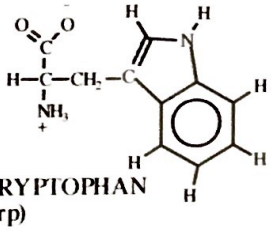
PROLINE
(pro)



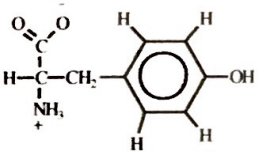
SERINE
(ser)



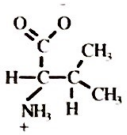
THREONINE
(thr)



TRYPTOPHAN
(trp)



TYROSINE
(tyr)



VALINE
(val)