1. Two molecules will be attracted to one another by van der Waals interactions as long as ....

- ❏ **A**. they are composed of different types of atoms
- ❏ **B**. they are composed of the same type of atoms
- X **C**. they are further away from one another than their van der Waals radii
- ❏ **D**. they each contain bonds between atoms of different electronegativities.

if they get closer, they repel each other.
the forces involved arise from the structure common to all atoms (as opposed to ions).
a and b and c: are wrong because it does not matter whether the atoms (or molecules) are different or not.

2. If the electronegativities of H and O were equal what would happen to the boiling point of water?

- ❏ **A**. it would be unchanged
- ❏ **B**. it would increase
- X **C**. it would decrease

because in such a scenario, the molecules would interact ONLY through van der Waals interactions; the H-bonds normally present between water molecules would be absent, so that the attraction between the molecules would be weaker.
a: is wrong because the absence of H-bonds would lead to a change in intermolecular interactions, which would influence the boiling point.
b: is wrong because less energy would be required to disrupt the interactions between water molecules, which would lead to a liquid to vapor transition at a lower temperature.

3. You are given samples of two compounds with similar molecular weights. One compound (A332) is composed of atoms of very different electronegativities, while the other (G221) is composed of atoms with very similar electronegativities. You are asked to predict which compound is likely to be more soluble in water - you are most likely to be right if you say ....

- X **A**. A332
- ❏ **B**. G221
- ❏ **C**. they will be equally water soluble

because the differences in electronegativities would produce bonded atoms capable of making H-bonds with water, which is the major determinant of solubility.
b: is wrong because the inability to make of H-bonds with water would lead to thermodynamically unfavorable entropic effects if the molecule were placed in the aqueous phase.
c: is wrong because the two compound differ in their ability to make H-bonds, a primary determined of water solubility, they are not the same and so will not be equally water soluble.

4. Lipids are characterized primarily by the fact that …

- ❏ **A**. they have a highly elongated shape
- X **B**. they contain both hydrophilic and hydrophobic domains
- ❏ **C**. they are composed 5 to 10 repeating amphipathic units
- ❏ **D**. they are found only in living organisms

which result in one part being water soluble and another discrete region being in soluble.
a: is wrong because a elongated shape is not the defining feature of a lipid (even though many lipid molecules are elongated
c: is wrong because lipids are not composed of repeating units, and certainly not “amphipathic” ones.
d: is wrong because lipids can be synthesized and occur outside of organisms. Also, this would not distinguish them from many other “organic” molecules.

5. You are studying a cell in a solution of Na+ where the [Na^+] is higher on the outside than on the inside. You observe that glucose flows into the cell. You measure the glucose concentration and find that it is higher inside the cell than outside. What type of membrane molecule could be responsible for the observed movement of glucose.

X **A**. a glucose-Na+ symporter
❑ **B**. a glucose carrier
❑ **C**. a glucose-Na+ antiporter
❑ **D**. a glucose channel

because the movement of glucose is driven AGAINST its concentration gradient by coupling to the movement of Na+ down its concentration gradient, and both Na+ and glucose are moving the same direction (i.e. into the cell, in this case).

b and d: are wrong because a glucose carrier or channel would lead to movement of glucose out of the cell (down its concentration gradient).

c: is wrong because we know glucose is moving into the cell. An antiporter would there require that Na+ move out of the cell. But both movement are against their respective concentration gradients, and so could not occur.

6. How does a catalyst work?

❑ **A.** by increasing temperature
❑ **B**. by decreasing the free energy of the products
X **C**. by decreasing the free energy of the reaction intermediate
❑ **D.** by increasing the free energy of the products ❑ **no idea**

since it is this step that determines the reaction rate.

a: is wrong because catalysts do not influence (directly) the temperature of the system, although if a thermodynamically favorable reaction occurs, energy (heat) can be released and temperature might increase.

b and d: are wrong because by definition a catalyst is not a part of the reaction, and does not contribute to or alter the free energy of reactants or products.

7. Increasing the temperature often increases the rate of a favorable reaction because ....

❑ **A**. the activation energy of the rate limiting step of the reaction is decreased
X **B**. more collisions transfer enough energy to make the rate limiting step likely
❑ **C**. the nature of the rate limiting step of the reaction is altered
❑ **D.** the free energy of the reactants is reduced, while the free energy of the products increases

Increasing temperature increases average and maximum kinetic energy of the molecules within the system, so there are more collisions that deliver enough energy to overcome the higher energy of the rate limiting step of the reaction.

a: is wrong because temperature does not effects activation energy of any step of the reaction.

c: is wrong because temperature does not alter the reaction per se.

d: is wrong because the effects of temperature on rate are not due to changes in free energy, that said the thermodynamic favorability of a reaction can be influenced by temperature (since $\Delta G = \Delta H - \Delta DS$)

8. A channel in a membrane is like a catalyst because it …

- ❏ **A**. alters lipid structure
- ❏ **B**. changes water structure
- ❏ **C**. increases the speed at which molecules collide with the membrane
- X **D.** decreases the free energy needed to pass though the membrane

because if provide an "open" hydrophilic (although constrained) path the membrane
a: is wrong because channels sit in the membrane, but do not alter the structure of the lipid molecules.
b: is wrong because the channel does not alter water structure
c: is wrong because that would mean temperature increases, which channels do not (cannot) do.

9. Plants are eukaryotes, and have within their cells endosymbiotically derived organelles. Based on this observation, we might well assume that the cell walls of plants and bacteria are

- ❏ **A**. homologous structures
- X **B**. analogous structures
- ❏ **C**. unrelated in terms of origin or function.

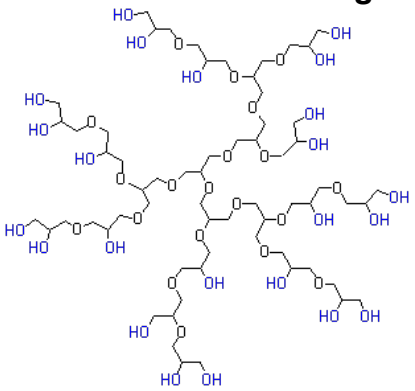
because to engulf the endosymbiont, the ancestral eukaryote lacked a cell wall.
a: is wrong because that would mean the ancestral eukaryote had a cell wall.
c: is wrong because the walls have similar functions

10. You find a species of plant without mitochondria, this could be possible if…

- ❏ **A**. its chloroplasts had retained all of their original respiratory functions
- ❏ **B**.its mitochondria never gained any non-respiratory functions
- X **C**. both A and B would **<u>have</u>** to be true
- ❏ **D**. the ancestor of plants did not have mitochondria

because our understanding is that all eukaryotes first acquired mitochondria, and later plants acquired chloroplasts. The mitochondria are specialized for respiratory function, the chloroplasts for photosynthesis.
a: is certainly true, assuming that b is also true. If either were not true, is has be the case.
d: is wrong because the ancestors of plants did not mitochondria, they are derived from the ancestral eukaryote after it acquired mitochondria.

11. Consider this strange compound. Based on its structure you might expect that it…



X **A**. dissolves in water
❑ **B**. forms micelles in water
❑ **C**. is insoluble in water
❑ **D**. would sit at the hydrophilic-hydrophobic interface of the membrane

because it can make and receive lots of H-bonds, a structure feature common to water soluble molecules.
b: is wrong because to make a micelle a molecule must have both hydrophilic and hydrophobic regions. This molecule is all hydrophilic.
c and d: are wrong because it can make H-bonds, and should be highly water soluble; there is no reason it would be localized to the hydrophilic-hydrophobic boundary of a membrane.

12. Assume that all of the Os in the molecule are replaced by Cs, then you would expect that the molecule would

❑ **A**. dissolve in water
❑ **B**. form micelles in water
X **C**. be insoluble in water
❑ **D**. would sit at the hydrophilic-hydrophobic interface of the membrane

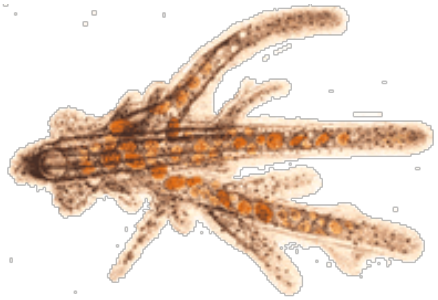
because it could not form H-bonds with water molecules.
a: is wrong because without H-bonding ability, it would be insoluble in water (due to entropic factors).
b: is wrong because to make a micelle a molecule must have both hydrophilic and hydrophobic regions. This molecule is all hydrophobic.
d: is wrong because there is no reason it would be localized to the hydrophilic-hydrophobic boundary of a membrane - it is not itself amphipathic.

13. Why are the oxidation of NADH, or other such molecules, and the hydrolysis of ATP similar?

❑ **A**. both are energetically unfavorable
X **B**. both can be used to drive thermodynamically unfavorable reactions
❑ **C**. both normally occur outside cell
❑ **D**. both occur only in the presence of light

Because they are both energetically favorable reactions, they can be coupled to, and use to drive energetically unfavorable reactions.
a: is wrong because both are energetically favorable
c: is wrong because both occur within cells (not outside of them).
d: is wrong because both can (and do) occur in the dark.

14. Consider an animal cell (like an amoeba) living in a fresh water pond. The amoeba engulfs some bacteria; these bacteria make and secrete a toxin that acts as an efficient H + ion channel and is able to enter all cellular membranes. The bacteria is immune to



the toxin because they also makes a specific inhibitor that blocks the ion channel's action within the bacteria. What happens to the amoeba ?

- ❏ **A**. Nothing
- ❏ **B**. its rate of ATP synthesis increases
- X **C**. water is no longer pumped out, so the cell swells and dies.

water pumping requires energy, which involves the synthesis of ATP, and then the coupling of the ATP hydrolysis reaction to the reaction that pumps out water. ATP synthesis, within the amoeba's mitochondria, depends upon H+ ion gradients, which are disrupted by the bacterial toxin, leading to decrease in ATP, decrease in pumping, net influx of water, bursting of amoeba.

a and b: are wrong because most ATP synthesis involves mitochondrial H+ gradients, and collapsing those gradients would decrease, not increase the ATP synthesis rate

15 . Consider the reactions (relax, read slowly, and take your time)

A + B + 3C ⇔ 2D + G (reaction 1)
G + H ⇔ N (reaction 2)
D ⇔ 2F (reaction 3)

Reactions 1 and 2 reach equilibrium very fast (in milliseconds), but are energetically highly unfavorable.

Reaction 3 does not occur to any significant extent, even though it is energetically very favorable (its equilibrium constant is 1000000).

You mix A + B + C + H and wait 10 minutes; then you add a catalyst that enables reaction 3 to reach equilibrium in 10 seconds. When you compare the concentration of H in the system before and after you added the catalyst, you will find that it has…

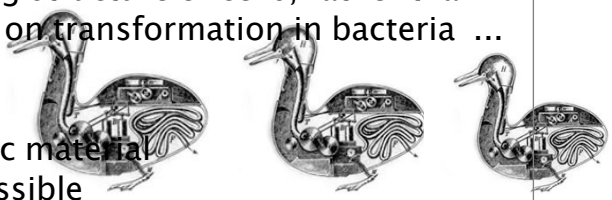
- ❏ **A**. increased
- X **B**. decreased
- ❏ **C**. remains unaltered

Allowing reaction 3 to proceed (by the addition of the catalyst, leads to the reaction (decrease) in [D]. This reduction in [D] will influence reaction 1, driving it to the right, leading to an increase in the [G]. Since G is component in reaction it, the increase in [G] will drive reaction 2 to the right (remember reactions 1 and 2 are at equilibrium). As reaction 2 occurs, **[H] will decrease.**

a: is wrong because (see logic above).

d: is wrong because the reactions are coupled.

1. If genetic information were encoded in the living structure of cells, rather than in the sequence of DNA molecules, Griffith's studies on transformation in bacteria ...



- ❏ would not have been effected
- X would not have worked
- ❏ would have identified proteins as the genetic material
- ❏ would have proved that evolution was impossible

a: is wrong because killing the bacteria would destroy the structure of the cell, so there would have been no information to transfer to the R cells.
c: is wrong proteins are not the "living structure of cells".
d: is wrong hereditable information could still be present in the living cell, and so this experiment would have no implications for evolution

2. A mutation occurs that leads to higher rates of mutation in actively dividing cells, but has no obvious effect in non-dividing cells. You would be justified in assuming that the mutation …

- ❏ inactivated the DNA-dependent DNA polymerase
- X inactivated the proof-reading activity associated with DNA polymerase
- ❏ inactivated DNA-dependent, RNA polymerase
- ❏ inactivated DNA repair enzymes

since division requires DNA replication, the higher rate of mutation must influence some part of the replication machinery.
a: is wrong because this would block DNA replication completely, no DNA replication, no division.
c: is wrong because it would block transcription but without obvious effects on mutation rates.
d: is wrong because it would effects dividing and non-dividing cells, increasing the mutation rate in both.

3. Non-sense suppressor mutations …

- X alter a tRNA's anti-codon
- ❏ alters the rate that DNA-dependent, RNA polymerase synthesizes RNA
- ❏ alter the ability of a ribosome to recognize an messenger RNA
- ❏ alters the specificity of an aminoacyl-tRNA synthetase

since the mutation is in a gene encoding a tRNA,
b: is wrong because the mutation would not alter RNA synthesis
c: is wrong because the ribosome would still recognize the mRNA; only if the non-sense suppressor mutation alter the anticodon of a methionine tRNA (which recognizes a translation start codon) and only if a single methionine tRNA gene were present in the cell would there be effects on ribosome-mRNA interaction.
d: is wrong because the synthetase does not "read" the anti-codon.

4. To say that a protein has a short half-life means….

❏ it is rarely synthesized
❏ it is inactive except in the presence of an allosteric effector
❏ it is short
X it is rapidly degraded ❏ no idea

half-life is a measure of stability, which is determined by degradation rate
a: is wrong because how often a protein is synthesized does not determine how rapidly it is degraded.
b: is wrong because allosteric factors typically regulate activity, not stability (although an allosteric factor could influence a protein's half-life.
c: is wrong because the length of a protein tells us nothing about its stability.

5. A mutation occurs in the region of a gene that is recognized by a negatively-acting transcription factor; such a mutation would most likely ….

❏ increase the rate of transcription in all genes
❏ decrease the rate of transcription of the mutant gene
❏ decrease the rate of translation of the mutant mRNA
X increase the rate of transcription in the mutant gene ❏ no idea

since this is a mutation in a region of a gene's regulatory region that normally binds a negatively acting transcription, it is likely to lead to the failure of that factor to bind, so the gene's transcription rate will increase.
a: is wrong because the mutation's effect would (most likely) be restricted to the mutated gene.
b: is wrong because the mutated region binds a negatively acting transcription factor
c: is wrong because the mutation would be unlikely to influence translation

6. You have two genes, *aya* and *bub*. Both encode cytoplasmic polypeptides (AYA and BUB). The rates of transcription and translation are similar. The BUB polypeptide is 10 times longer than the AYA polypeptide. PREDICT the overall rate of AYA synthesis (# of polypeptides made per minute) compared to the BUB synthesis.

❏ both rates are similar
❏ AYA synthesis is 10 time faster than BUB synthesis
X AYA synthesis is more than 10 time faster than BUB synthesis
❏ the BUB synthesis rate is faster than that for AYA

the question asks for the effect on # of polypeptide made per minute. which is a function of both the time required for transcription (a function of transcript length) AND the time required for translation (again a function of mRNA length).
a: is wrong because it takes ~10X longer to make the BUB mRNA and ~10X longer translate it. Both rates are involved in the total polypeptide synthesis rate within a cell
b: this would be the case if only translation were considered
d: this cannot be true, since it BUB is longer than AYA, and so takes longer to synthesize

7. A mutation occurs in the region of a polypeptide that, in the normal case, is buried within the molecule's interior. The mutation replaces a hydrophobic amino acid with a positively charged amino acid. You would be justified in predicting that such a mutation would …

❏ alter the polypeptide's location within the cell
❏ have little effect on the polypeptide's three dimensional structure
❏ function normally since it only effects the polypeptide's primary structure
X produce a dramatic change in protein folding and activity

such a change, from hydrophobic to highly hydrophilic, would be likely to dramatically disrupt the polypeptide's tertiary structure (which would influence it interactions with other polypeptides, if it were part of a multiple subunit protein, and its function).

a: is wrong because there is no reason to believe that the change would a "targeting" sequence

b: is wrong because such a dramatic change would be likely to influence 3D structure

d: is wrong because primary structure (sequence) determines 3D structure and function

8. Mutations can occur throughout the sequence of gene. Consider a non-sense mutation that occurs at codon 42 of a 544 amino acid long polypeptide, and consider a similar mutation that occurs at codon 536 of a the same polypeptide. You would be justified in predicting that …

❏ both mutations would have similar effects on polypeptide function
X the mutation at codon 42 would have a more severe effect
❏ the mutation at codon 536 would have a more severe effect
❏ more information is required to answer this question

Given that the normal polypeptide is 544 amino acids long, a non-sense mutation at codon 42 would lead to a 41 amino acid long polypeptide, must of the polypeptide would be missing. It is very unlikely that this polypeptide would retain any biological function.

a: is wrong because the two mutations have dramatically different effects on polypeptide length, and so likely polypeptide function.

c: is wrong because it would produce a 535 amino acid long polypeptide, only 9 amino acids shorter than the wild type protein. This slightly shorter protein could retain some function.

d: is wrong because there is enough information to make an educated guess.

9. Assume an organism used single-stranded DNA (rather than double stranded DNA) as its genetic material. If you knew the percentage of A in the DNA of that organism, you would know

- ❏ the percentage of T
- ❏ the percentage of G
- ❏ the percentage of C
- ❏ the percentage of C + G
- X nothing else (or rather the percentage of T + C + G)

Since the DNA is single stranded, there are no constraints on nucleotide composition.
a, b, c, and d are wrong because there no constraints on nucleotide composition

10. Assume that mutations in a single gene, encoding a polypeptide, are responsible for the change from the disease causing (virulent) S strain of Streptococcus to avirulent R strains. Based on this information you would predict that ….

- X the rate of S to R mutation are more frequent than R to S mutations
- ❏ the rate of R to S mutation are more frequent than S to R mutation
- ❏ R to S and S to R mutations occurs with equal frequency
- ❏ only nonsense mutations at the start of the gene's coding region can explain the S to R phenotype

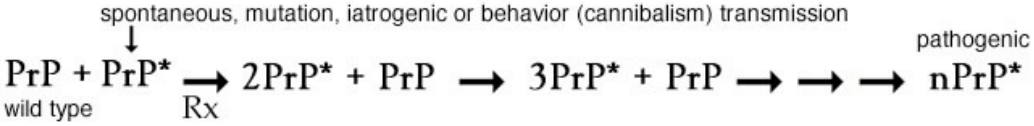
there are many ways to mutate a gene to produce a change a polypeptide that makes it non-functional. Once non-functional, however, there are many fewer ways to reverse the effect. The probably of mutating from functional to non-functional is higher than mutations that have the opposite effect
b: R to S involves a much smaller subset of possible mutation that does S to R
c: is wrong because the two events are distinct differ in terms of functional effects.
d: is wrong because non-sense mutations are not necessarily involved in either process

11. Through the studies of Avery et al, it became clear the molecules that carried genetic information in cells were nuclease sensitive. Knowing what we now know about prion disease, which type of enzyme would be most likely to destroy the "infectious" activity of a disease sample?

- X protease
- ❏ nuclease
- ❏ lipase
- ❏ reverse transcriptase

because the infectious agent appears to be a misfolded protein.
b: is wrong because nucleic acids do not appear to be involved in prion disease transmission
c: is wrong because lipids do not appear to be involved
d: is wrong because making a DNA based on an RNA does not appear to be involved in prion disease

12. In prion disease wild type PrP is converted into the



pathogenic PrP* form. This reaction can be influenced by mutation; alternatively the formation of PrP* can be initiated by surgical or behavioral "infection". Once present PrP* drives the transformation of PrP into PrP* (Rx). In the case of cannibalism-based disease vast majority of the PrP* found in the sick person differs from PrP...

- ❏ in its primary structure
- X in its secondary and tertiary structure
- ❏ in the sequence of the gene that encodes PrP

Since this is cannibalism-based transmission, the victim (the cannibal) has the wild type protein, and the prion induces the misfolding of this normally normal prion.
a: is wrong because the host's protein's primary sequence is not altered
c: is wrong because the host's gene is not mutated