Solutions to 7.014 Quiz I

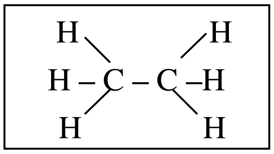
3/2/11

Class Ave = 69
Standard Dev = 15

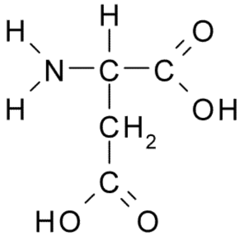
Approximate grade	Range	%
A	82 - 100	24%
B	67 - 81	36%
C	52 - 66	27.5%
D	40 – 51	9.5%
F	0 – 40	3%

Question 1 (10 points)

a) An example of a structural representation is shown in the adjacent box.

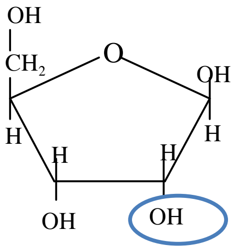


Draw a structural representation of the amino acid, Aspartic acid, which has the side chain of: CH_2COOH.



b) The molecule drawn above is a monomer found in *Proteins*

c) Below is a pentose found in RNA. On the diagram circle the hydroxyl that differs between ribonucleotides and deoxyribonucleotides.

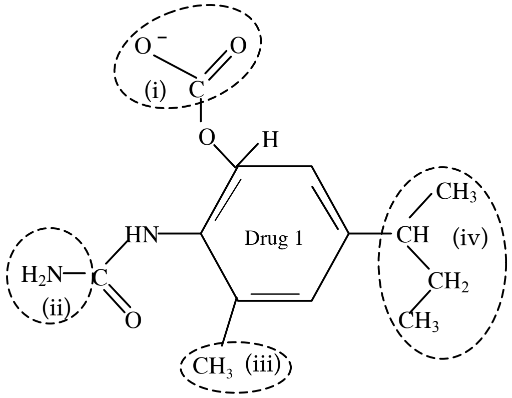


d) You find an organism that lives in thermal pools with temperatures as high as 160 °F. You find that many of this organism's proteins have a high percentage of cysteine. Briefly explain why this might be the case.

The amino acid cysteine has a terminal S – H group on the side chain. Under the appropriate conditions, adjacent cycteines can for disulfide bonds. A disulfide bond is a covalent interaction, and these strong covalent bonds can stabilize the tertiary and quaternary structure at higher temperatures. Because the protein structure dictates the function, these bonds would be important for an organism that lives in thermal pools.

Question 2 (25 points)

Shown below is the structure of Drug 1, that binds to the *E. coli* ribosome. Indicate whether each circled region could possibly form ionic bonds, hydrogen bonds, or hydrophobic interactions with another molecule by filling out the table below. Fill in the table with "yes" if that type of bond is possible, "no" if it is not.



a)

Part	Could this part form **ionic bonds**	Could this part form **hydrogen bonds**	Could this part be involved in a **hydrophobic interaction**
(i)	*yes*	*yes*	*no*
(ii)	*no*	*yes*	*no*
(iii)	*no*	*no*	*yes*
(iv)	*no*	*no*	*yes*

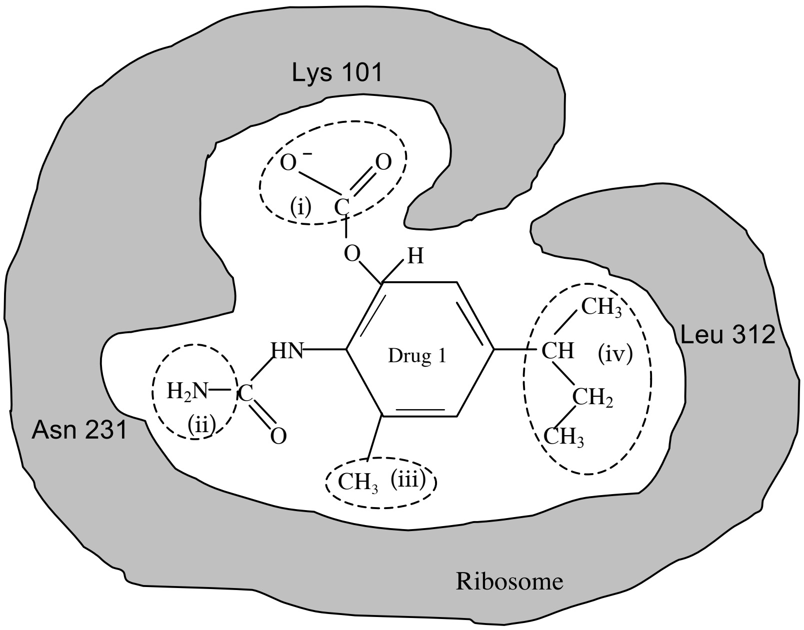
b) What is the general function of the ribosome?
The ribosome is the large complex that synthesizes polypeptides using an mRNA template.

c) Of what is the ribosome composed?
The ribosome is composed of Proteins and rRNA

d) List two macromolecules that temporarily associate with the ribosome when it performs the function listed in (b) above.
Two macromolecules that temporarily associate with the ribosome when it performs its function are tRNA and mRNA, *the growing polypeptide is also associated.*

Question 2, continued

A representation of the drug bound to the *E. coli* ribosome is shown below. Three amino acids important for binding are shown. If this drug can bind to many different bacterial ribosomes, it may be useful as an antibiotic. The ability of this drug to bind to the ribosome of two different species is examined. The drug binds to the ribosome of species 1, but does **not** bind to the ribosome of species 2.



For your information:

Amino acid	Side chain
Ile	$CHCH_3CH_2CH_3$
Val	$CHCH_3CH_3$
Asn	CH_2CONH_2
Glu	$CH_2CH_2COO^-$
Lys	$(CH_2)_4NH_3+$
Ser	CH_2OH
Leu	$CH_2CHCH_3CH_3$
Arg	$(CH_2)_3NHC(NH_2)_2+$

e) The table shows the differences between the ribosomes. Given this information, complete the table indicating which would be from species 1 (drug binds) and which would be from species 2 (drug does not bind).

Ribosome from:	Amino acid found at		
	101	231	312
E. coli	Lys	Asn	Leu
Species 2	Glu	Ser	Val
Species 1	Arg	Glu	Ile

f) What specific amino acid or amino acids prevents the ribosome from species 2 from binding Drug 1?
The glutamic acid at position 101.

g) In terms of the specific non-covalent interactions, explain why the ribosome from species 2 will NOT bind Drug 1, but the ribosomes from *E. coli* and species 1 will.
The ribosomes of E. coli and species 1have positively charged amino acids (lysine and arginine, respectively), at position 101. Hence both can form an ionic bond with the carboxyl of drug 1. The glutamic acid at position 101 in species 2 is negatively charge and will repel the carboxyl of drug 1 and prevent binding.

Question 3 (13 points)

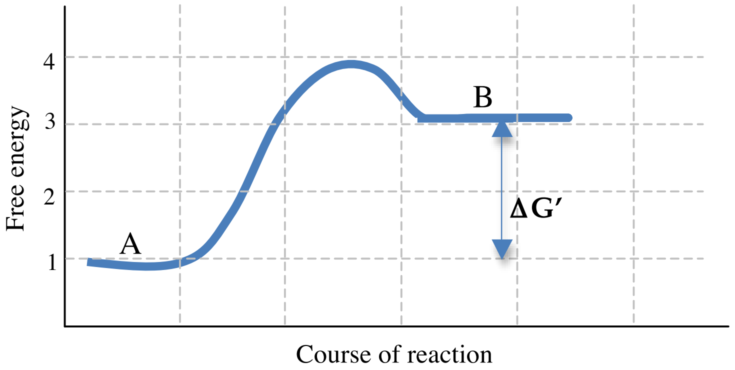
a) The energy profile for the reaction 1 is drawn on the axes below.

- Label A, B, and ΔG′ on the graph below.

- What is the value for the energy of activation?

The energy of activation for the forward reaction is 3, The energy of activation for the reverse reaction is 1.

Reaction 1) **A** $\rightleftharpoons$ **B, where ΔG′ = +2**



Compare reaction 1 (above) to reactions 2 and 3 (below).

Reaction 2) C $\rightleftharpoons$ D, where ΔG′ = -3, Energy of activation = +0.5

Reaction 3) E $\rightleftharpoons$ F, where ΔG′ = +0.3, Energy of activation = +2

b) Which of these reactions, 1, 2, or 3 is most likely to proceed in the forward direction in the absence of an enzyme? If you do not have enough information to answer this question, write *"Can't tell"* below. Explain your answer.

Reaction 2 is most likely to proceed in the forward direction in the absence of an enzyme because it is exergonic (the ΔG is negative) and the energy of activation is low compared to the other two reactions.

c) When an appropriate enzyme is added to each of these reactions, the rate of the reaction increases. Which reaction will proceed the fastest? If you do not have enough information to answer this question, write *"Can't tell"* below. Explain your answer.

You Can't tell because the rate of a reaction is a function of the enzyme, not the thermodynamic. One enzyme may be more efficient than another, regardless of the thermodynamics of the reaction, so you do not have enough information to answer the question.

d) Assume that you have a reaction X $\rightleftharpoons$ Y where ΔG = 0 and the energy of activation = +0.6 kcal/mole. In a cell, you find that the reaction proceeds almost exclusively in the forward direction. Explain why this might be the case.

In a cell, the product can be used as soon as it is produced. This consumption of the product prevents the reverse reaction for occurring and drives the reaction in the forward direction.

Question 4 (25 points)

You inoculate two test tubes with the same amount of identical growth medium and with the same number of identical yeast cells and grow these cells under identical conditions except for the presence or absence of oxygen.

a) After 12 hours, all of the glucose in each culture has been consumed. You determine the number of total cells found in each culture and find that one culture has more cells than the other.

- Which culture would have the greater cell density, the one grown aerobically or the one grown anaerobically?
  Aerobic

- Explain why the culture you chose above can make more cells with the same amount of glucose than the other culture.
  For a cell to grow and divide, it needs a large supply of ATP. The aerobic culture will perform respiration, which produces about 36 ATP/glucose. The anaerobic culture will ferment which gives 2 ATP/glucose. Thus there is more energy to make more yeast cells in aerobic conditions.

b) The cells of both cultures convert glucose to pyruvate via glycolysis, and then further metabolize pyruvate.

- Are the cells of both cultures able to obtain the same amount of ATP from **glycolysis**? Explain.
  Yes, glycolysis does not require oxygen, and give a net 2 ATP regardless. The difference in energy production is determined by what happen after glycolysis, i.e., respiration or fermentation.

- Under anaerobic conditions, the carbon from pyruvate will ultimately be found in which molecule?
  Lactic acid or ethanol

- Under aerobic conditions, the carbon from pyruvate will ultimately be found in which molecule?
  CO_2

c) Under aerobic conditions, when glucose is metabolized some of the energy is used to reduce NAD^+ to $NADH + H^+$. In the mitochondria, NADH donates its electrons to NADH-Q reductase, and from there the electrons move through the electron transport chain.

- Explain why this process requires aerobic conditions.
  Each consecutive protein in the electron transport chain is more electronegative than the last. The final electron acceptor is oxygen, which is highly electronegative.

- Briefly describe how the transfer of electrons from one protein to another in the electron transport chain results in the production of ATP.
  *As the electrons pass from one protein to another, H+ ions pass across the membrane to form a **charge** and **concentration** gradient . H+ ions of the gradient flow down the **charge** and **concentration** gradient through ATP synthase. ATP synthase can use the stored energy to make ATP from ADP.*

Question 4, continued

d) In oxygenic photosynthesis, electrons from the cholorphyll found in photosystem II are donated to the primary electron carrier. How are the donated electrons replaced?
The electrons are replace by splitting water, which generates the O_2.

e) Anoxygenic photosynthetic organisms make ATP using an electron transport chain, but do **not** produce O_2 as a waste product. What is a common source of electrons for the conversion of $NADP^+$ to NADPH for in this type of organism?
Many highly reduced compounds whose redox potential will allow transfer of electrons to $NADP^+$ *could serve as a source of electron. One common compound is* H_2S.

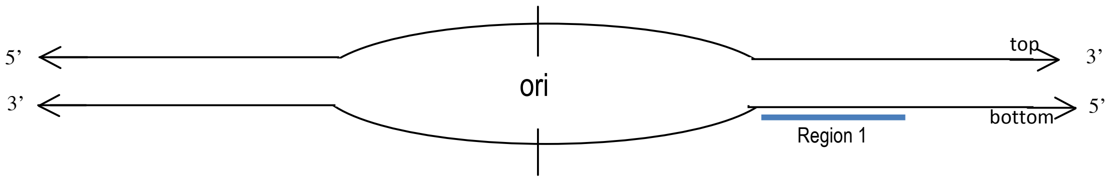
f) Circle **all** of the metabolic processes that occur in **organisms** that perform oxygenic photosynthesis.

[✓ Glycolysis] [✓ Citric acid Cycle] [✓ Oxidative phosphorylation]

[✓ Calvin Cycle] Cyclic photophosphorylation [✓ Non-cyclic photophosphorylation].

Question 5 (6 points)

Consider the following origin of replication that is found on a chromosome. The sequence of region 1 is shown below.



`Region 1:        5'…CTGACTGACA…3'`
`                 3'…GACTGACTGT…5'`

a) Within Region 1, which strand will be the template for leading strand synthesis, the top or the bottom?
The bottom strand will be the template for leading strand synthesis.

b) If we assume that a lagging strand fragment is made from region 1, what will be its sequence? Label the 5′ and the 3′ ends.
3′…GACTGACTGT…5′ or 5′…GTCAGTCAG… `3'`

c) DNA polymerase can add many thousands of nucleotides before it falls off. How does the DNA polymerase achieve this processive quality?
DNA polymerase function in conjunction with a protein, called the processivity factor. This protein is shaped like a donut or clamp that encircles the DNA template and helps anchor the polymerase.

Question 6 (21 points)

Below are 210 consecutive base pairs of DNA that includes part of the sequence of gene X. The underlined sequence represents the promoter for gene X and the underlined and italicized sequence encodes the gene X ribosome binding (RBS) site. Transcription begins at the T/A base pair at position 60 (bold)

```
    1        10        20         30        40        50        60        70
    I--------I---------I---------I---------I---------I---------I---------I
5’  ATCGGTCTCGGCTACTACGTAAACGCGCGCATATATCGATATCTAGCTAGCTATCGGTCTCGGCTACTAC
3’  TAGCCAGAGCCGATGATGCATTTGCGCGCGTATATAGCTATAGATCGATCGATAGCCAGAGCCGATGATG
                                 Promoter

             80        90        100       110       120       130       140
    ---------I---------I---------I---------I---------I---------I---------I
5’  CAGGTATCGGTATAATCTAGCTAGCTTCTCTTCTCTCTCTCCCCCGCGGGGGCTGTACTATGTATCGTCG
3’  GTCCATAGCCATATTAGATCGATCGAAGAGAAGAGAGAGAGGGGGCGCCCCCGACATGATACGTTGCAGC
                                     RBS

             150       160       170       180       190       200       210
    ---------I---------I---------I---------I---------I---------I---------I
5’  TCTCGGCTACTACGTAAACGCGCGCATATATCGATATCTAGCTAGCTATCGGTCTCGGCTACTACGTAAA
3’  AGAGCCGATGATGCATTTGCGCGCGTATATAGCTATAGATCGATCGATAGCCAGAGCCGATGATGCATTT
```

a) What are the first 10 nucleotides of the mRNA from gene X?

5′ ***U*** *C G G C U A C U A 3′*

b) What are the first 4 amino acids encoded by gene X? (A codon chart is found on page 10)

N --- met - tyr - arg - arg --- C

c) You have found two different mutations of gene X, mutation 1 and mutation 2.

i) In mutation 1, there is an insertion of the following four base pairs immediately **after** the G/C base pair at position 80 (shown in bold).

```
5’ ATGT
3’ TACA
```

- Would the mRNA expressed from this version of gene X be longer, shorter, or the same as that produced from the normal gene X? Explain and if longer or shorter, indicate by how many in bases.
  The mRNA expressed from this version of gene X would be longer by 4 bases because the insertion is after the promoter.

- If the mRNA can be translated, what are the first four amino acids produced?
  N --- met - tyr - arg - arg --- C

- If the mRNA can be translated, do you expect that the protein produced will have the same function as the normal protein X? Explain your thinking.
  This will produce normal protein X. The insertion is before the ribosome binding site and the ATG, so it will not have an effect on the protein.

Question 6, continued

c) ii) In mutation 2, you find the same four base pair insertion, but in this case the insertion is immediately **after** the A/T base pair at position 130 (shown in bold).

```
5' ATGT
3' TACA
```

- Would the mRNA expressed from this version of gene X be longer, shorter, or the same as that produced from the normal gene X? Explain and if longer or shorter, indicate by how many in bases.
  The mRNA expressed from this version of gene X would be longer by 4 bases because the insertion is after the promoter.

- If the mRNA can be translated, what are the first four amino acids produced?

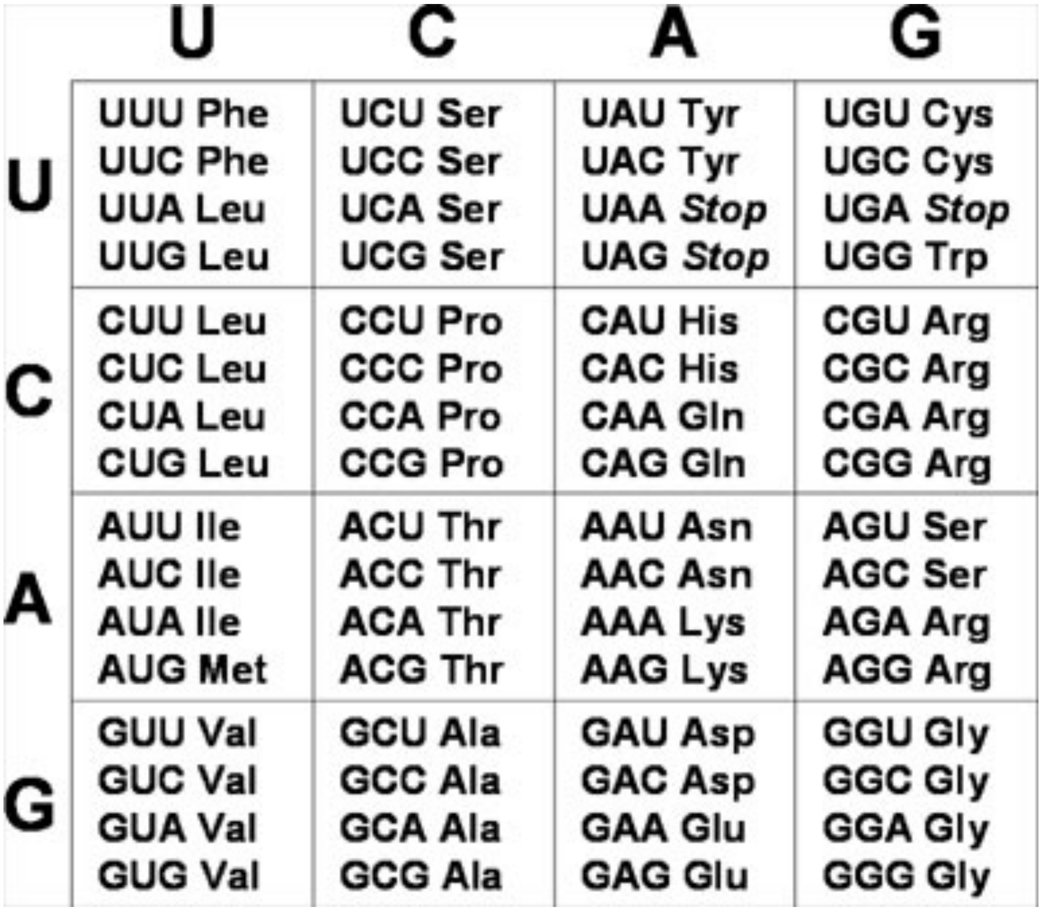
  N --- met - leu - tyr - arg --- C

- If the mRNA can be translated, do you expect that the protein produced will have the same function as the normal protein X? Explain your thinking.

  This will function as a normal protein. This insertion disrupts the normal start codon of the protein, but because it also contains an ATG, translation can begin. The new sequence will be:

```
 80        90       100       110       120       130       140       150
   ---------I---------I---------I---------I---------I---------I---------I----
5' TATAATCTAGCTAGCTTCTCTTCTCTCTCCCCCGCGGGGGCTGTACTAATGTTGTATCGTCGTCTCGGCTAC
3' ATATTAGATCGATCGAAGAGAAGAGAGAGGGGGCGCCCCCGACATGATTACAACGTTGCAGCAGAGCCGATG
```

This will be translated in the frame: AUG UUG UAU CGU CGU, which is the same reading frame as the normal gene X. Thus the protein produced from this mutation will have one additional amino acid just after the starting methionine, and this is unlikely to cause a problem.



	U	C	A	G
U	UUU Phe UUC Phe UUA Leu UUG Leu	UCU Ser UCC Ser UCA Ser UCG Ser	UAU Tyr UAC Tyr UAA *Stop* UAG *Stop*	UGU Cys UGC Cys UGA *Stop* UGG Trp
C	CUU Leu CUC Leu CUA Leu CUG Leu	CCU Pro CCC Pro CCA Pro CCG Pro	CAU His CAC His CAA Gln CAG Gln	CGU Arg CGC Arg CGA Arg CGG Arg
A	AUU Ile AUC Ile AUA Ile AUG Met	ACU Thr ACC Thr ACA Thr ACG Thr	AAU Asn AAC Asn AAA Lys AAG Lys	AGU Ser AGC Ser AGA Arg AGG Arg
G	GUU Val GUC Val GUA Val GUG Val	GCU Ala GCC Ala GCA Ala GCG Ala	GAU Asp GAC Asp GAA Glu GAG Glu	GGU Gly GGC Gly GGA Gly GGG Gly