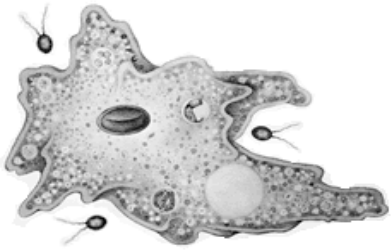
MCDB 1150-3:Biofundamentals 2015 Midterm 3 Name:_____

Directions: There are 20 questions, each worth 5 points. Remember, you can check "no idea" and you will receive 1 point (no reasoning is required), but if you do, we not grade any part of the question.



Q1: Which is correct? the binding of a transcription factor to DNA …

□ A. has no effect on the direction of transcription
□ B. determines exactly where translation begins
□ C. determines where in the cell the encoded polypeptide will end up □ no idea
➜ D. determines which strand will be used to generate an RNA
□ E. determines when and where RNA primers are synthesized

Explain what will happen to the transcript (RNA) made if you were able to remove, rotated 180º, and reinsert back into to DNA the transcription factor's binding site (a diagram could be useful).

You'd get transcription the opposite direction

Q2: Consider a cell. Which of the following processes are absolutely required to produce a functional transcription factor?

□ A. DNA replication □ no idea
□ B. transcription
□ C. translation
➜ D. both transcription and translation

Explain the logic of your answer.

TFs are proteins. Proteins need to be translated from mRNAs that in turn must be transcribed from DNA

Q3: A protein has a short half-life, meaning that ….

□ A. it is rapidly synthesized □ no idea
□ B. it is rarely synthesized
□ C. the mRNA that directs its synthesis is unstable
➜ D. it is rapidly degraded after it has been synthesized

Explain the logic of your answer.

Half-life isn't about synthesis, it's about degradation. The half-life of the mRNA does not influence the half-life of the protein.

Q4: You are asked to genetically engineer an organism so that it now incorporates a new type of amino acid (not one of the normally used set of amino acids). Which molecule or molecular complex would you NOT need to change?

□ A. one of the genes encoding a tRNA □ no idea
➜ B. the genes that encode the ribosome
□ C. the gene that encodes the enzyme that adds the new amino acid to the tRNA
□ D. the genes encoding the enzymes involved in synthesizing the new amino acid (assuming that it is not normally made by the organism) **Explain** the logic of your answer.

The ribosome doesn't have to change to use the new tRNA; the other do.

Q5: We discussed a type of mutation that allows a stop codon to be read as an amino acid. Such a mutation would occur in a gene that encodes a …

□ A. ribosomal RNA □ no idea
□ B. messenger RNA
➜ C. transfer RNA
□ D. a gene's regulatory region
Explain the logic of your answer (and why the other choices are wrong).

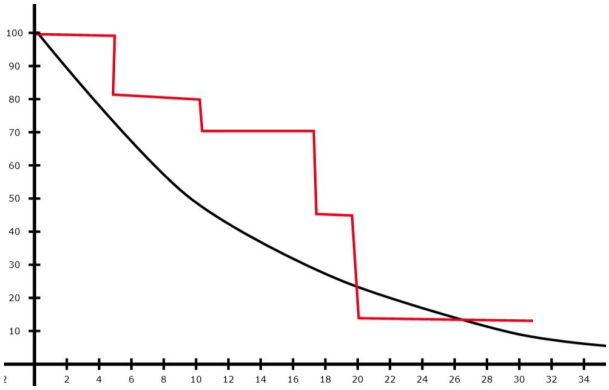
tRNA: A mutation has to occur that changes the tRNA's anticodon region so that it can a stop codon and bring into the ribosome an amino for addition to the end of the growing polypeptide change. Of course that mutant tRNA will not recognize the codon it originally recognized.

Q6: The time between the synthesis and degradation of particular RNA or protein is noisy (stochastic), like radioactive decay, because …

➜ A.it depends upon random collisions between molecules □ no idea
□ B. it is determined by the molecule's structure
□ C. it is based on radioactive decay
□ D. it can be regulated by other factors **Explain** the logic of your answer.

The random (and effective) collisions with a ribonuclease are the cause of the degradation of RNA.

Q7: You are studying a particular polypeptide; it has a half-life of 10 minutes. The cell contains 300,000 copies of this polypeptide.
At time 0 the synthesis of polypeptide stops completely.
Using a solid line draw a graph that represents the amount of polypeptide that remains as a function of time.



How will your graph will change if there are only 10 copies of this polypeptide in the cell □ no idea
How might a cell could benefit from making a protein with a short half life?

It would be able to respond quickly by changing conditions, one type of protein can be removed (quickly) replaced by another.

Q8: You isolate total <u>tRNA</u> from a cell and analyze its base composition (i.e. the ratio of the various nucleotides). This ratio will be …

□ A. A = U □ no idea
□ B. A = G
□ C. the same as the bulk composition of the cell's DNA (but with Us instead of Ts)
➜ D. impossible to know based on the information supplied
Explain the logic of your answer.

tRNA is single stranded. You don't have the 1:1 ratio of A:T and G:C that you have in dsDNA. There is therefore no basis for making conclusions about the base composition of a tRNA (or that it will reflect composition as the organism as a whole, since only a small region is transcribed to form a tRNA.

Q9: A mis-sense mutation can alter a polypeptide's 3D folding because ...

➜ A. a different amino acid is inserted at the site of the mutation □ no idea
□ B. the polypeptide's synthesis stops prematurely
□ C. any change at any position of a polypeptide will lead to misfolding
□ D. it will alter the rate at which mRNA is synthesized
Explain the logic of your answer.

Missense mutations change the codon which changes the amino acid inserted in a particular position along the polypeptide chain.

Q10: For an organism to be able to survive a mutation that creates a non-sense suppressor, which <u>must</u> be true?

□ A. the mutated gene must be relatively unimportant □ no idea
□ B. the original mutation (the mutation that is suppressed) must be in a non-coding region
➜ C. there must be multiple genes encoding specific tRNAs
□ D. the mutation must alter the region of the tRNA that determines which amino acid is attached to the tRNA **Explain** the logic of your answer.

A non-sense suppressor (NSS) mutation involves changes in a tRNA gene (and the tRNA transcribed from it). If there were only one gene for a particular tRNA, then a NSS mutation both create an anti-codon able to read a stop codon and remove the anti-codon needed to read normal (wild type) polypeptides. This would be lethal. To generate a NSS mutation, there must be at least two distinct genes that recognize a particular codon.

Q11: A non-sense mutation will <u>always</u> …

□ A. lead to the production of a longer polypeptide □ no idea
➜ B. lead to the production of a shorter polypeptide
□ C. lead to the production of a dysfunctional polypeptide
□ D. generally have no effect on polypeptide function
Explain how the position of a non-sense mutation would be likely to influence polypeptide activity.

The closer to the beginning, the shorted the translated polypeptide. The larger the truncation the larger the chance of an influence on activity.

Q12: You are studying the XUP gene of the speckled trout (a eukaryote). The XUP gene encodes a negatively acting transcription factor. You identify a mutation in the XUP gene and you find that the mutant Xup protein is secreted from the cell. Which is the most likely effect on the expression of genes whose transcription is directly regulated by the Xup protein?

□ A. no effect, since it normally acts negatively □ no idea

➜ B. their expression would increase

□ C. their expression would decrease

□ D. the expression of all genes would increase

Explain the logic of your answer.

XUP encodes a repressor. The mutant secretes XUP out of the cell so it can no longer play its repressive role inside the cell. Breaking a (negatively acting) repressor ➜ more gene expression.

Q13: A polypeptide passes through a membrane once, and only once. Which is the most likely to be the case for the region of the polypeptide that that passes through the membrane? In will form …

□ A. an unstructured polypeptide with both hydrophobic and hydrophilic R-groups □ no idea

□ B. a β-sheet like structure with hydrophilic R-groups

➜ C. an α-helix with hydrophobic R groups

□ D. it is impossible to make a plausible model based on the information given

Explain the logic of your answer.

The α-helix will engage the H-bond donor and receptor groups of the polypeptide backbone, while the hydrophobic R groups will be surrounded by the hydrophobic (lipid tail) region of the membrane.

Q14: Draw and label: How could a membrane channel protein be generated using a single polypeptide? □ no idea

Hydrophobic residues where it interacts with the hydrophobic region of the membrane, hydrophilic residues lining the central channel, where the water soluble molecule can pass through. We imagine that the polypeptide passes through the membrane in an α-helical configuration, with four or passages (but it could be otherwise, as long as it makes sense).

Q15: If you were trying to devise a simple system that could recognize unfolded (denatured) proteins in the cytoplasm of a cell, you might look for …

□ A. acidic amino acid residues within the interior of the molecule □ no idea

□ B. non-peptide bonds on the surface

□ C. a net positive surface charge

➜ D. multiple hydrophobic R groups on the surface

Explain the logic of your answer and describe what is likely to happen if the unfolded protein is not refolded correctly.

A well folded cytoplasmic protein will have most of its hydrophobic R groups in the interior of the structure. There presence on the protein's surface is a sign that it is unfolded (incorrectly folded).

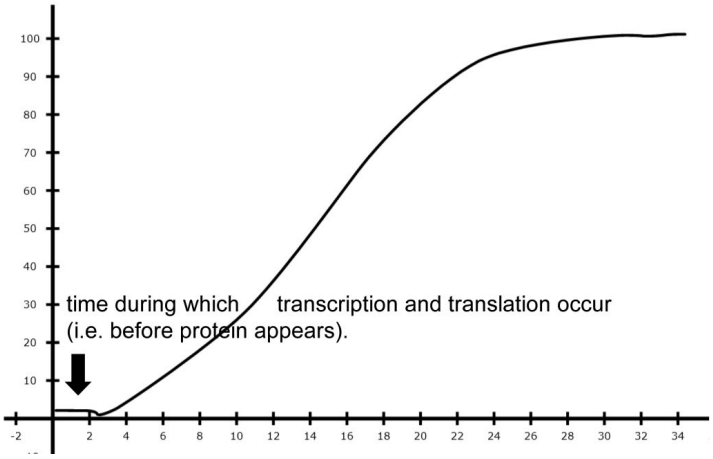
Q16: A protein kinase phosphorylates a normally cytoplasmic protein; the phosphorylated form of the protein is found in the nucleus. Which of the following most likely explains the observation?

□ A. phosphorylation inactivates a nuclear localization sequence □ no idea
□ B. phosphorylation activates a signal sequence
➜ C. phosphorylation activates a nuclear localization sequence
□ D. phosphorylation activates a nuclear export sequence

Explain the logic of your answer.

After phosphorylation, the protein will be localized to the nucleus

Q17: In a bacterium the expression of the CHL gene is regulated by the transcription factor ZIP. Expression of the ZIP gene depends on another transcription factor, ZNG.



The ZNG gene is always expressed, but the ZNG protein is active only when the allosteric effector molecule ZOUP is present.

At time = 0 we add enough ZOUP to the culture to activate all of the ZNG protein present. Draw a graph of the accumulation of the CHL polypeptide as a function of time after the addition of ZOUP. □ no idea

Describe the assumptions you made in drawing your graph.

CHL regulated by ZIP, ZIP regulated by ZNG, ZNG always on but only active after addition ZOUP

Lag: new ZIP and CHL have to be transcribed and translated which takes time. CHL will not appear instantaneously after the addition of ZOUP

Decay: The proteins all have a half-life and will degrade. Eventually the system will turn back off again… (assuming that ZOUP disappears).

Q18: Some genes are transcribed but not translated; pick the type of RNA that is both transcribed and translated.

➜ A. mRNAs □ no idea
□ B. rRNAs
□ C. tRNAs
□ D. depends on the gene

Explain the logic of your answer (include why are the wrong choices wrong).

rRNA and tRNA are functional RNA molecules, they are not translated (although used in the process of translation). mRNAs encode proteins, they must be transcribed (synthesized) and translated.

Q19: How is regulation by an allosteric effector different from regulation by proteolytic cleavage? Allosteric regulation is …

□ A. irreversible

➜ B. reversible

□ C. always positive

□ D. always negative

□ no idea

Explain the logic of your answer.

Proteolytic cleavage is irreversible, the binding of an allosteric regulator is not.

Q20: A mutation occurs that replaces an mRNA's normal start codon with a stop codon. Draw and explain what can happen ….

If there is another start codon downstream the protein will start translation there. If there is not (something very unlikely since ATGs occur frequently), then no protein will get made.

Translation form a downstream ATG is likely (2 out of 3 times) to be out of frame with respect to the original coding frame. Polypeptide synthesized likely to be gibberish (biologically).