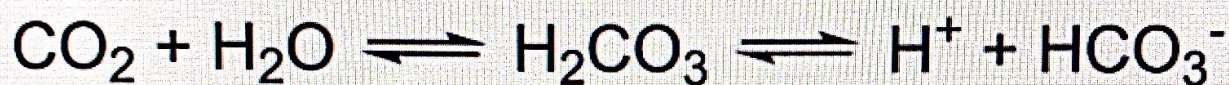


Question 11

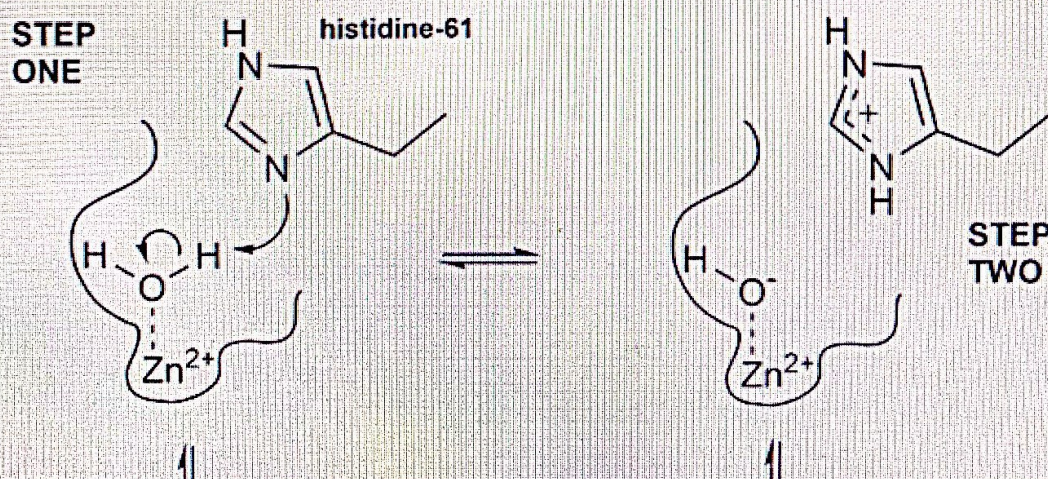
1 pts

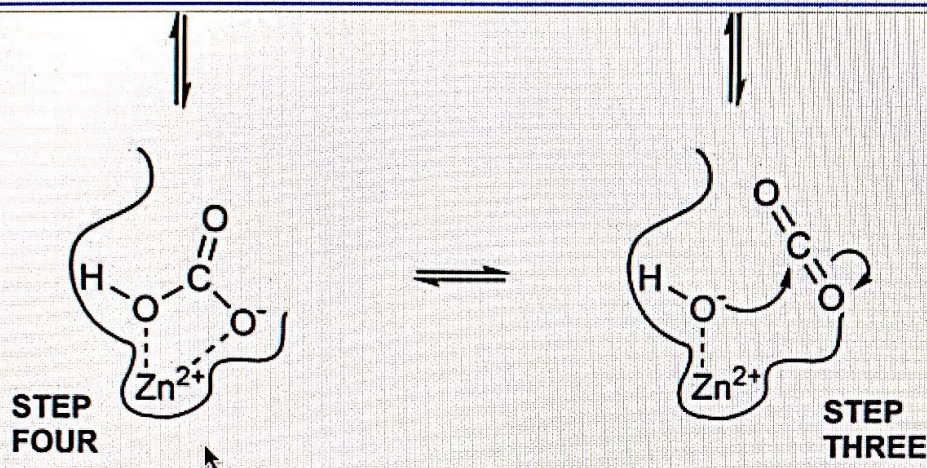
Again, use the following to answer question 11.

The enzyme carbonic anhydrase catalyses the reversible hydration of carbon dioxide to form bicarbonate.



The enzyme has a Zn^{2+} ion in its active site that promotes the catalysis. A simplified enzymatic mechanism for carbonic anhydrase is shown below. Only the zinc ion, a critical histidine side chain, and substrate and product molecules are shown.

Carbonic anhydrase mechanism of CO_2 conversion to bicarbonate:



Consider the following statements about the carbonic anhydrase mechanism (in the figure).

- Histidine-61 acts as a catalytic acid. It becomes protonated in the process.
- Zinc provides a binding site to bring substrates together in the correct orientation to react together.
- Zinc increases the polarity of the bound water molecule. The polarised water molecule is more likely to donate its proton to histidine-61.
- The carbon dioxide carbon atom has a partial negative charge. The zinc ion attacks this oppositely-charged carbon atom.

Which of the statements above is/are **CORRECT**?

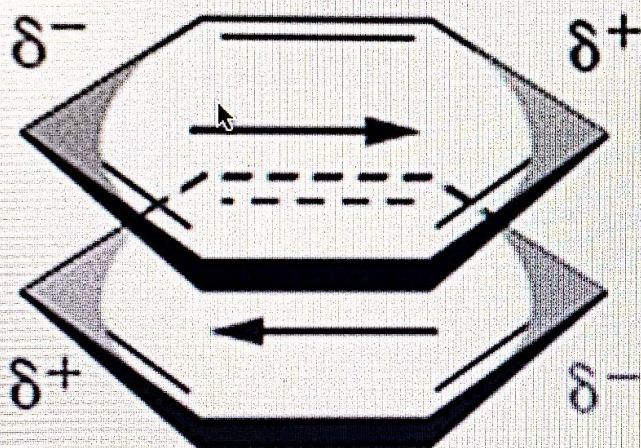
- ☐ Statements ii and iii only are correct.
- ☐ Statements i, ii and iii only are correct.
- ☐ Statement iii only is correct.
- ☐ Statements ii and iv only are correct.



Question 12

1 pts

How can we describe the interaction between two aromatic molecules (for example two benzenes as shown) stacked on top of each other?



- ☐ Electrons freely flow between the two benzene molecules. This process of electron movement is called "ring charge switching".
- ☐ Benzene rings contain electronegative atoms that produce polar bonds. Opposite charges in the polar bonds are attracted to each other.
- ☐ Benzene molecules have permanent dipoles. The positive and negative partial charges attract each other.
- ☐ The attractive interaction between benzene rings comes from mutually induced dipoles.

- ☐ The attractive interaction between benzene rings comes from mutually induced dipoles.

Question 13

1 pts

Which of the following statements **CORRECTLY** identify the type(s) of interactions that stabilise the structure of the DNA double helix?

- i. van der Waals interactions between base-pairs stacked up and down the helix.
- ii. Hydrogen bonds between bases to form base pairs.
- iii. Hydrogen bonds between phosphates and water molecules surrounding the DNA molecule.

- ☐ Statement i only is correct.
- ☐ Statements ii and iii only are correct.
- ☐ Statements i, ii, and iii are all correct.
- ☐ Statements i and ii only are correct.

Question 14

1 pts

Which statement is **INCORRECT**?



MacBook Air

☐ Statements i and ii only are correct.



Question 14

1 pts

Which statement is **INCORRECT**?

- ☐ Water is predominantly in the liquid state on our planet because of its inability to form hydrogen bonds in ice.
- ☐ A protonated water molecule or hydronium ion (H_3O^+) is a better way to represent the hydrogen ion (H^+) in aqueous solution.
- ☐ The hydrophobic effect relates to how water molecules interact with other water molecules and also with non-polar molecules.
- ☐ Water forms a hydration shell around both negatively-charged ions (anions) and positively-charged ions (cations).



Question 15

1 pts

Which of these processes involve the hydrophobic effect?

- i. Membrane protein folding with the hydrophobic amino acid side chains buried in the lipid bilayer.
- ii. Water-soluble protein folding with hydrophobic amino acid side chains buried inside the protein interior.



Question 15

1 pts

Which of these processes involve the hydrophobic effect?

- i. Membrane protein folding with the hydrophobic amino acid side chains buried in the lipid bilayer.
- ii. Water-soluble protein folding with hydrophobic amino acid side chains buried inside the protein interior.
- iii. Formation of the DNA double helix with the DNA bases hidden from solvent.
- iv. The binding of a hydrophobic drug molecule inside a hydrophobic pocket of a protein.
- v. The formation of lipid bilayers.

- ☐ Processes i, iv, and v only are correct.
- ☐ Processes i, ii, iii, iv and v are all correct.
- ☐ Processes ii and iv only are correct.
- ☐ Processes i and iii only are correct.



Question 16

1 pts

Which statement is **CORRECT**?

Question 16

1 pts

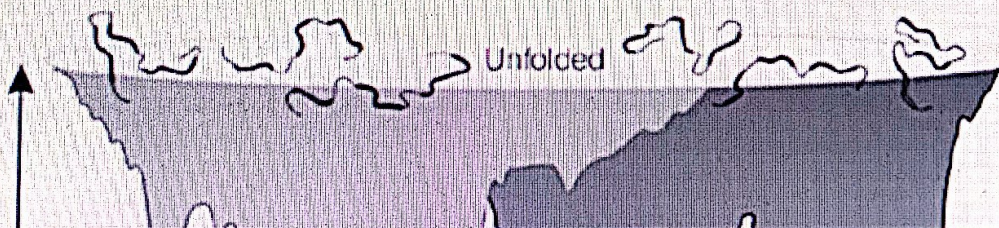
Which statement is **CORRECT**?

- ☐ Metamorphic proteins exist as more than one structure. There is a large energy barrier in converting between the different forms and a chaperone is required for this to occur.
- ☐ The amyloid diseases Parkinson's, Creutzfeldt-Jakob and kuru are each associated with the misfolding of a unique protein.
- ☐ Disease forms of amyloid proteins do not fold up following the same rules as the native form of the protein.
- ☐ Kuru is a genetic disease carried by a large proportion of the Fore people in Papua New Guinea.

Question 17

1 pts

Consider the energy landscape below describing a generic amyloid disease.



Question 17

1 pts

Consider the energy landscape below describing a generic amyloid disease.

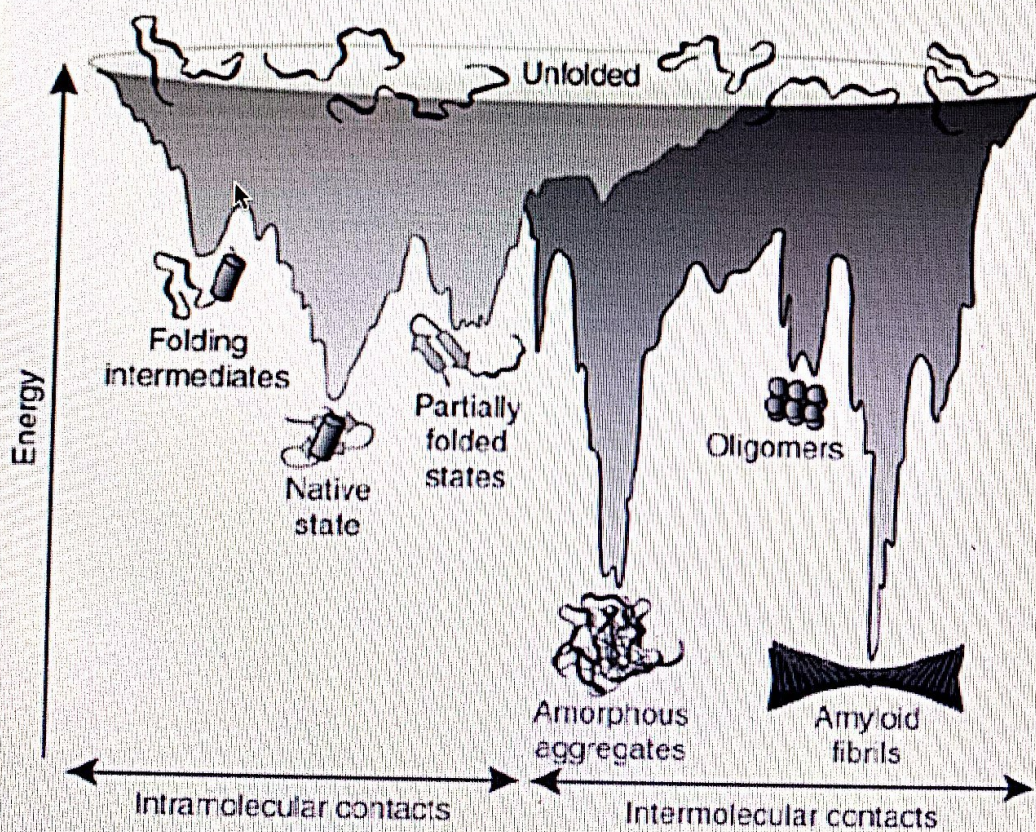


Figure from: Hartl and Hayer-Hartl, 2009.

Which statement is CORRECT?

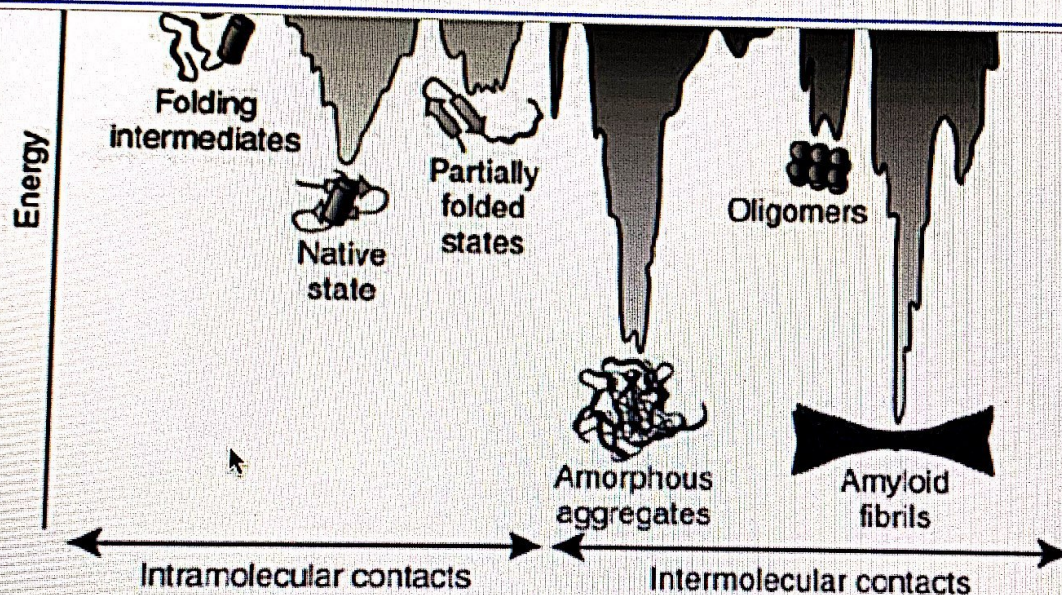


Figure from: Hartl and Hayer-Hartl, 2009.

Which statement is **CORRECT**?

- ☐ Disease forms of amyloid proteins are characterised by multiple copies of the protein stabilised by extensive intermolecular interactions.
- ☐ Folding intermediates, partially-folded states, and the native protein are primarily held together by intermolecular contacts.
- ☐ Energy barriers between different forms of the protein are low. Interconversion between all the protein forms is easy.
- ☐ Amorphous aggregates, oligomers, and amyloid fibrils form extended α -helical structures with extensive hydrogen bonding interactions stabilising their structures.

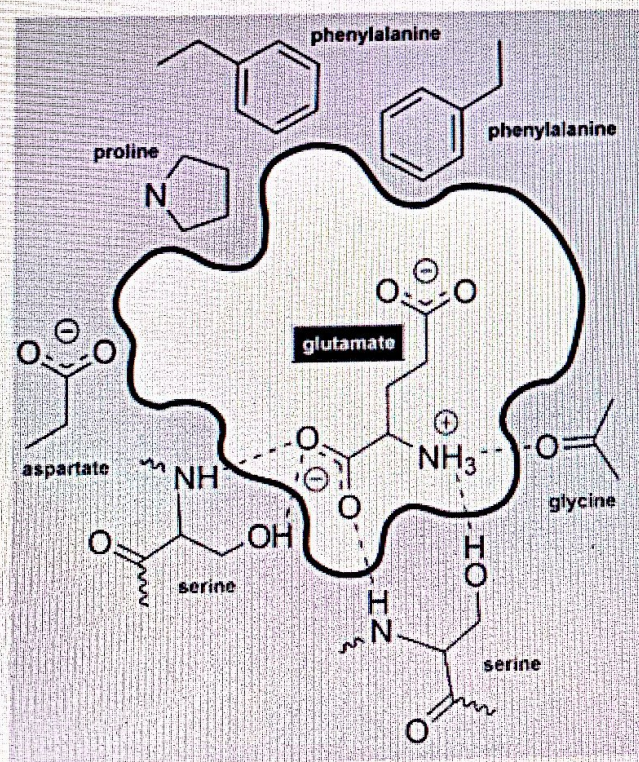


Question 18

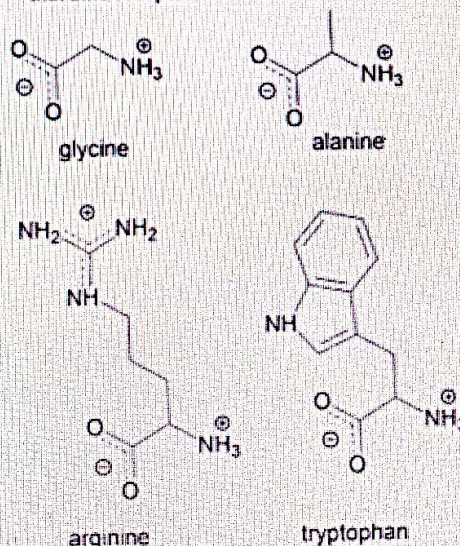
1 pts

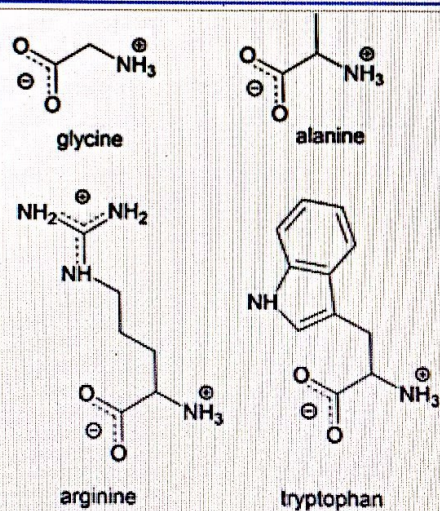
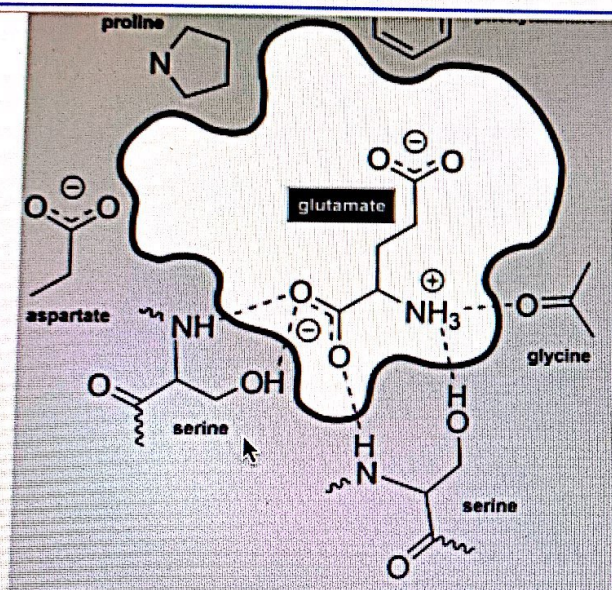
Do you like the taste of mushrooms or fermented fish sauce? The umami (Japanese for "good taste") receptors on your tongue recognise the "taste" of specific amino acids - a classic example of molecular recognition. The amino acids induce the receptor to change shape and this signals the sensation of taste.

X-ray structures of the umami receptor from the Japanese rice fish show how glycine, alanine, glutamate, and arginine are recognised by the receptor. A diagram showing glutamate binding is provided below. The protein is shaded grey and dark curved lines represent the outer edges of the binding pocket.



other amino acids that bind receptor:





Which statement is **INCORRECT**?

- ☐ The tryptophan side chain could bind in the pocket formed by the proline and two phenylalanines, making numerous van der Waals interactions.
- ☐ The arginine side chain is long and flexible and could reach around to the aspartate to form a charge-charge interaction.
- ☐ The pocket that is formed by two serines and a glycine would recognise the carboxylate and amine groups of any amino acid.
- ☐ Glycine and alanine lack the functional groups that bind to the receptor as shown in the figure (for glutamate).

**Question 19****1 pts**

In a COVID-19 infection, the SARS-CoV-2 spike protein binds to the human ACE2 receptor to enable the virus to enter the host cell. This interaction is similar to that previously seen between ACE2 and the SARS-CoV virus from 2002-2004. SARS-CoV-2 has caused pandemic disease in humans because:

- ☐ its spike protein has adapted to the human ACE2 receptor making the virus highly transmissible between humans.
- ☐ pigs have bat type receptors in their upper respiratory tract; pigs transmit the viral infection to humans.
- ☐ it has acquired a new spike protein from influenza and can bind to sialic acid receptors on human cells in the upper respiratory tract.
- ☐ the human host cells in the upper respiratory tract have adapted to bind the virus spike protein making the virus more transmissible between humans.

**Question 20****1 pts**

The interfaces formed between the human ACE2 receptor and the spike protein of both SARS-CoV and SARS-CoV-2 are illustrated below.

The (not so brilliant) Dr Squire forgot to label his images. Use your knowledge of protein-protein interactions to determine which interface involves SARS-CoV2.



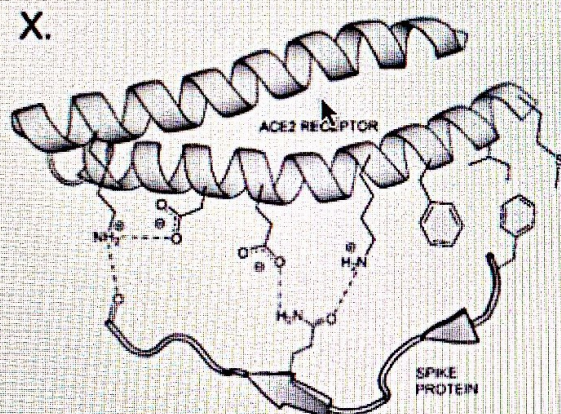
Question 20

1 pts

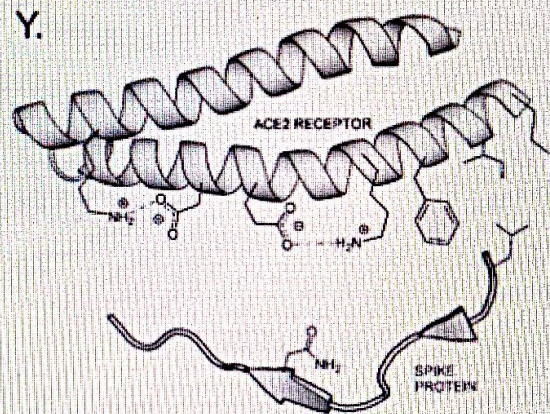
The interfaces formed between the human ACE2 receptor and the spike protein of both SARS-CoV and SARS-CoV-2 are illustrated below.

The (not so brilliant) Dr Squire forgot to label his images. Use your knowledge of protein-protein interactions to determine which interface involves SARS-CoV2.

X.



Y.



The interface between human ACE2 and SARS-CoV-2:

- ☐ is shown in image X. Intermolecular interactions are formed by amino acid side chains that would otherwise form intramolecular interactions.
- ☐ is shown in image Y. The lack of hydrophobic interactions makes this interface stronger.
- ☐ is shown in image Y. This interface is stronger than the SARS-CoV interface because it contains two charge-charge interactions
- ☐ could be shown in either image X or image Y - there is not enough information to decide.



Question 21

1 pts

Which statement is **CORRECT**?

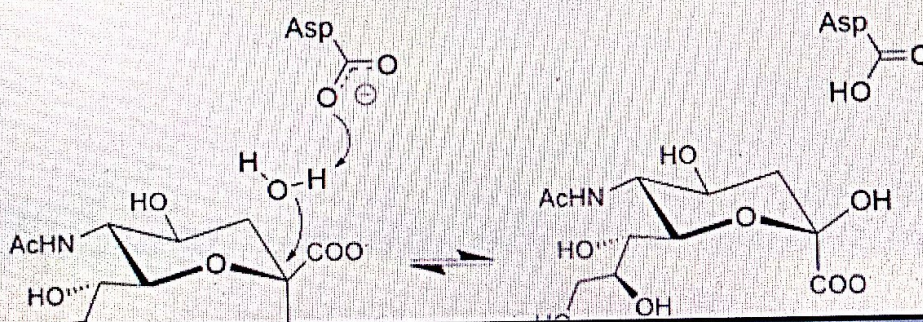
- ☐ Neuraminidase is required to cleave sialic acid from host cell proteins to allow influenza to enter the host cell.
- ☐ The removal of terminal sialic acid in influenza infection requires molecular recognition by the viral enzyme that can cleave a glycosidic bond.
- ☐ The intermediate hosts for influenza A infection are bats and rats.
- ☐ There are no intermediate hosts for influenza A infection.



Question 22

1 pts

In Post Lecture Quiz 6 you analysed the first steps of the sialic acid cleavage reaction catalysed by influenza neuraminidase. The final step is hydrolysis and the release of sialic acid as shown in the mechanism below:

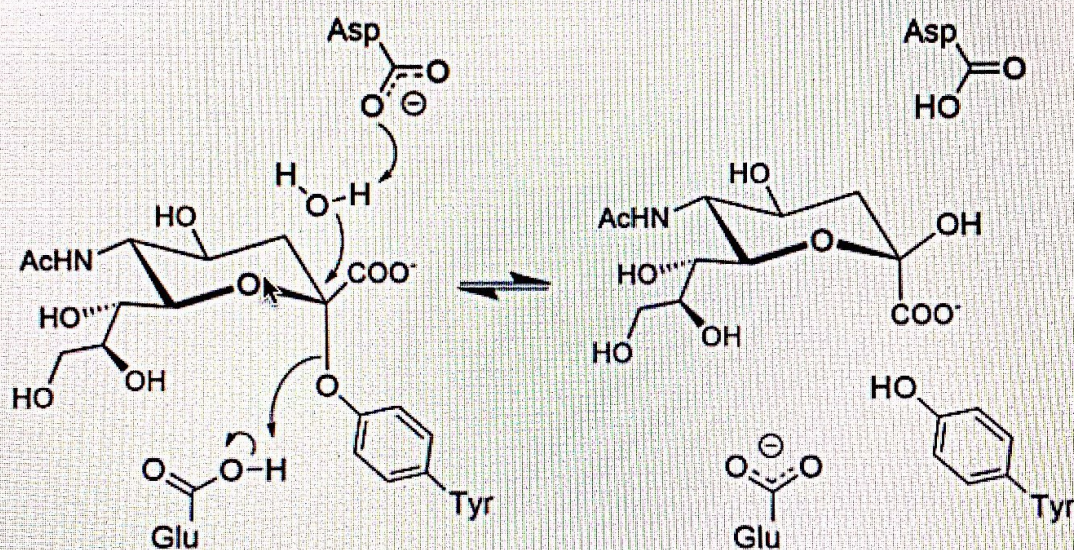




Question 22

1 pts

In Post Lecture Quiz 6 you analysed the first steps of the sialic acid cleavage reaction catalysed by influenza neuraminidase. The final step is hydrolysis and the release of sialic acid as shown in the mechanism below:



Which statement is **CORRECT**?

- ☐ The Glu side chain acts as a catalytic base.
- ☐ The Asp side chain acts as a catalytic acid.
- ☐ The water molecule attacks the sialic acid ring and breaks it open to give the linear form of the sugar.
- ☐ The water molecule can be considered a nucleophile that attacks sialic acid.

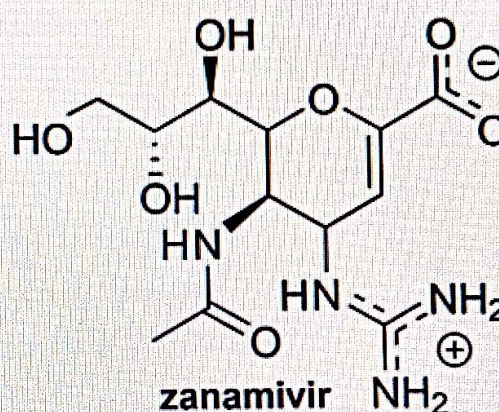
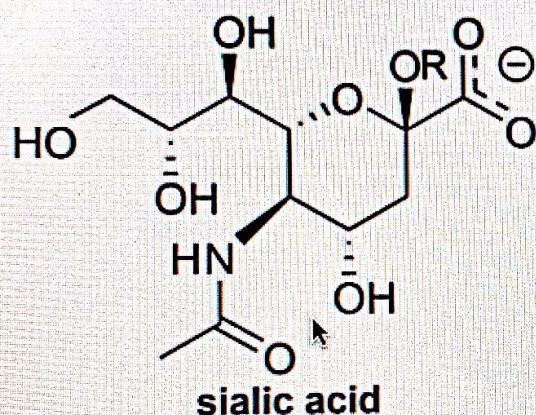


MacBook Air

Question 23

1 pts

The neuraminidase substrate sialic acid and the neuraminidase inhibitor zanamivir are shown below:



Which statement about zanamivir is **CORRECT**?

- ☐ Zanamivir will form a covalent bond with sialic acid to prevent hemagglutinin from binding to the host cell.
- ☐ Zanamivir binds weakly to neuraminidase and only acts as a drug at high concentrations.
- ☐ Zanamivir binds neuraminidase with greater affinity than sialic acid by forming a new charge-charge interaction.
- ☐ Zanamivir is unlikely to bind in the same site as sialic acid and is an allosteric inhibitor.



MacBook Air



Question 24

1 pts

A reversible binding interaction between a protein (P) and a ligand (L) to form a protein-ligand complex ($P \cdot L$), follows the equation $P + L \rightleftharpoons P \cdot L$. The affinity (i.e. "strength") of the protein/ligand interaction is conventionally described by:

- ☐ the rate constant for the dissociation reaction.
- ☐ the rate constant for the association reaction.
- ☐ the equilibrium binding constant for the dissociation reaction.
- ☐ the equilibrium binding constant for the association reaction.



Question 25

1 pts

For the interaction described in Question 24, when the concentration of ligand, $[L]$ is greater than the K_d , what is the fractional occupancy, f , of the protein?

- ☐ $f < 0.5$
- ☐ $f > 0.5$
- ☐ $f = 0.5$
- ☐ $f = 0.9$



MacBook Air



Question 26

1 pts

Enzymes enhance the rate of a chemical reaction converting substrate to product because:

- ☐ they recognise the product by non-specific hydrophobic interactions.
- ☐ they bind to the product more tightly than they bind to the transition state.
- ☐ they recognise the substrate by complementary binding interactions.
- ☐ they bind to the substrate more tightly than they bind to the product.



Question 27

1 pts

The active site of an enzyme is mutated such that it now binds to its substrate as tightly as it binds to the transition state of the reaction. How will this change the activity of the enzyme?

- ☐ It will decrease the enzyme's activity slightly, as it will now bind to the product more tightly.
- ☐ It will increase the enzyme's activity slightly, as it will now bind to the substrate more tightly.
- ☐ The enzyme's activity will greatly increase, as the change in $\Delta G^\ddagger$ for the catalysed reaction will now be larger.
- ☐ The enzyme will no longer increase the rate of the reaction, as the change in $\Delta G^\ddagger$ for the catalysed reaction will now be zero.



Question 28

1 pts





Question 28

1 pts

Which of the following statements is **INCORRECT**?

- ☐ Enzymes are always exquisitely specific to one reaction.
- ☐ Dietary vitamins are the source of many enzyme co-factors in humans.
- ☐ Nucleic acids can act as enzymes.
- ☐ Over 30% of enzymes need to bind to metal ions to function as catalysts.



Question 29

1 pts

Which of the following strategies to regulate enzyme activity is irreversible?

- ☐ Proteolytic activation e.g. pro-enzyme cleavage
- ☐ Changes in substrate concentration i.e. substrate-level control
- ☐ Non-covalent binding e.g. heterotropic allostery
- ☐ Covalent modification e.g. phosphorylation



Question 30

1 pts



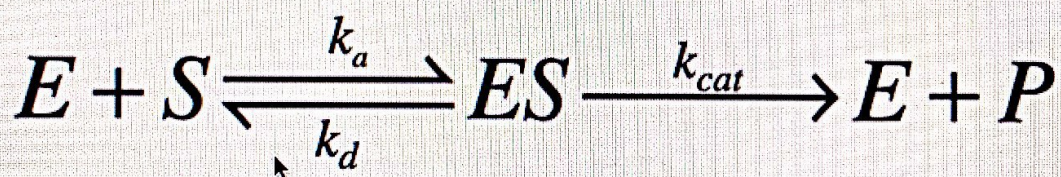
MacBook Air



Question 30

1 pts

In 1913, Leonor Michaelis and Maud Menten proposed a simple model of enzyme activity that considers the conversion of substrate, S, to product, P, by the enzyme, E, to be a two-step process as shown in the figure below:



For this model to be useful in predicting enzyme activity, several assumptions need to be made. Which of the following assumptions is made in the Michaelis-Menten model?

- ☐ The starting concentrations of enzyme and substrate must be roughly equal.
- ☐ The enzyme-substrate complex, ES, quickly builds up after the addition of substrate, and will continue to increase in concentration as the reaction proceeds.
- ☐ The enzyme-substrate complex, ES, quickly builds up after the addition of substrate, and then remains at a constant concentration.
- ☐ The rate of the dissociation of the substrate from the enzyme, k_d , limits the overall rate of catalysis.



Question 31

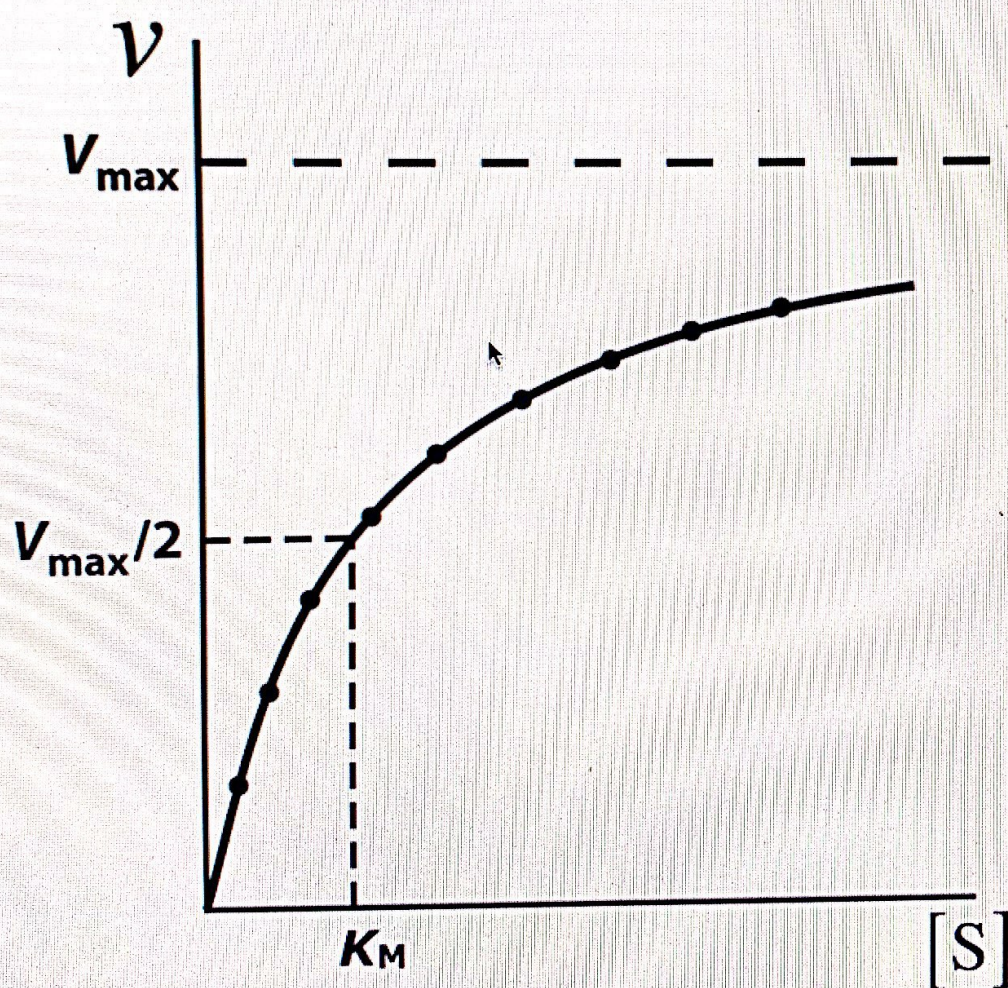
1 pts

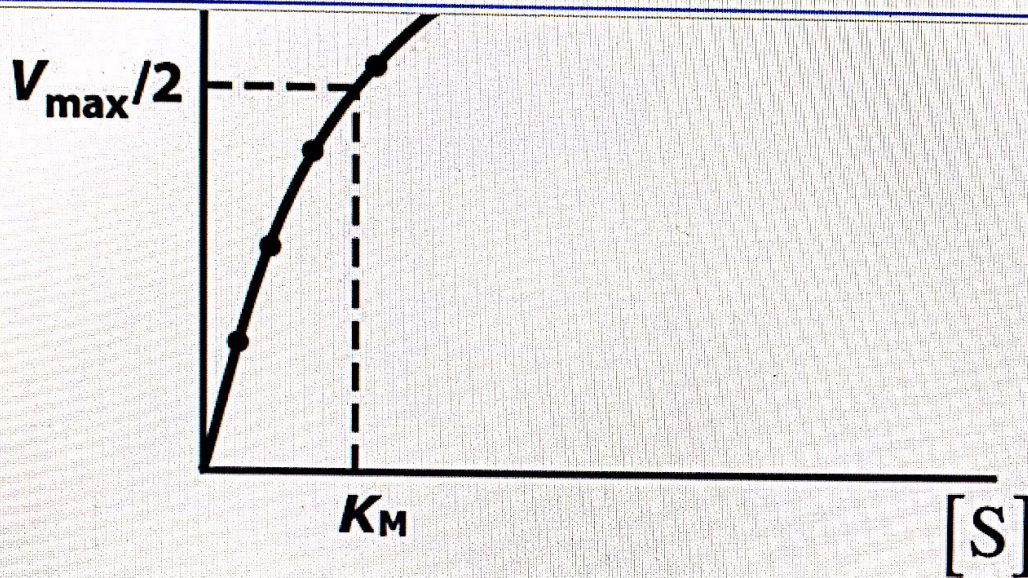


Question 31

1 pts

The following graph shows the dependence of the reaction rate, v , on the concentration of the substrate $[S]$, for an enzyme-catalysed reaction that obeys the Michaelis-Menten model.





Which of the following statements is **INCORRECT**?

- ☐ When the enzyme is saturated with substrate, the observed reaction rate is equal to k_{cat} multiplied by the total enzyme concentration.
- ☐ At high substrate concentrations, every molecule of enzyme is bound by substrate.
- ☐ At low substrate concentrations, the reaction rate is proportional to substrate concentration, whereas at high substrate concentrations, the reaction rate is independent of substrate concentration.
- ☐ $V_{\max}$ cannot be estimated from this graph, even with modern computational curve-fitting.

- ☐ $V_{\max}$ cannot be estimated from this graph, even with modern computational curve-fitting.



Question 32

1 pts

Which of the following statements is **INCORRECT**? The Michaelis constant (K_M):

- ☐ is always a good measure of the enzyme's affinity for its substrate.
- ☐ is expressed in units of concentration.
- ☐ is equivalent to the substrate concentration when the enzyme is functioning at half its rate when saturated with substrate.
- ☐ is a ratio of rate constants, and hence is characteristic of a specific enzyme-catalysed reaction.



Question 33

1 pts

The Michaelis-Menten equation can be rearranged in a number of ways to give a straight-line graph. One of these is the Lineweaver-Burk graph, shown below.

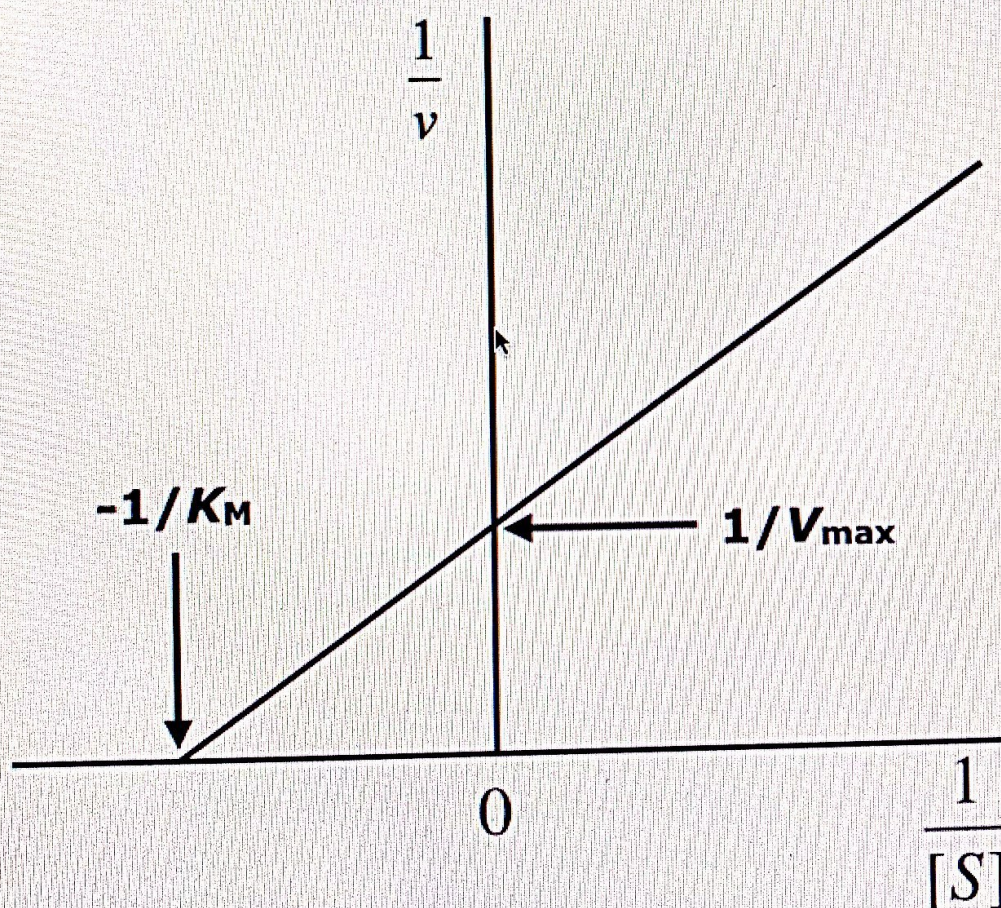
$$\frac{1}{v}$$



Question 33

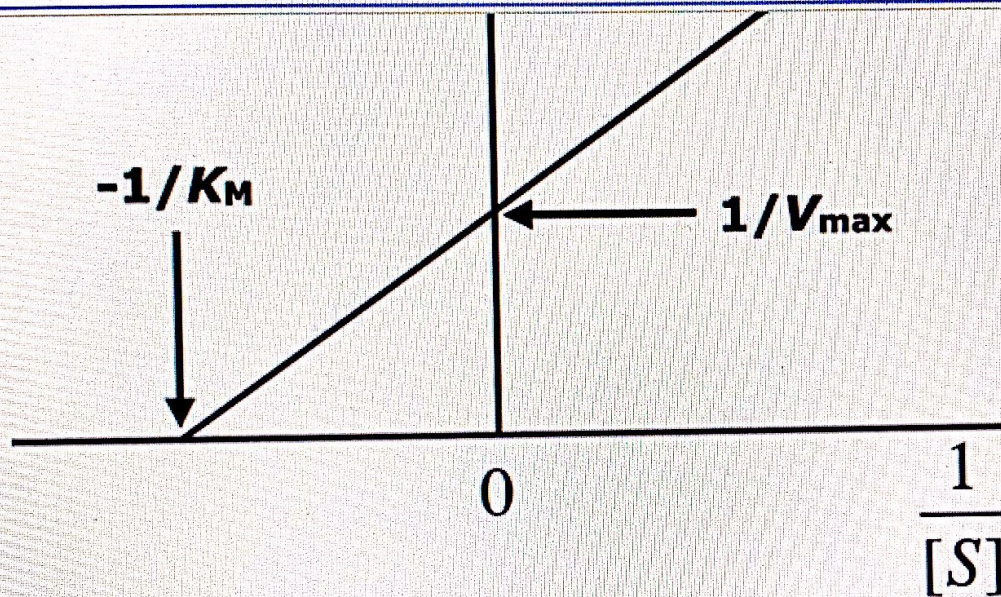
1 pts

The Michaelis-Menten equation can be rearranged in a number of ways to give a straight-line graph. One of these is the Lineweaver-Burk graph, shown below.



Which of the following statements is CORRECT?





Which of the following statements is **CORRECT**?

- ☐ The double-reciprocal nature of the Lineweaver-Burk graph makes it unaffected by experimental errors.
- ☐ The Lineweaver-Burk transformation can only be used to obtain K_M and $V_{\max}$ values using modern computational curve-fitting techniques.
- ☐ It is not possible to use Lineweaver-Burk graphs to distinguish between different types of reversible enzyme inhibitors.
- ☐ At the y-intercept of the Lineweaver-Burk graph, the substrate concentration is infinitely large.



Question 34

1 pts

Which of the following statements about reversible, non-competitive enzyme inhibitors is **CORRECT**?

- ☐ they only bind to free enzyme
- ☐ they appear to reduce K_M
- ☐ they appear to increase V_{max}
- ☐ they appear to reduce k_{cat}



Question 35

1 pts

Consider the following statement:

"Uncompetitive inhibitors have a greater effect at high $[S]$ than at low $[S]$."

- ☐ This is **CORRECT**, because they bind equally to the free enzyme, E, and to the enzyme-substrate complex, ES.
- ☐ This is **CORRECT**, because they only bind to the enzyme-substrate complex, ES.
- ☐ This is **INCORRECT**, because they bind to the free enzyme less with lower apparent affinity as $[S]$ increases.
- ☐ This is **INCORRECT**, because they bind in a different site on the enzyme to the substrate.





Question 36

1 pts

For Question 36 and 37, assume that the K_M of an enzyme for its substrate has been measured to be $25\mu\text{M}$.

In the presence of a **competitive** inhibitor, I , at a concentration equal to the K_i of the inhibitor (i.e. $[I] = K_i$), what will the K_M of the enzyme now appear to be when re-measured?

- ☐ $25\mu\text{M}$
- ☐ $50\mu\text{M}$
- ☐ $2.5\mu\text{M}$
- ☐ $12.5\mu\text{M}$



Question 37

1 pts

For Question 36 and 37, assume that the K_M of an enzyme for its substrate has been measured to be $25\mu\text{M}$.

In the presence of a **uncompetitive** inhibitor, I , at a concentration equal to the K_i of the inhibitor (i.e. $[I] = K_i$), what will the K_M of the enzyme now appear to be when re-measured?



Question 37

1 pts

For Question 36 and 37, assume that the K_M of an enzyme for its substrate has been measured to be $25\mu\text{M}$.

In the presence of a **uncompetitive** inhibitor, I , at a concentration equal to the K_i of the inhibitor (i.e. $[I] = K_i$), what will the K_M of the enzyme now appear to be when re-measured?

- ☐ $25\mu\text{M}$
- ☐ $50\mu\text{M}$
- ☐ $2.5\mu\text{M}$
- ☐ $12.5\mu\text{M}$



Question 38

1 pts

A Russian politician has been poisoned, allegedly by the Russian Government, using a compound that acts as a substrate-mimetic, suicide inhibitor of an essential enzyme. Doctors decide to treat the politician by injecting a large dose of the enzyme's substrate, in order to relieve the inhibition. Will this strategy work?

- ☐ Maybe. It will only work if the inhibitor is uncompetitive.
- ☐ Maybe. It will only work if the inhibitor is non-competitive.



Question 38

1 pts

A Russian politician has been poisoned, allegedly by the Russian Government, using a compound that acts as a substrate-mimetic, suicide inhibitor of an essential enzyme. Doctors decide to treat the politician by injecting a large dose of the enzyme's substrate, in order to relieve the inhibition. Will this strategy work?

- ☐ Maybe. It will only work if the inhibitor is uncompetitive.
- ☐ Maybe. It will only work if the inhibitor is non-competitive.
- ☐ Yes. The substrate will compete with the inhibitor for the active site of the enzyme.
- ☐ No. The inhibitor will be covalently bound to the active site.



Question 39

1 pts

The best way to compare the efficiency of an enzyme towards different potential substrates is by comparing:

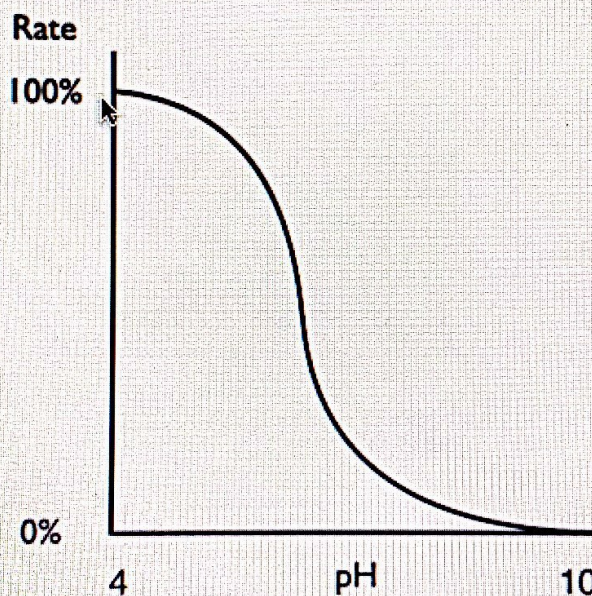
- ☐ $V_{\max}$ values for each substrate.
- ☐ K_M values for each substrate.
- ☐ K_d values for each substrate.
- ☐ k_{cat}/K_M values for each substrate.



Question 40

1 pts

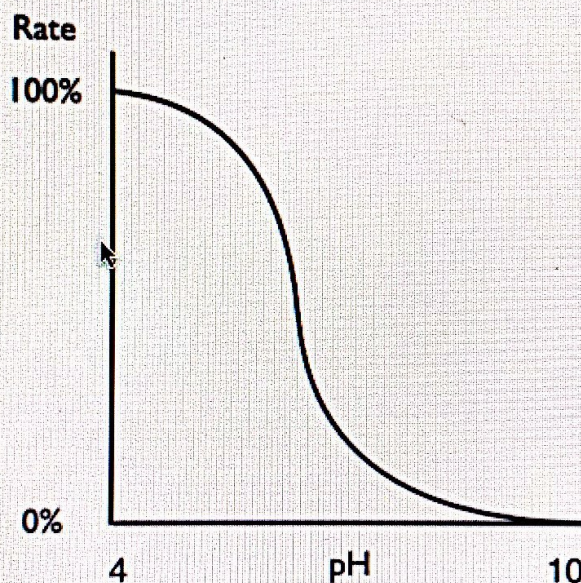
The activity of an enzyme as a function of pH is shown in the graph below.



Which of the following statements is **CORRECT**?

- ☐ The active site of this enzyme has a single ionisable amino acid side chain that is initiating catalysis by accepting a proton.
- ☐ The active site of this enzyme has a single ionisable amino acid side chain that is initiating catalysis by donating a proton.
- ☐ The active site of this enzyme has two ionisable amino acid side chains that sequentially accept and then donate a proton during the catalytic cycle.

The activity of an enzyme as a function of pH is shown in the graph below.



Which of the following statements is **CORRECT**?

- ☐ The active site of this enzyme has a single ionisable amino acid side chain that is initiating catalysis by accepting a proton.
- ☐ The active site of this enzyme has a single ionisable amino acid side chain that is initiating catalysis by donating a proton.
- ☐ The active site of this enzyme has two ionisable amino acid side chains that sequentially accept and then donate a proton during the catalytic cycle.
- ☐ The active site of this enzyme has two ionisable amino acid side chains that sequentially donate and then accept a proton during the catalytic cycle.



Question 41

1 pts

The advantage of homotropic allosteric regulation in the initial step of a metabolic pathway is that:

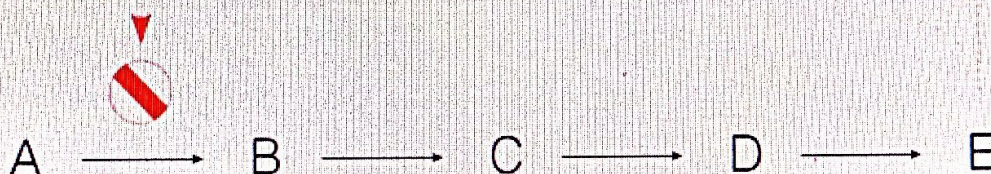
- ☐ the enzyme is less sensitive to changes in temperature.
- ☐ the enzyme can be effectively regulated by feedback inhibition by the end-product of the pathway.
- ☐ the enzyme transitions from a less active to a more active state over a narrow range of [S].
- ☐ the enzyme is less influenced by changes in the pH.



Question 42

1 pts

Consider the following biosynthetic pathway for questions 42 and 43, where compound A is converted to compound E by four enzyme-catalysed reaction steps. The red symbol indicates inhibition of the first reaction step (from compound A to compound B) by compound E.

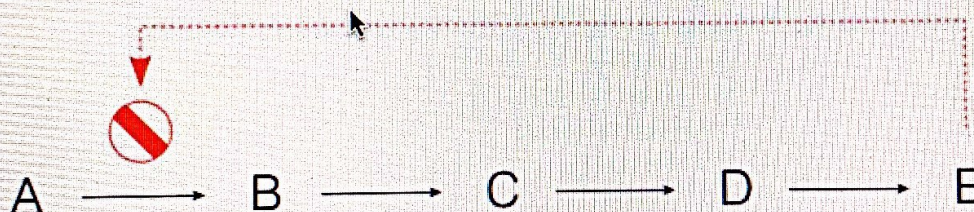




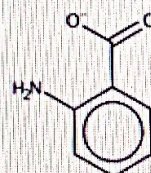
Question 42

1 pts

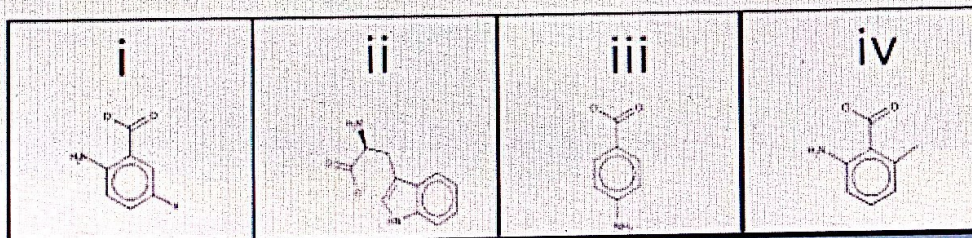
Consider the following biosynthetic pathway for questions 42 and 43, where compound A is converted to compound E by four enzyme-catalysed reaction steps. The red symbol indicates inhibition of the first reaction step (from compound A to compound B) by compound E.

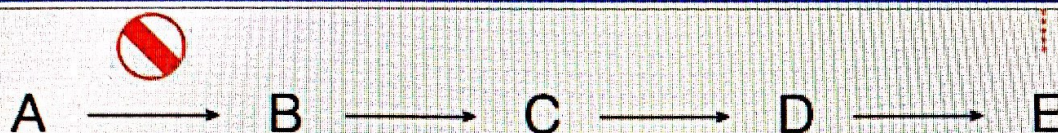


This is the structure of compound A:

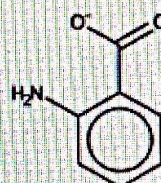


Which of the following compounds, labelled i -iv, is most likely to be compound E?

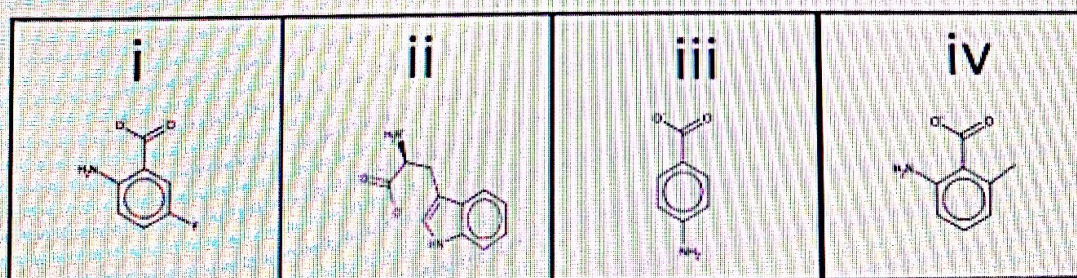




This is the structure of compound A:



Which of the following compounds, labelled i-iv, is most likely to be compound E?



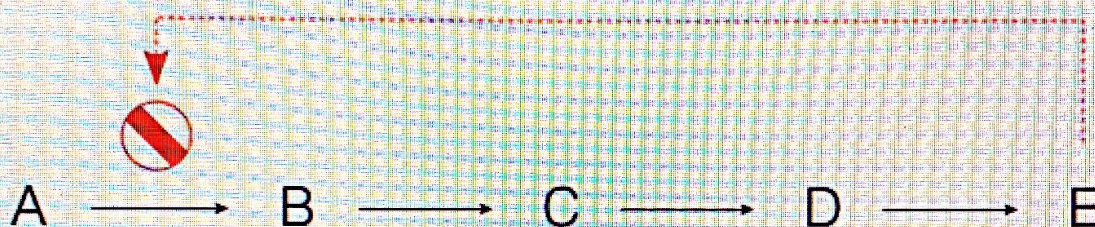
- ☐ i
☐ iii
☐ ii
☐ iv



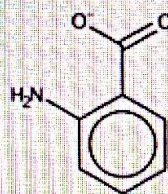
Question 43

1 pts

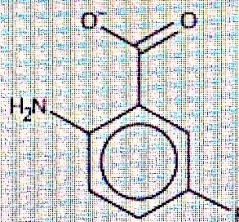
Consider the following biosynthetic pathway for questions 42 and 43, where compound A is converted to compound E by four enzyme-catalysed steps.



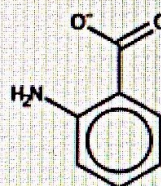
This is the structure of compound A:



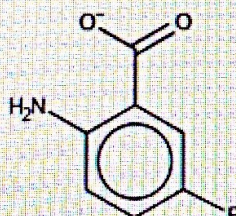
The compound below is an inhibitor of the enzyme that converts A to B:



This is the structure of compound A:



The compound below is an inhibitor of the enzyme that converts A to B:



What is its most likely mode of inhibition?

- ☒ A mixture of non-competitive and uncompetitive
- ☒ Uncompetitive
- ☐ Non-competitive
- ☐ Competitive



Question 44

1 pts

The standard reduction potential (ΔE°) for a redox reaction involving the transfer of two electrons is +0.82V. What is the standard free energy change (ΔG°) for this reaction? (You should assume that the Faraday constant is $100 \text{ kJ mol}^{-1}\text{V}^{-1}$, and that the reaction is taking place under standard conditions: pH 7 and 25°C .)

- ☐ +16.4 kJ mol^{-1}
- ☐ -82 kJ mol^{-1}
- ☐ -164 kJ mol^{-1}
- ☐ +164 kJ mol^{-1}



Question 45

1 pts

Which one of the following things does the coupling of ATP hydrolysis to chemical reactions NOT do?

- ☐ It changes the equilibrium ratio of reactions.
- ☐ It accelerates reactions towards equilibrium.
- ☐ It allows the energy acquired from catabolism to be transferred to anabolism.
- ☐ It allows unfavourable reactions to occur in the cell.