Chem153A Exam 1

VIBHA GURUNATHAN

TOTAL POINTS

90.5 / 100

QUESTION 1

1 4 / 4

✓ **- 0 pts** **Correct**

- 1 pts Did not state false for 1a

- 1 pts Did not state true for 1b

- 1 pts Did not state false for 1c

- 1 pts Did not state true for 1d

QUESTION 2

2 6 / 6

✓ **+ 0.5 pts** **Correctly identified endergonic pathway**

✓ **+ 0.5 pts** **Correctly identified exergonic pathway**

✓ **+ 1 pts** **Correctly labelled first arrow**

✓ **+ 1 pts** **Correctly labelled second arrow**

✓ **+ 1 pts** **Correctly labelled third arrow**

✓ **+ 1 pts** **Correctly labelled fourth arrow**

✓ **+ 1 pts** **Correctly labelled fifth arrow**

QUESTION 3

3 3 / 4

✓ **+ 1 pts** **Ester**

+ 1 pts Amide

✓ **+ 1 pts** **Amine/Amino**

✓ **+ 1 pts** **Carboxylic Acid/Carboxyl**

1 Although amines can be called amino groups, it's not the same for amides. The correct terminology is amide not amido.

QUESTION 4

4 3 / 4

- 0 pts Correct

✓ **- 1 pts** **Didn't mention coupling with specifically an exergonic rxn**

- 1 pts You would couple it with an exergonic reaction that has dG=-20 or less. Enzymes do not change thermodynamics.

- 2 pts Did not discuss coupling the unfavorable reaction with an favorable reaction or specifically say an exergonic reaction/example of such (ATP hydrolysis)

- 3 pts Enzymes do not change thermodynamics, only kinetics

- 3 pts Did not discuss thermodynamics, coupling the reaction with a favorable reaction, or state coupling to an exergonic rxn or list an example of an exergonic example

- 4 pts No answer

QUESTION 5

5 6 / 6

✓ **- 0 pts** **Correct**

- 2 pts Incorrect structure of alanine

- 2 pts incorrect stationary phase

- 2 pts incorrect exchanger

QUESTION 6

6 6 / 6

✓ **- 0 pts** **Correct**

Excellent!

QUESTION 7

7 5 / 5

- 2.5 pts Answer: B, bicarbonate and phosphate

✓ **- 0 pts** **Correct**

QUESTION 8

8 5 / 5

✓ **+ 5 pts** **0.1 M NaOH, because the solution will be at a pH of 13, which deprotonates the compound to have a charged species that will soluble in water**

+ **0 pts** incorrect

QUESTION 9

9 5 / 5

✓ **- 0 pts Correct**

- **2.75 pts** Peptide backbone is incorrect
- **0.5 pts** Structure of valine is incorrect
- **0.5 pts** Structure of methionine is incorrect
- **0.5 pts** Structure of arginine is incorrect
- **0.25 pts** Charge of N-terminus is incorrect (should be neutral)
- **0.25 pts** Charge of C-terminus is incorrect (should be negative)
- **0.25 pts** Charge of arginine is incorrect (should be positive)
- **5 pts** No submission

QUESTION 10

10 5 / 5

✓ **- 0 pts Correct**

- **1 pts** Incorrect N-terminus charge
- **1 pts** Incorrect C-terminus charge
- **1 pts** Incorrect asparagine charge
- **1 pts** Incorrect glutamate charge
- **1 pts** Incorrect tyrosine charge

QUESTION 11

11 5 / 5

✓ **- 0 pts Correct**

- **4 pts** Wrong pKa used, should be pKas in between zwitterion
- **5 pts** Click here to replace this description.

QUESTION 12

12 0 / 5

- **0 pts** Correct

✓ **- 5 pts Angle drawn does not match angle specified, and/ or angle drawn is askew**

- **5 pts** Angle drawn does not match ~-90 to ~-140 degrees
- **0.5 pts** Angle drawn and specified is either -80 or -160 degrees
- **1 pts** Drawing does not modeled after dihedral angle model

QUESTION 13

13 5 / 5

✓ **+ 5 pts Correct**

+ **1 pts** identifies R group deprotonated >pH 7 and/or protonated @pH2

+ **1 pts** identifies net charge - >pH7 and/or 0 @pH 2

+ **2 pts** identifies repulsion between R groups destabilizes the ordered alpha helix

+ **1 pts** identifies that hydrogen bonds between NH and C=O groups **(not R groups)** contribute to alpha helix formation

+ **0 pts** no response written

QUESTION 14

14 5 / 5

✓ **+ 5 pts Correct, beta-mercaptoethanol**

+ **2.5 pts** indicates reducing agent is required

+ **0 pts** no response written

QUESTION 15

15 5 / 5

✓ **- 0 pts Correct**

- **1.5 pts** Need to mention that the conformational change is to planar state for full credit
- **1.5 pts** Need to mention that the starting conformation is puckered in shape
- **3 pts** Need to mention which state is "puckered" and which is "planar"
- **5 pts** No answer written
- **5 pts** Need to describe how the conformation of the ring changes
- **1 pts** Rings cannot be "linear", they are planar

QUESTION 16

16 2.5 / 5

- **0 pts** Correct

✓ **- 2.5 pts incorrect varient**

- **2.5 pts** incorrect effect on Hb affinity

QUESTION 17

17 4 / 4

✓ **- 0 pts** **Correct**

- 1 pts ATP curve should be sigmoidal

- 2 pts Curves should be sigmoidal

- 1 pts CTP curve should be sigmoidal

- 0.5 pts Curves should begin at same point

- 3 pts Curve labels should be switched

- 4 pts No answer

- 2 pts ATP curve should be a sigmoidal curve above original curve

- 4 pts Curves should be sigmoidal, ATP on top of line, CTP below

QUESTION 18

18 5 / 5

✓ **+ 5 pts** **substrate B**

+ 0 pts incorrect

QUESTION 19

19 6 / 6

✓ **- 0 pts** **Correct**

- 3 pts Incorrect Vmax- apparent value

- 3 pts Incorrect Km - apparent value

QUESTION 20

20 5 / 5

✓ **- 0 pts** **Correct**

Chem153A
Biochemistry: Introduction to Structure, Enzymes and Metabolism
Exam 1

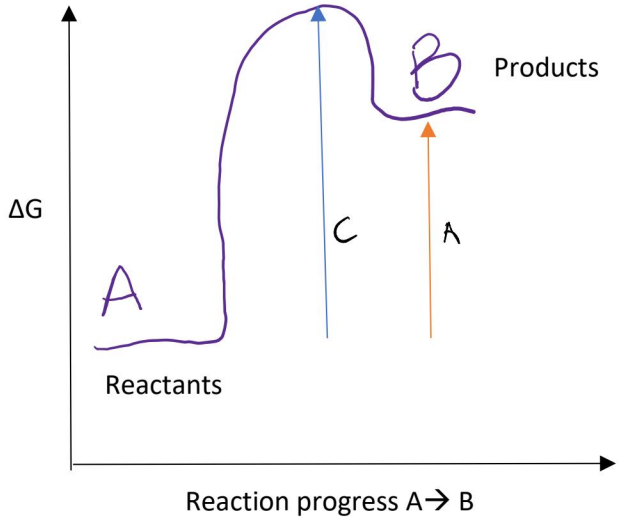
Name: VIBITA GURUNATHAN Date: OCT 15, 2021

Instructions: Refer to page 10 for pKa values to use in Exam1. Limit your answers to 2 brief sentences. Graders are not required to grade more than 2 sentences per question. This exam is open notes/ book. Follow the honor code specified in the syllabus.

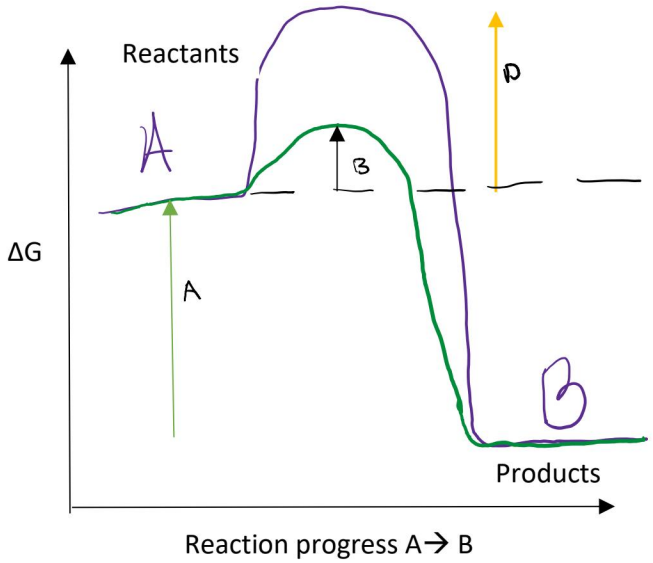
1. Label the following statements as True or False (4 points):
   a. Bacteria lack membrane bound organelles; however, they contain a well-defined nucleus. False
   b. Gram positive bacteria have a thick peptidoglycan layer. true
   c. The mitochondrion is the location of protein synthesis. false
   d. The Golgi apparatus is the site of protein processing and packaging. true

2. Below are 2 free energy diagrams for 2 different reactions. State whether each diagram is exergonic or endergonic. Label the 5 **arrows** correctly based upon the below choices, which may or may not be used more than once. (6 points)
   a. ΔG
   b. ΔG‡catalyzed
   c. ΔG‡
   d. ΔG‡uncatalyzed

‡ → transition state



endergonic



exergonic

1 4 / 4

✓ **- 0 pts** **Correct**

- 1 pts Did not state false for 1a

- 1 pts Did not state true for 1b

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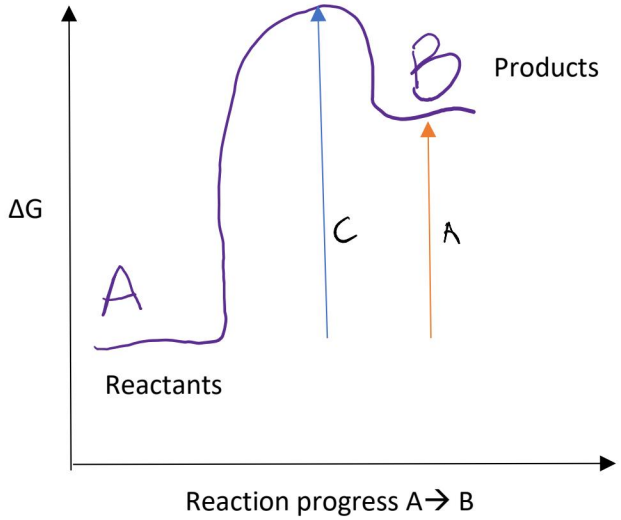
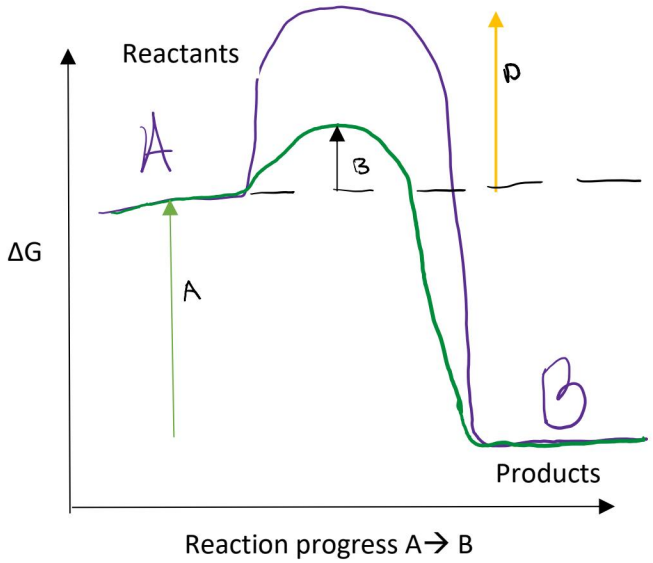


endergonic

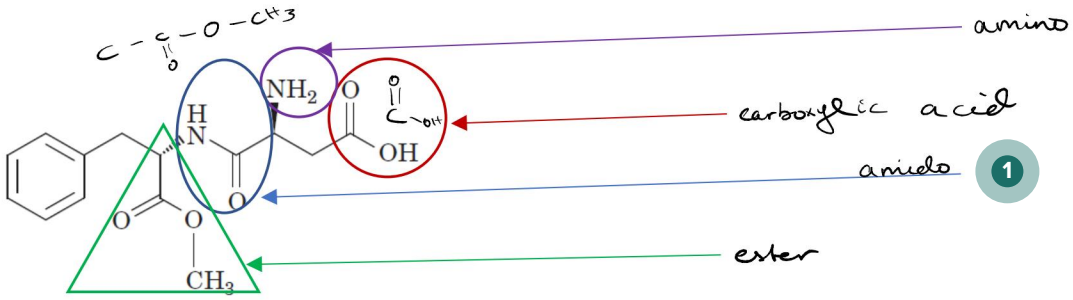


exergonic

2 6 / 6

- ✓ **+ 0.5 pts** Correctly identified endergonic pathway
- ✓ **+ 0.5 pts** Correctly identified exergonic pathway
- ✓ **+ 1 pts** Correctly labelled first arrow
- ✓ **+ 1 pts** Correctly labelled second arrow
- ✓ **+ 1 pts** Correctly labelled third arrow
- ✓ **+ 1 pts** Correctly labelled fourth arrow
- ✓ **+ 1 pts** Correctly labelled fifth arrow

3. Identify the functional groups that are circled (and in the triangle) in the diagram below (4 points).

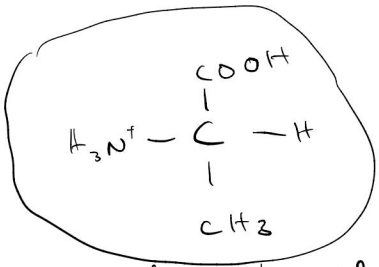


4. Can a reaction that is nonspontaneous with a ΔGo value of +20 kJ/mol be made to become favorable? If so, then how? (4 points)

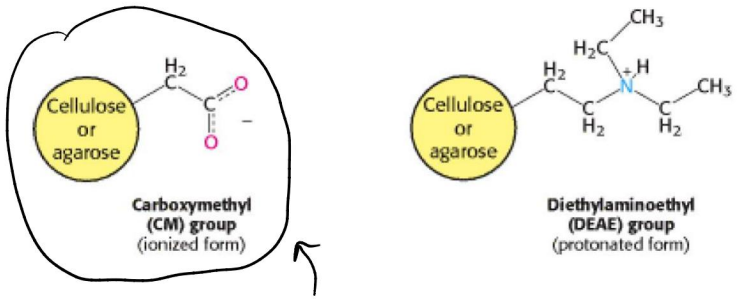
Yes. It can be paired with a highly spontaneous, favorable reaction, and the reactions can be coupled to make the overall reaction exergonic and favorable.

5. Draw the species of alanine that dominates at pH 1.0. Circle the stationary phase that will better retain the species that dominates at pH 1.0, and state whether the circled stationary phase is a cation exchanger or anion exchanger. (6 points)

$pH = 1.0$ $pK_1 = 2.34$, $pK_2 = 9.69$



fully protonated form dominates



Cation exchanger

3 **3 / 4**

✓ **+ 1 pts** **Ester**

+ 1 pts Amide

✓ **+ 1 pts** **Amine/Amino**

✓ **+ 1 pts** **Carboxylic Acid/Carboxyl**

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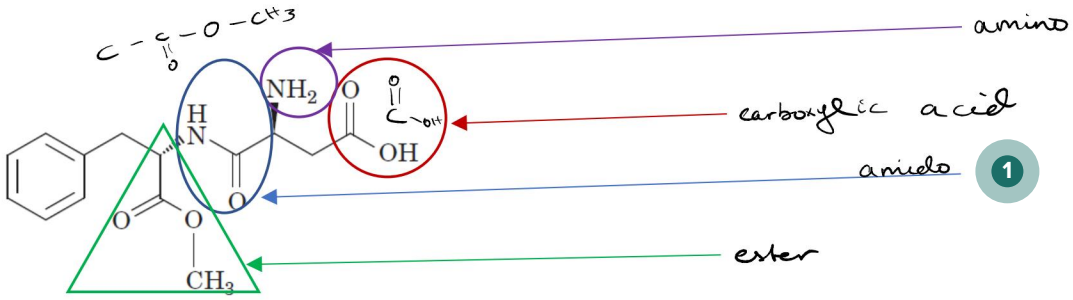

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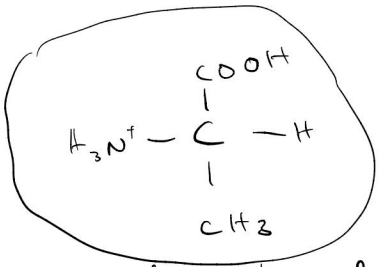

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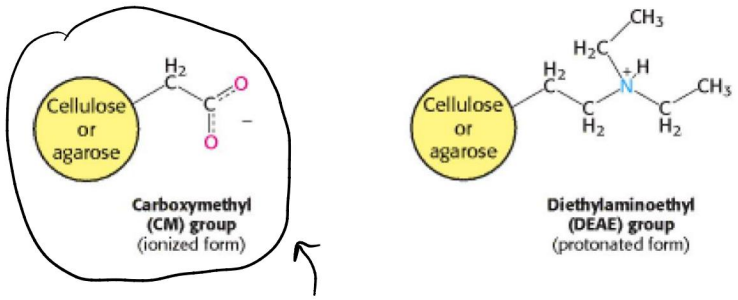

Cation exchanger

4 3 / 4

- 0 pts Correct

✓ **- 1 pts** **Didn't mention coupling with specifically an exergonic rxn**

- 1 pts You would couple it with an exergonic reaction that has dG=-20 or less. Enzymes do not change thermodynamics.

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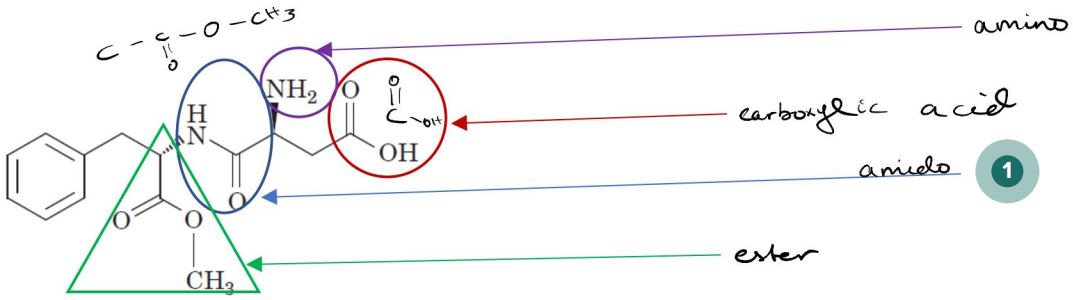

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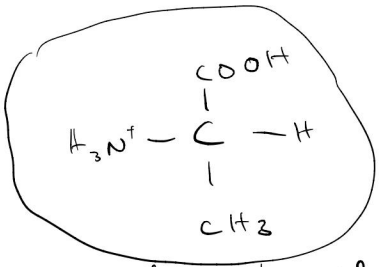

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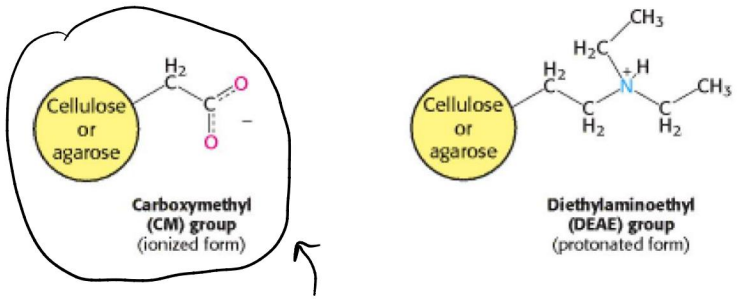


Cation exchanger

5 **6 / 6**

✓ **- 0 pts** **Correct**

- 2 pts Incorrect structure of alanine

- 2 pts incorrect stationary phase

- 2 pts incorrect exchanger

6. Calculate the ratio of conjugate base to weak acid at pH 7.0 for a molecule with a pKa of 8.2. (6 points)

$pH = pKa + \log [CB/WA]$

$7.0 = 8.2 + \log [CB/WA]$

$\log [CB/WA] = 7.0 - 8.2 = -1.2$

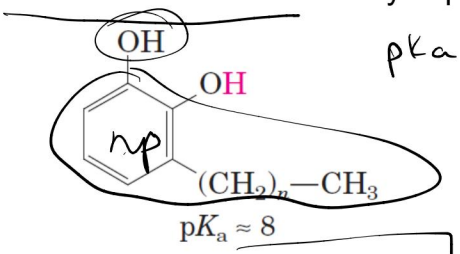
$10^{[CB/WA]} = 10^{-1.2}$

$[CB/WA] = 0.063$

Ratio of conjugate base to weak acid is 0.063.

7. What is the name of the buffering system that buffers the blood and cytoplasm of the cell, respectively? (5 points)
   a. Bicarbonate only
   b. Bicarbonate and phosphate
   c. Phosphate and ammonium
   d. None of the above

8. Is the following compound more water soluble in an aqueous solution of 0.1 M NaOH or 0.1 M HCl? Briefly explain why. (5 points)



pKa ≈ 8 @ pH = 8 it starts getting deprot. past

pH > 8 gets deprot

↑ solubility → ↑ charge

charged molecules are polar & dissolve better in polar.

NaOH ↑ pH past 8 deprotonate & increase solubility

The compound has a pKa of 8, so past pH of 8, it slowly starts to get deprotonated, and it becomes deprotonated, the molecule gains a negative charge, making it more polar. Polar substances dissolve better in water, as water is also polar & like dissolves like (due to intermolecular forces of attraction) — to increase the pH past 8, we would add strong base, and therefore the compound is more water soluble in 0.1 M NaOH.

6 6 / 6

✓ - 0 pts Correct

Excellent!

6. Calculate the ratio of conjugate base to weak acid at pH 7.0 for a molecule with a pKa of 8.2. (6 points)

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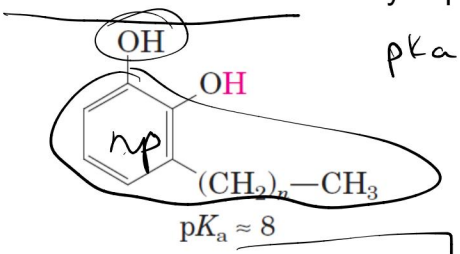

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7 5 / 5

- **2.5 pts** Answer: B, bicarbonate and phosphate

✓ - **0 pts** **Correct**

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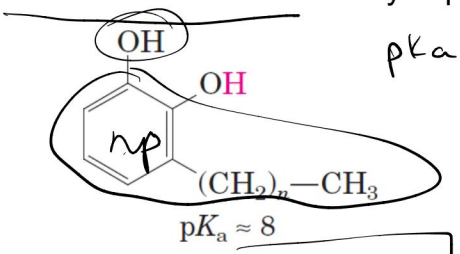

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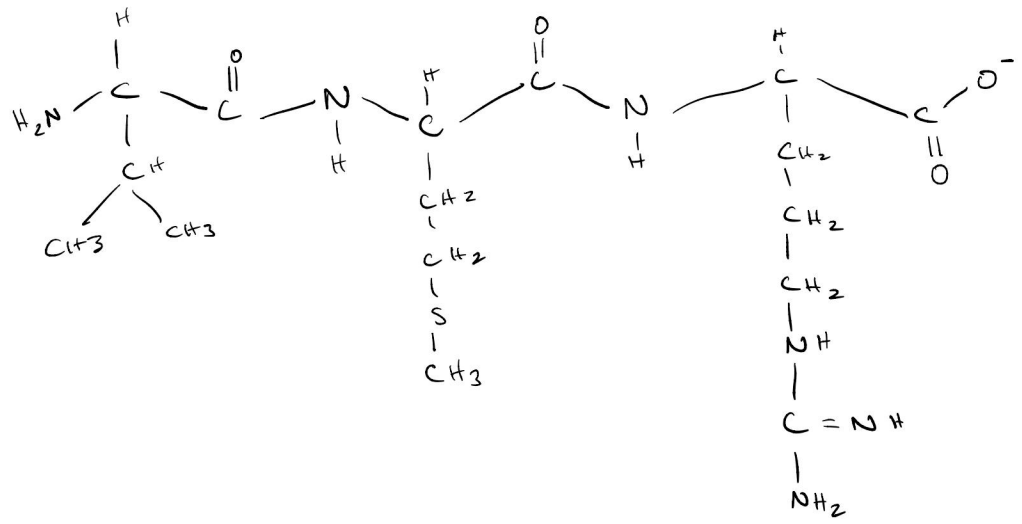
8 **5 / 5**

✓ **+ 5 pts** **0.1 M NaOH, because the solution will be at a pH of 13, which deprotonates the compound to have a charged species that will soluble in water**

+ 0 pts incorrect

valine - met - arg

9. Draw the structure of the oligopeptide V-M-R at pH 10. (5 points)



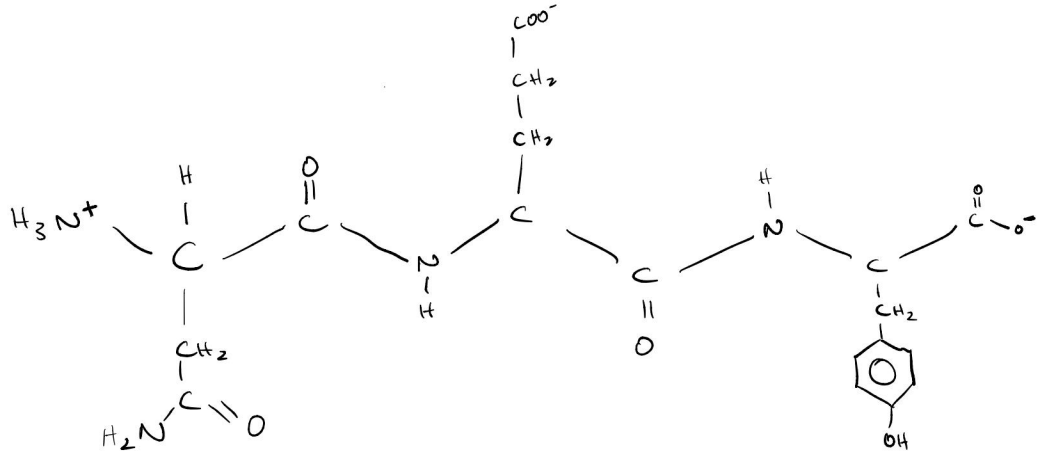
10. What is the net charge of the oligopeptide N-E-Y at pH 7.5? (5 points)

net charge : −1

glu - tyr ← deprot carboxy, not deprot pK_R

pK_R deprot.

asp ← NH_3^+ still prot



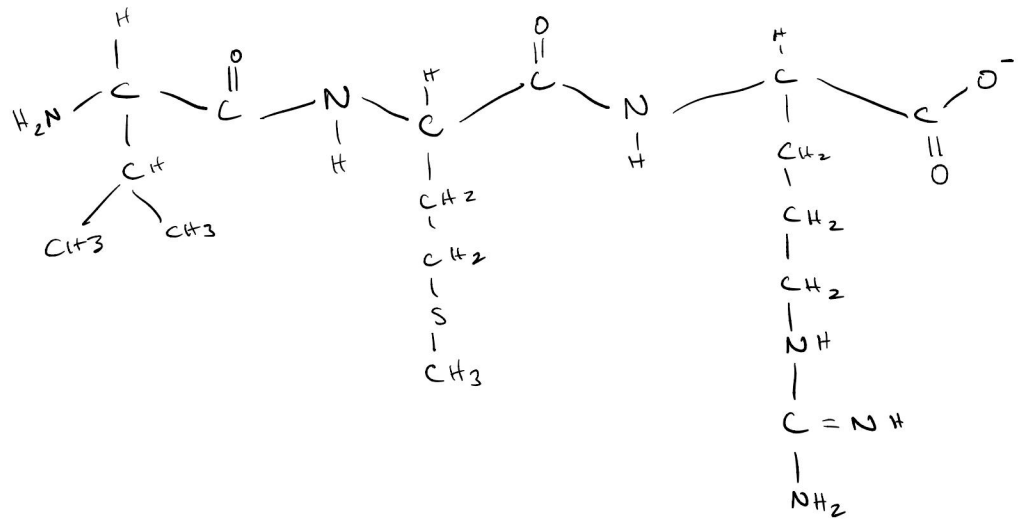
9 5 / 5

✓ - 0 pts Correct

- 2.75 pts Peptide backbone is incorrect
- 0.5 pts Structure of valine is incorrect
- 0.5 pts Structure of methionine is incorrect
- 0.5 pts Structure of arginine is incorrect
- 0.25 pts Charge of N-terminus is incorrect (should be neutral)
- 0.25 pts Charge of C-terminus is incorrect (should be negative)
- 0.25 pts Charge of arginine is incorrect (should be positive)
- 5 pts No submission

valine - met - arg

9. Draw the structure of the oligopeptide V-M-R at pH 10. (5 points)



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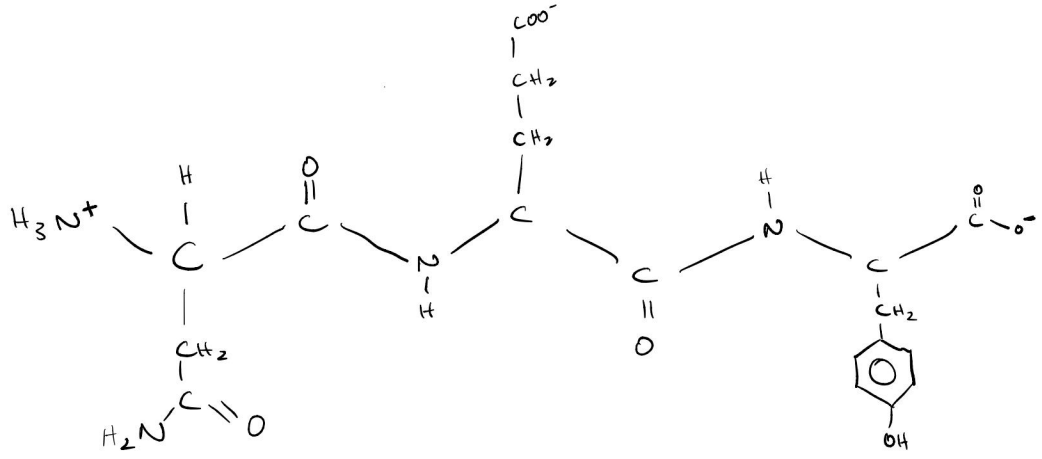


10 **5 / 5**

✓ **- 0 pts Correct**

- 1 pts Incorrect N-terminus charge

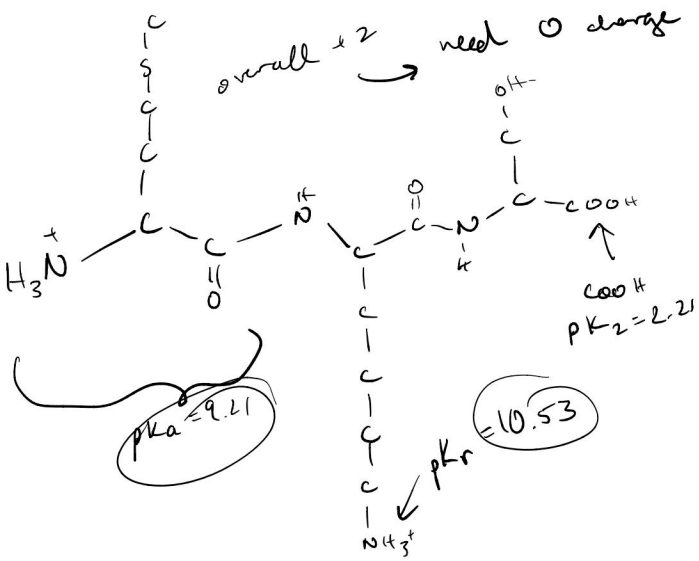
- 1 pts Incorrect C-terminus charge

- 1 pts Incorrect asparagine charge

- 1 pts Incorrect glutamate charge

- 1 pts Incorrect tyrosine charge

11. Calculate the pI of the oligopeptide M-K-S. (5 points)



between 9.21 & 10.53

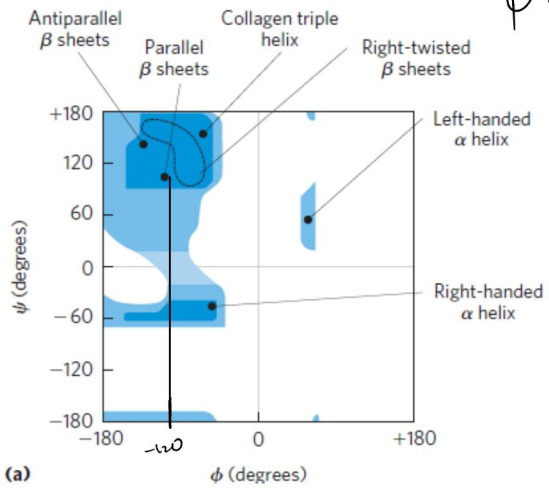
Zwition ⇒ 2 deprots

$$pI = \frac{9.21 + 10.53}{2}$$

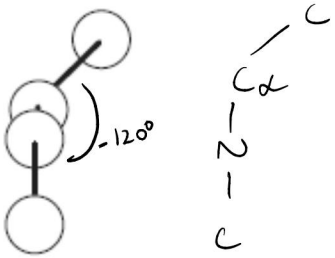
pI = 9.87

12. Below is the Ramachandran plot depicting the location of several secondary structures. Draw the phi dihedral angle for parallel β sheets in the designated box. Also state the degree of the dihedral angle in the box. Use the structure of a dihedral angle below (adjacent to the Ramachandran plot) as a model to draw your dihedral angle. (5 points)

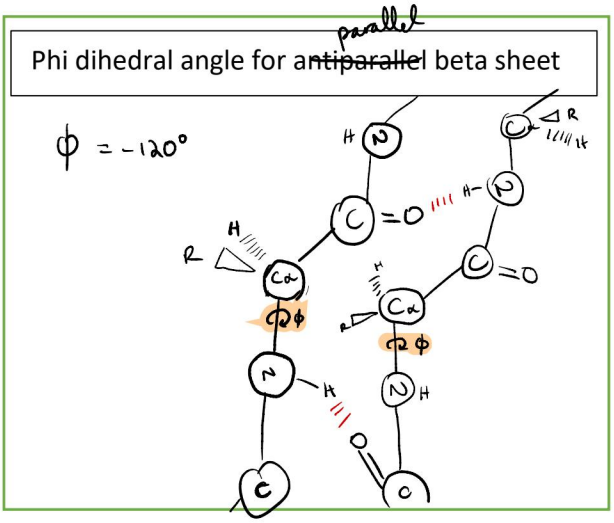
ϕ: N – C_α rotation



Model Dihedral angle



Phi dihedral angle for ~~antiparallel~~ parallel beta sheet



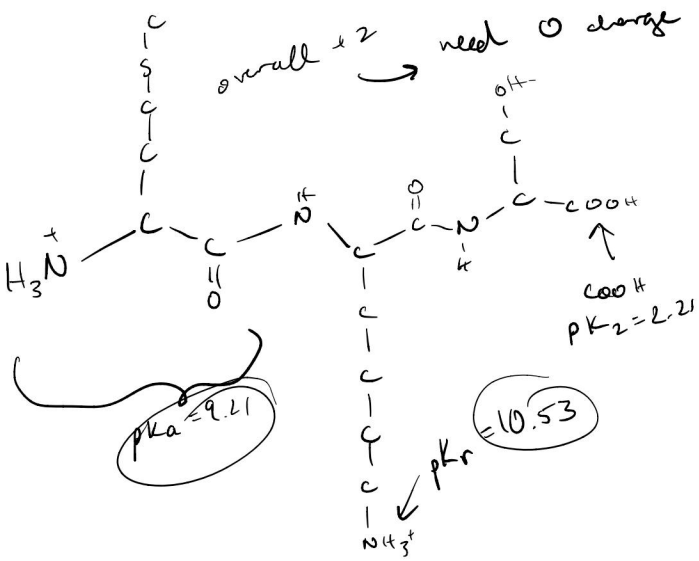
11 5 / 5

✓ **- 0 pts** **Correct**

- 4 pts Wrong pKa used, should be pKas in between zwitterion

- 5 pts Click here to replace this description.

11. Calculate the pI of the oligopeptide M-K-S. (5 points)



between 9.21 & 10.53

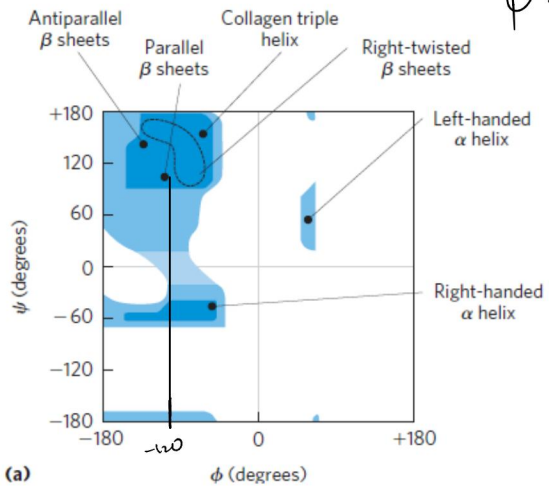
Zwition ⇒ 2 deprots

$$pI = \frac{9.21 + 10.53}{2}$$

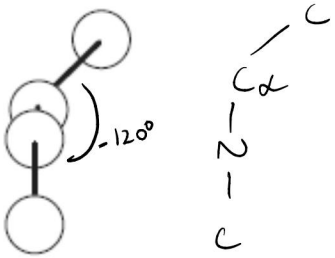
pI = 9.87

12. Below is the Ramachandran plot depicting the location of several secondary structures. Draw the phi dihedral angle for parallel β sheets in the designated box. Also state the degree of the dihedral angle in the box. Use the structure of a dihedral angle below (adjacent to the Ramachandran plot) as a model to draw your dihedral angle. (5 points)

ϕ: N – C_α rotation



Model Dihedral angle



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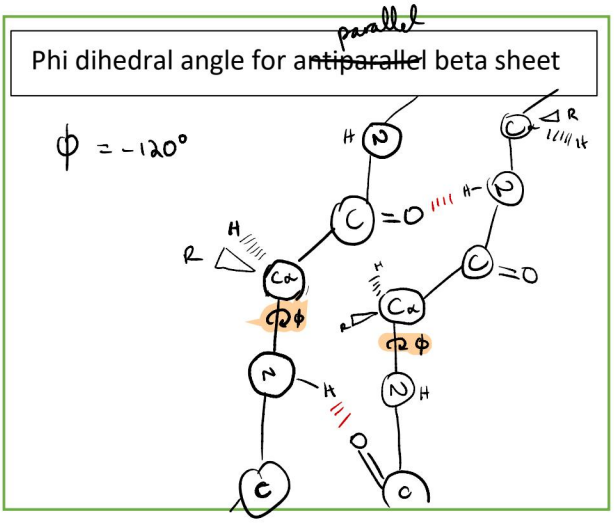


12 **0 / 5**

- **0 pts** Correct

✓ - **5 pts** **Angle drawn does not match angle specified, and/ or angle drawn is askew**

- **5 pts** Angle drawn does not match ~-90 to ~-140 degrees
- **0.5 pts** Angle drawn and specified is either -80 or -160 degrees
- **1 pts** Drawing does not modeled after dihedral angle model

13. A polyaspartate polypeptide, made of only L-Asp residues, adopts a random coil structure at a pH above 7.0; however, it adopts an alpha helix conformation at pH of 2.0. Provide a brief explanation of this phenomenon. (5 points)

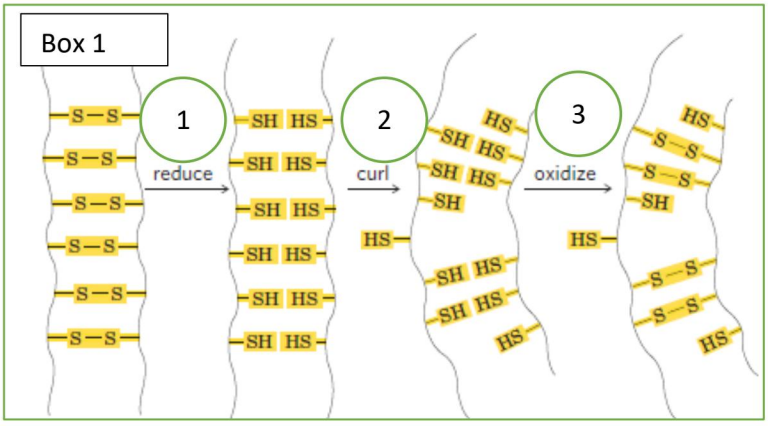
aspartate

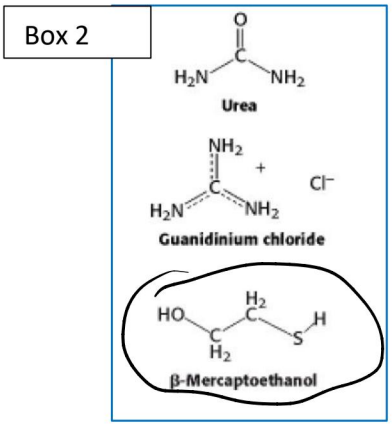
above 7.0, pKa & pKr deprot.

Aspartate's R group has a pKa of 3.65; at pH's above 7, the R group's will be deprotonated, causing a negative charge (as it is a pH above its buffer region), and these negative charges cause random coils due to ionic/electrostatic repulsions. (The individual residues comprising the polypeptide have R groups w/ negative charges).

In contrast, at pH 2.0, the L-asp residues have protonated, neutral (neutrally charged) R groups, therefore causing stabilization of the polypeptide into an α helix.

14. The process of hair, which is made up of α-keratin helices, getting permed is depicted in the diagram below in box 1. Circle the reagent in Box 2 that will most likely be used in step1 of Box 1. (5 points)





urea disrupts H-bonding interactions

13 **5 / 5**

✓ **+ 5 pts** **Correct**

+ 1 pts identifies R group deprotonated >pH 7 and/or protonated @pH2

+ 1 pts identifies net charge - >pH7 and/or 0 @pH 2

+ 2 pts identifies repulsion between R groups destabilizes the ordered alpha helix

+ 1 pts identifies that hydrogen bonds between NH and C=O groups **(not R groups)** contribute to alpha helix formation

+ 0 pts no response written

13. A polyaspartate polypeptide, made of only L-Asp residues, adopts a random coil structure at a pH above 7.0; however, it adopts an alpha helix conformation at pH of 2.0. Provide a brief explanation of this phenomenon. (5 points)

aspartate

above 7.0, pKa & pKr deprot.

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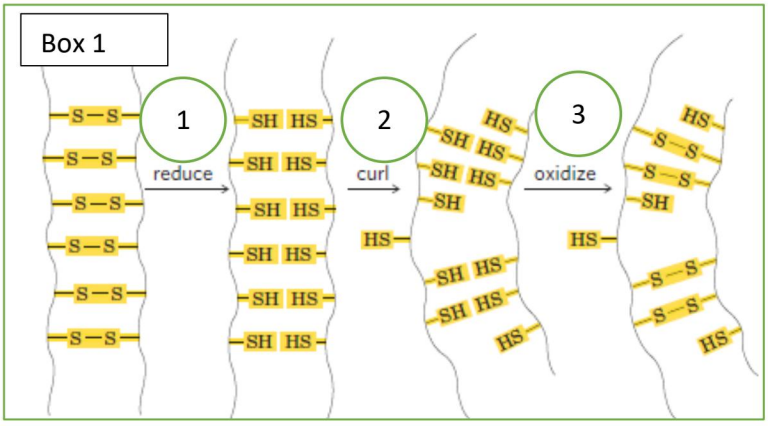
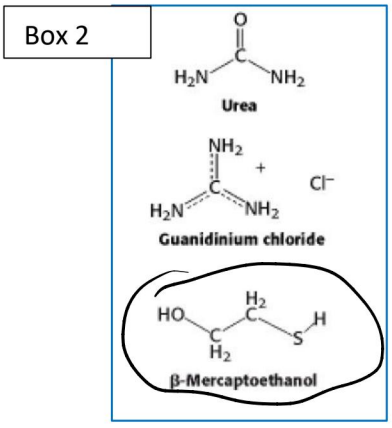




urea disrupts H-bonding interactions

14 **5 / 5**

✓ **+ 5 pts** **Correct, beta-mercaptoethanol**

+ **2.5 pts** indicates reducing agent is required

+ **0 pts** no response written

15. Briefly explain how the heme protoporphyrin ring changes from the deoxygenated state to the oxygenated state of hemoglobin. (5 points)

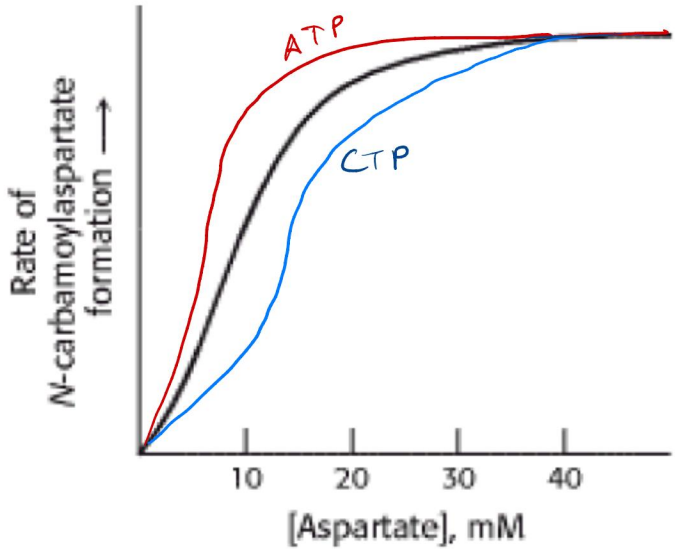
The heme protoporphyrin ring binds an iron atom in its 2^+ state (Fe^{2+}) - the heme group is nonplanar when it is in its deoxygenated state, or not bound to an oxygen - it has sort of a domed shape. This is because of e^- clouds which increase repulsions, pushing Fe out and away. Once the iron binds the oxygen, however, it becomes Fe^{3+}, the porphyrin ring becomes planar.

16. Below is a list of hypothetical Hemoglobin variants. Circle the name of the variant that is most likely to show an increase in BPG binding. Does such a hypothetical variant cause an increase or decrease in hemoglobin's affinity for oxygen? (5 points)

   a. Hb Minnesota: substitutes Pro for Leu in an alpha helix np aliphatic R groups
   b. Hb Towncow: substitutes Lys for Val
   c. Hb New Orleans: substitutes Met for Tyr, which disrupts the hydrogen bonding at the $\alpha_1\beta_1$ interface.
   d. All of the above

It would likely cause a decrease in hemoglobin's affinity for O_2.

17. Below is a rate vs [substrate] curve for the enzyme aspartate transcarbamolyase (ATCase). ATP is known to stabilize the R-state of ATCase and makes it easier for the aspartate substrate to bind. While CTP, on the other hand stabilizes the T-state of ATCase. Draw the curves for the binding of ATP and CTP and label the curves clearly with ATP or CTP. (4 points)



15 **5 / 5**

✓ **- 0 pts** **Correct**

- 1.5 pts Need to mention that the conformational change is to planar state for full credit

- 1.5 pts Need to mention that the starting conformation is puckered in shape

- 3 pts Need to mention which state is "puckered" and which is "planar"

- 5 pts No answer written

- 5 pts Need to describe how the conformation of the ring changes

- 1 pts Rings cannot be "linear", they are planar

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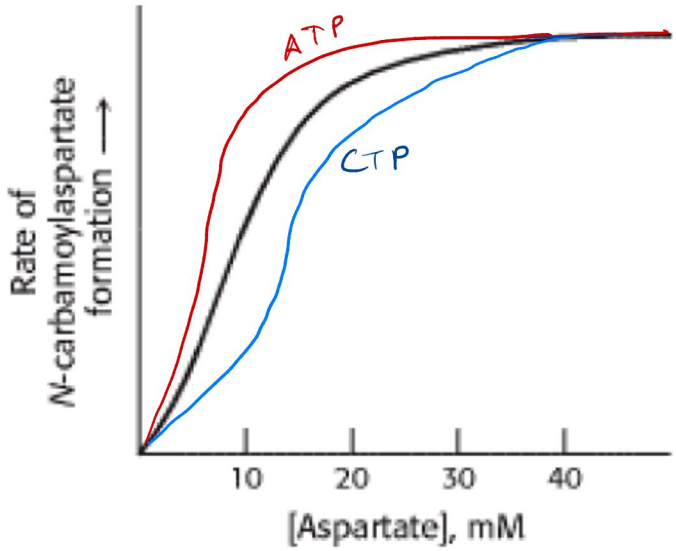

16 **2.5 / 5**

- **0 pts** Correct

✓ - **2.5 pts** **incorrect varient**

- **2.5 pts** incorrect effect on Hb affinity

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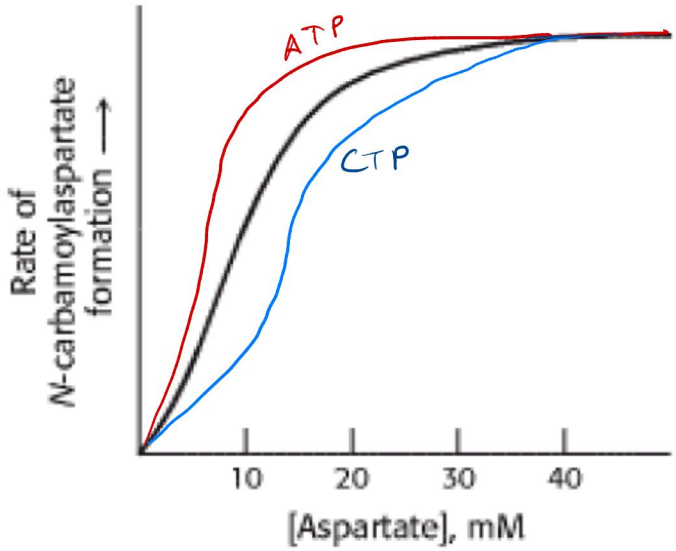


17 4 / 4

✓ **- 0 pts** **Correct**

- 1 pts ATP curve should be sigmoidal

- 2 pts Curves should be sigmoidal

- 1 pts CTP curve should be sigmoidal

- 0.5 pts Curves should begin at same point

- 3 pts Curve labels should be switched

- 4 pts No answer

- 2 pts ATP curve should be a sigmoidal curve above original curve

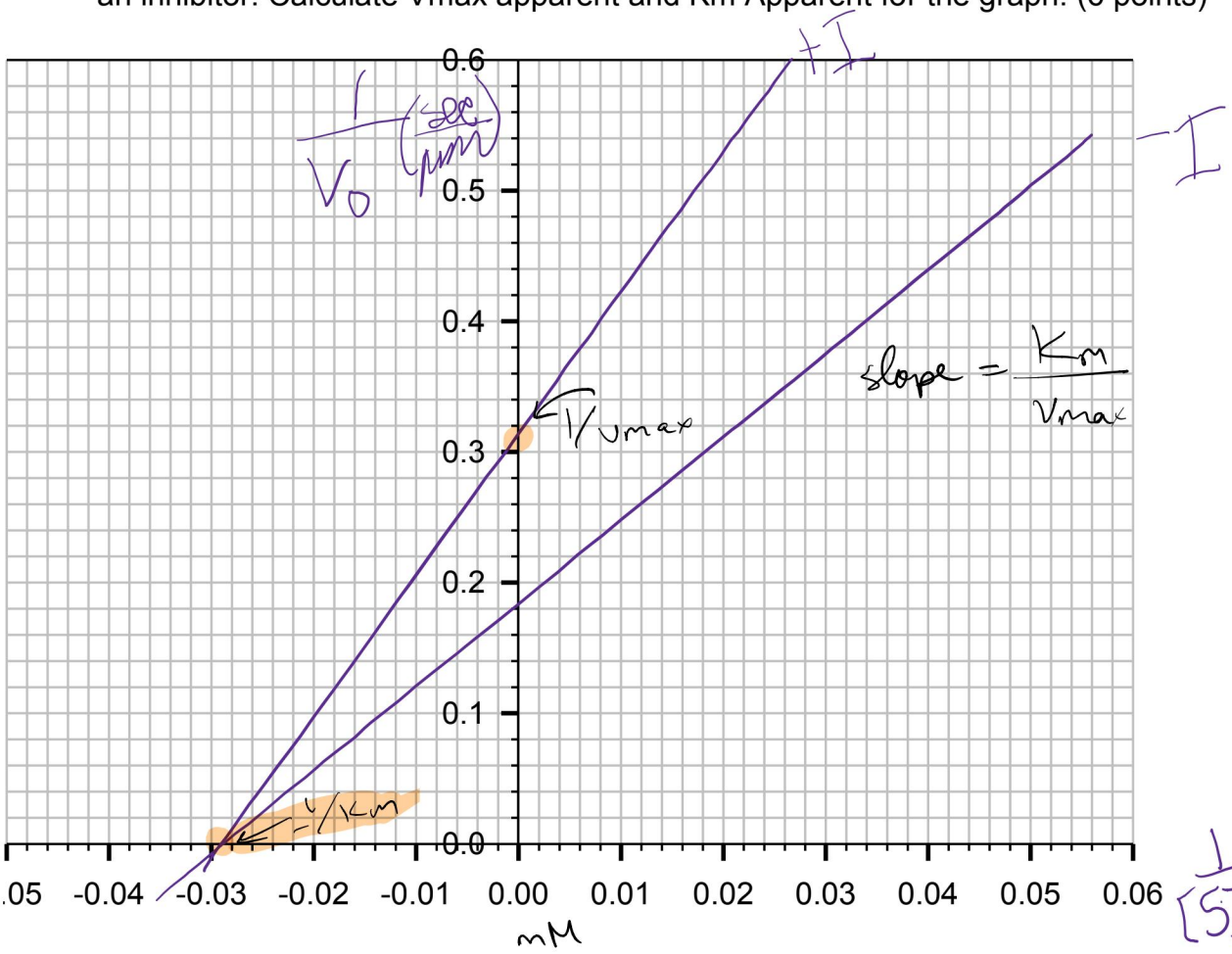
- 4 pts Curves should be sigmoidal, ATP on top of line, CTP below

↑ Km, low aff. ↓ Km, high aff.

18. Enzyme X follows simple Michaelis-Menten kinetics and has different affinities for substrates A and B. Km for substrate A is equal to 20mM and the Km for substrate B is 15mM. What is the preferred substrate for enzyme X? (5 points)

Substrate B — substrate B has a lower Km than substrate A, B a lower Km indicates higher binding affinity of the substrate to the enzyme (as only a small amt of substrate needs to be present to saturate the enz.) Thus, substrate B is preferred, as you need less of it/ it has a higher binding affinity.

19. Below is a Lineweaver-Burke plot for an enzyme in the absence and presence of an inhibitor. Calculate Vmax apparent and Km Apparent for the graph. (6 points)



$-\frac{1}{K_{m\ apparent}} = -0.028 \quad [s]^{-1} \Rightarrow$ **Km apparent = 35**

$\frac{1}{V_{max\ apparent}} = 0.31$ sec/mM $\quad V_{max\ apparent} = 1/0.31$

Vmax apparent = 3.22

18 **5 / 5**

✓ **+ 5 pts** substrate B

+ 0 pts incorrect

↑ Km, low aff. ↓ Km, high aff.

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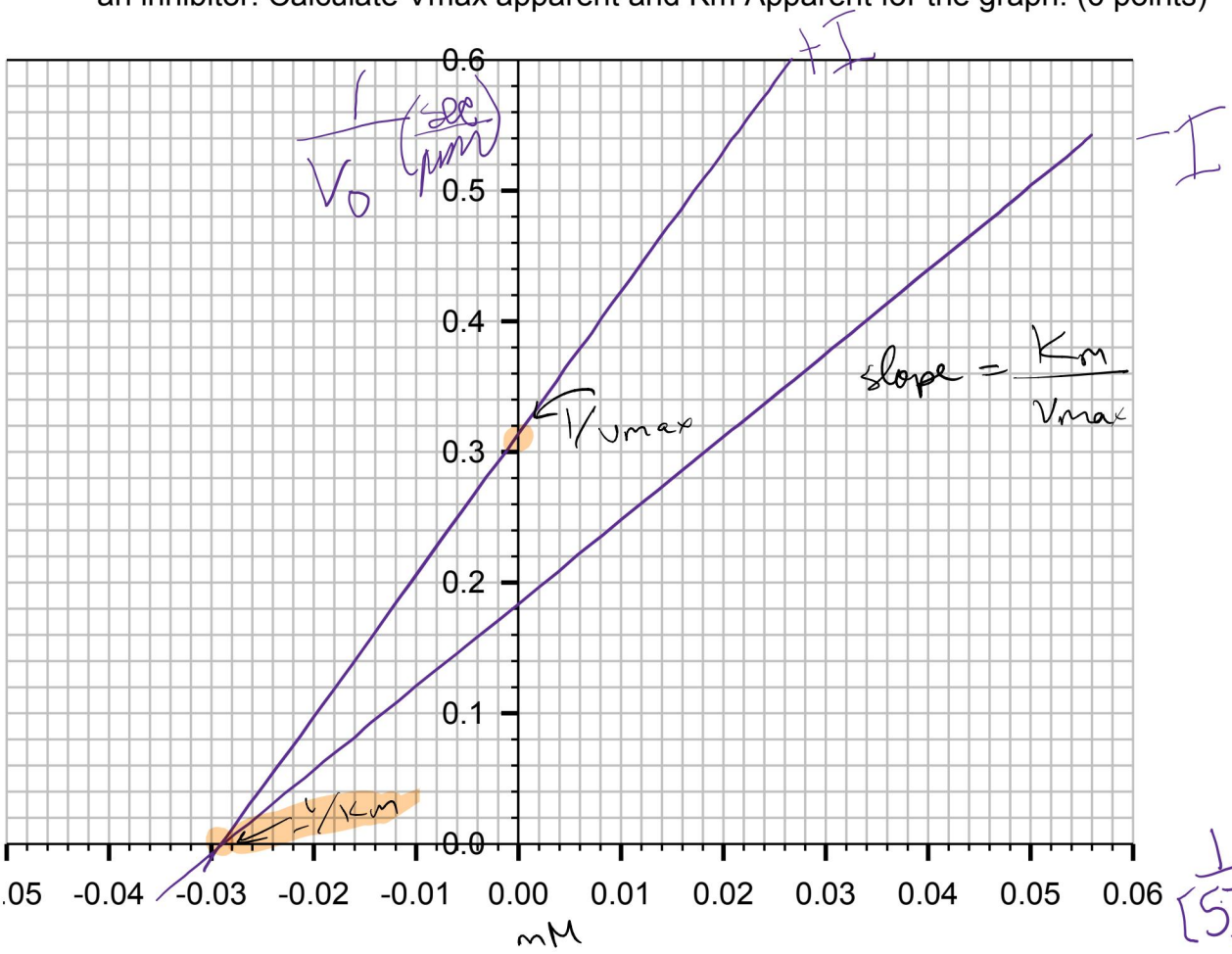

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$\frac{1}{V_{max\ apparent}} = 0.31$ sec/mM $\quad V_{max\ apparent} = 1/0.31$

Vmax apparent = 3.22

19 **6 / 6**

✓ **- 0 pts** **Correct**

- 3 pts Incorrect Vmax- apparent value

- 3 pts Incorrect Km - apparent value

20. Based upon the graph in question ~~17~~ 19, what type of inhibitor is depicted, and does this inhibitor have a greater affinity for the enzyme only, enzyme-substrate complex only, or both? (5 points)

It is a non competetive inhibitor. This is because it has a constant Km value & a decreased Vmax value (as it has an increase in $1/V_{max}$), which means that it has a roughly equal affinity for both the enzyme & the enzyme - substrate complex.

20 **5 / 5**

✓ **- 0 pts** Correct