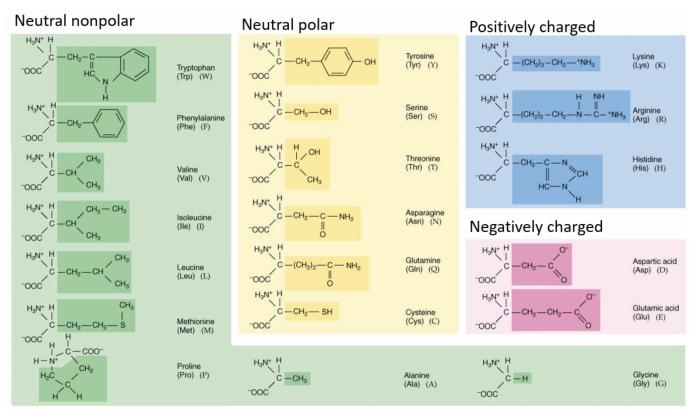
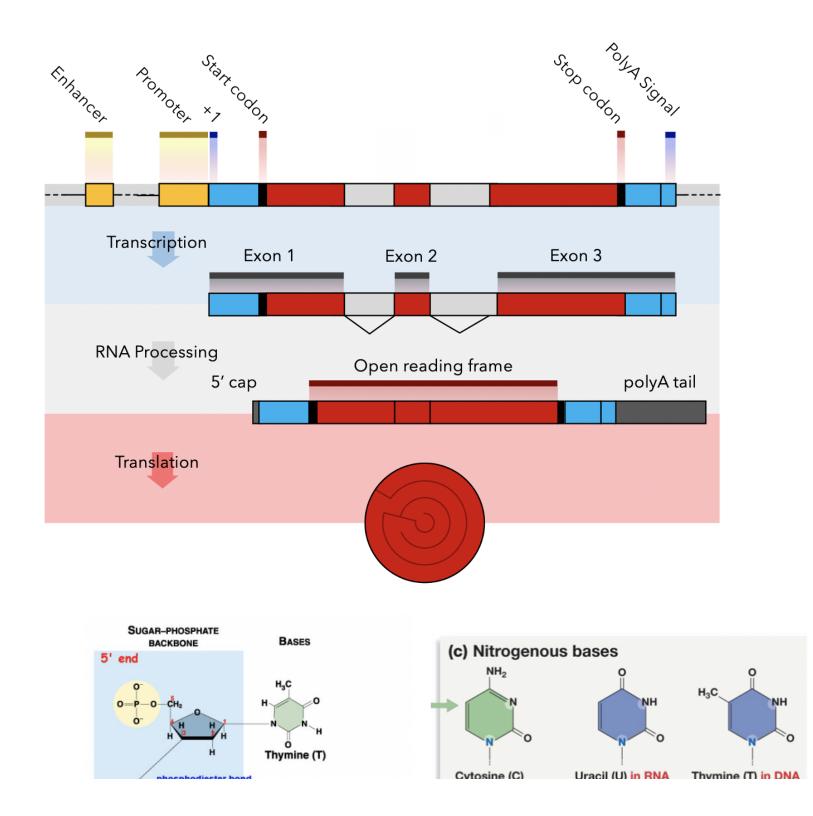
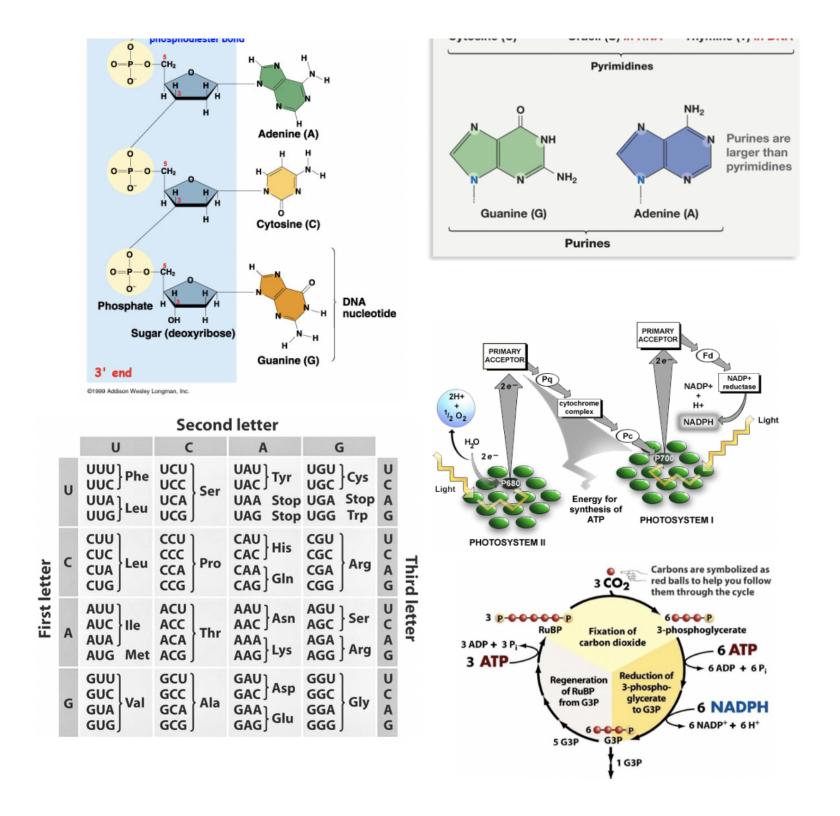
In addition to the figures associated with different problems throughout the exam, you may refer to the following figures if you find them useful:







#### Information

You are interested in joining a lab at UCLA to study SARS-CoV-2, the coronavirus that causes COVID. Your lab is hoping to learn more about the virus to develop new treatments. To study this virus in the lab, you plan on infecting cells obtained from mice. You learn from your new lab mates that the mouse genome follows the same rules of DNA base composition and base pairing that you learned about in class. Given this information, what can you conclude about the genome of your mouse cells?

Question 1	
Complete	
Not graded	

Mouse DNA must contain equal amounts of thymine and cytosine.

- 🔵 a. True
- b. False

Question <b>2</b>	
Complete	
Not graded	
Mouse DNA must o	ontain the same number of purines and pyrimidines.
Select one:	
a. True	
🔵 b. False	
Question <b>3</b>	
Complete	
Not graded	

Select one:

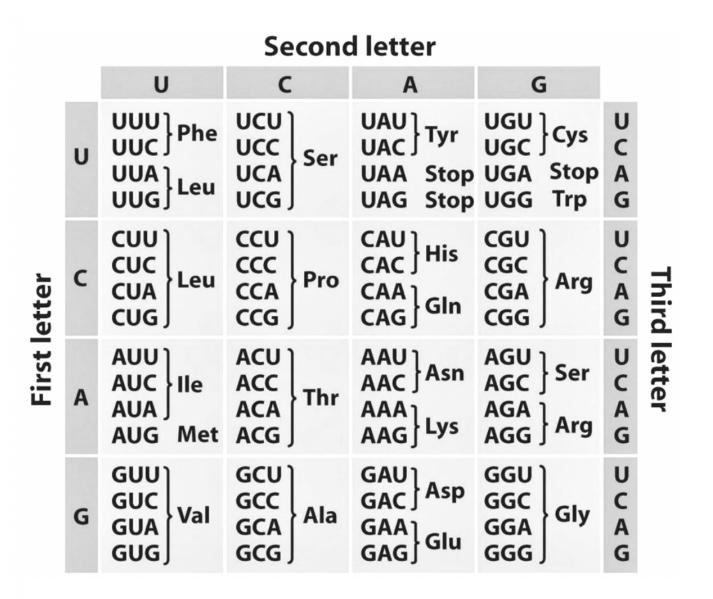
🔵 a. True

b. False

SARS-CoV-2 uses a protein on its surface called "S Protein" to bind to and infect human cells. To study this protein, you create a double stranded DNA sequence that contains the gene for S Protein. Since you learned in LS 7A that a double stranded piece of DNA can contain multiple genes that are transcribed in opposite directions, you also include the sequence for another unrelated gene (Gene X) on the opposite strand. Your double stranded DNA sequence is shown below.

This DNA sequence contains no introns. The three dots in the middle of the sequence indicate that there are an additional 3,735 base pairs in the middle of this DNA sequence that are not shown here, which can be assumed to not contain any stop codons. The boxed base pairs represent the +1 transcription start site for the two genes. The three dots on either side of the DNA sequence indicate that this sequence can be assumed to extend beyond your computer screen on both sides, and the promoter(s) for the S Protein gene and Gene X are located somewhere off of your computer screen. Use this figure and the codon chart below to answer the following questions.

# 3,735 bp DNA 5' ... CTACCTAAGTGTAATGCAGCTT ... AAGAAAGATGAACATTAAATTGTAAT ... 3' 3' ... GATGGATTCACATTACGTCGAA ... TTCTTTCTACTTGTAATTTAACATTA ... 5'



Question 4	
Complete	
Not graded	
The amir	no acid sequence of Protein X begins Met-GIn-Leu. Which strand is the template strand for the Protein X gene?
) a.	The top strand shown in the diagram
b.	The bottom strand shown in the diagram
Question 5	
Complete	
Not graded	
What is t	he second to last amino acid in S Protein?
) a.	lle
○ b.	Thr
○ c.	Tyr
🔾 d.	Met
🔾 e.	None of these

Q	Question 6
С	Complete
N	lot graded
	T/F: When transcribing Gene X, RNA polymerase will read the DNA sequence from the right side of your computer screen to the left side of your computer screen.
	Select one:
	🔿 a. True
	b. False

Question 7	
Complete	
Not graded	

The S Protein gene and Gene X most likely have different promoter regions on your DNA sequence.

Select one:

a. True

Question <b>8</b>	
Complete	
Not graded	
RNA polymerase will read t	he sequence for the S Protein gene from the 3' end to the 5' end of the template strand.
Select one:	
🖲 a. True	
🔵 b. False	
Question 9	
Complete	
•	

Select one:

🔘 a. True

Question 10	
Complete	
Not graded	
	in and the metain symposed from Come V will meet likely he the same
The tertiary structure of S Prote	in and the protein expressed from Gene X will most likely be the same.
Select one:	
🔵 a. True	
b. False	
Question 11	
Complete	
Not graded	

- 🔵 a. 1,253
- b. 1,255
- oc. 1,254
- od. 3,765
- e. 3,768
- f. A different number not shown above
- $\bigcirc$  g. Not possible to say without more information

Complete

Not graded

Which of the following changes to a codon would you expect to be LEAST damaging to the resulting protein (all codons are written 5'->3')?

- a. GCC -> CUG
- b. GAG -> AAG
- c. AGC -> AGA
- Od. CAA -> GAA

You suspect that regulation of the transcription of the SARS-CoV-2 S Protein gene might play an important role in infection. To identify important regulatory elements for this gene, you isolate a piece of DNA that includes the sequence before the transcribed region of the gene. You first take the wild-type sequence, allow transcription to occur, and run a Northern blot to determine how much RNA is produced. You then change the first nucleotide in this region (labeled -24 to indicate that it is 24 nucleotides upstream from the transcription start site) to a different nucleotide and measure how much RNA is produced. You then change the second nucleotide (-23) and measure how much RNA is produced. You then change the second nucleotide (-23) and measure how much RNA is produced. You then change the second nucleotide experiment are shown below. Using these data, mark each of the following statements true or false.

	-24	-23	-22	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1
WT	А	С	G	С	Т	А	А	G	С	А	Т	С	G	А	А	А	G	С	А	Т	С	G	А	А
-	-	-	-			-	-	-	-	-	-	-		-					-		-		-	-

#### Question 13

Complete

Not graded

T/F: The nucleotide at position -22 could be part of a promoter sequence.

Select one:

🔘 a. True

Question 14			
Complete			
Not graded			
Nucleotides -21 and -20 do not ap	pear to play a role in transci	ription.	
Select one:			
a. True			
🔘 b. False			
Question 15			
Complete			
Not graded			
Nucleatides 14 and 12 could be	transariation factor hindin	a oito	
Nucleotides -14 and -13 could be		y site.	

Select one:

💿 a. True

Complete

Not graded

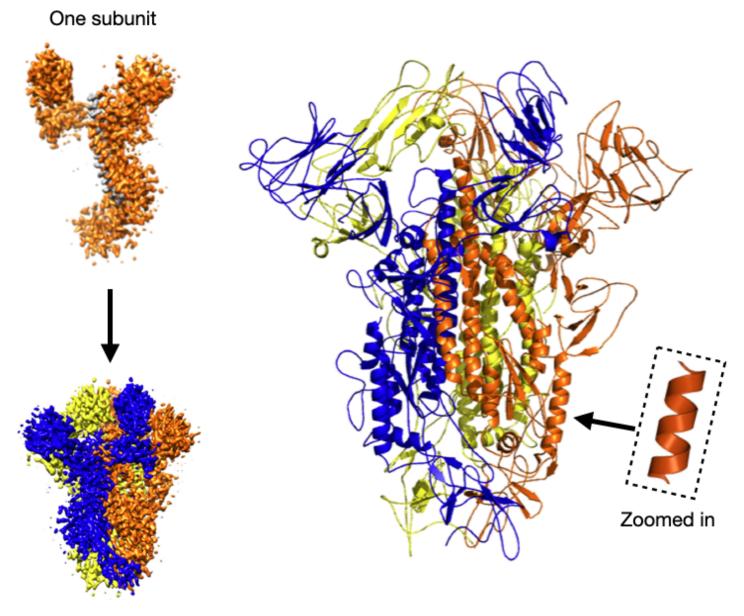
When nucleotide -19 is mutated, transcription of this gene increases.

Select one:

a. True

Information

The image below depicts the structure of the SARS-CoV-2 S Protein. S Protein is made up of three identical polypeptide chains, or subunits, that associate with each other and form a spike-like structure on the surface of SARS-CoV-2. The left side of this image shows the structure of a single subunit (top) and the assembled S Protein spike structure (bottom). The right side of this image is a different model of the same S Protein structure that shows more detail of the protein structure. The arrow on the right side of the image points to a specific part of this structure, and a zoomed in view of that part of the structure is shown to the right of the arrow in a dotted box. Use this information to answer the following questions.



Three subunits

Question 1	7
------------	---

Complete

Not graded

What is the highest level of protein structure in S Protein?

Select one:

- 🔵 a. Primary
- b. Secondary
- c. Tertiary
- d. Quaternary

Question 18	
Complete	
Not graded	

T/F: If heat were added to S Protein, the primary structure would be the first level of structure to be disrupted.

- 🔵 a. True
- b. False

Question <b>19</b>	
Complete	
Not graded	
T/F: Addition of one nucle	otide in the open reading frame of the S Protein gene would probably not affect the function of S Protein.
Select one:	
🔵 a. True	
🖲 b. False	
Question <b>20</b>	
Complete	

What level of protein structure is shown in the boxed zoomed in region?

- 🔵 a. Primary
- b. Secondary
- oc. Tertiary
- 🔘 d. Quaternary

Question 21		
Complete		
Not graded		

T/F: Disrupting the tertiary structure of S Protein would most likely affect its primary structure.

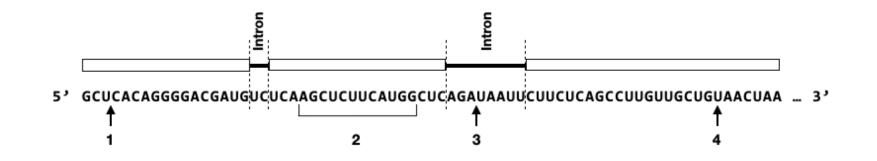
Select one:

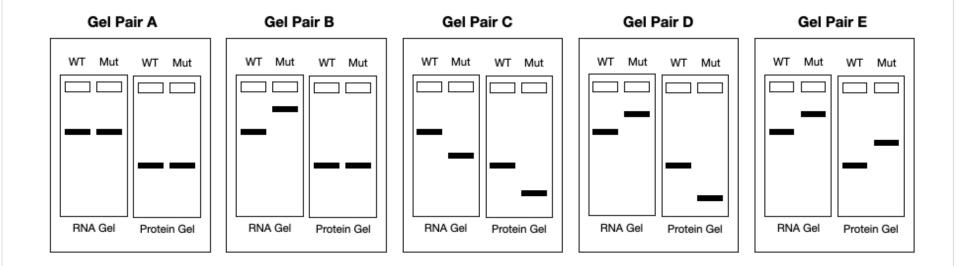
True

False

Information

Angiotensin Converting Enzyme 2 (ACE2) is a membrane protein on the surface of human cells in the lungs, arteries, and heart. To infect human cells, SARS-CoV-2 uses its S Protein to bind to ACE2 on cell surfaces in the lungs. The first part of the sequence of the primary RNA transcript encoding ACE2 is shown below (the full sequence is actually much longer, encoding a total of 805 amino acids, and extends beyond your computer screen, as indicated by the three dots to the right of the sequence). A diagram above the sequence highlights certain features of this primary RNA transcript. Exons are depicted as white boxes, and introns are indicated by lines. The numbered regions represent areas of this gene where mutations will be made. Each of the questions below describes a different mutation that could occur in the ACE2 gene. Below the sequence are five possible gel pairs showing the potential consequences of different mutations in the ACE2 gene. The gel pairs each contain an RNA gel showing the mature mRNA product and a protein gel showing the protein produced from that mRNA. On each gel, "WT" is the normal wild type version of ACE2 and MUT is the mutated version. Assume any difference in size of a molecule (even one nucleotide!) from WT is detectable on a gel. Use the gel pairs as answer choices to describe the result you would be most likely to observe as a consequence of each mutation. Answer choices may be used more than once or not at all.





Complete

Not graded

Gel pair that could result from the addition of AAUAC at point 1.

- 🔵 a. Gel Pair A
- b. Gel Pair B
- C. Gel Pair C
- 🔘 d. Gel Pair D
- 🔘 e. Gel Pair E
- $\bigcirc$  f. None of these

Complete

Not graded

Gels that could result from the deletion of the region indicated at point 2.

- 🔵 a. Gel Pair A
- b. Gel Pair B
- C. Gel Pair C
- 🔘 d. Gel Pair D
- 🔘 e. Gel Pair E
- $\bigcirc$  f. None of these

Complete

Not graded

Gel pair that could result from inserting AAUUGU at point 3

- a. Gel Pair A
- b. Gel Pair B
- C. Gel Pair C
- d. Gel Pair D
- e. Gel Pair E
- $\bigcirc$  f. None of these

Complete

Not graded

Gel pair that could result from changing the U at point 4 to an A.

- a. Gel Pair A
- b. Gel Pair B
- C. Gel Pair C
- 🔘 d. Gel Pair D
- 🔘 e. Gel Pair E
- $\bigcirc$  f. None of these

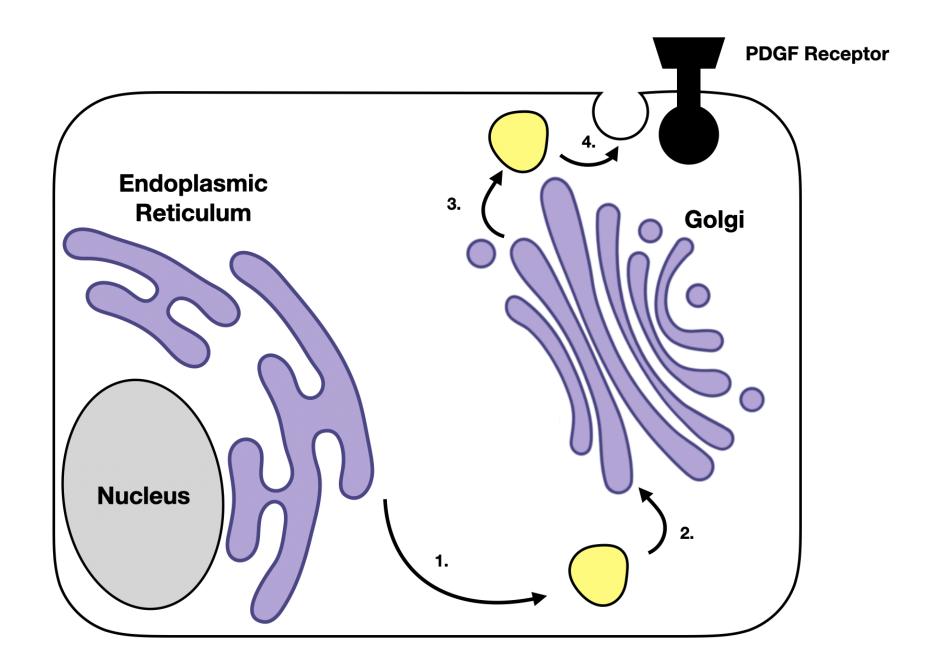
Complete

Not graded

Gel pair that could result from a mutation making the spliceosome nonfunctional.

- 🔵 a. Gel Pair A
- b. Gel Pair B
- C. Gel Pair C
- 🔵 d. Gel Pair D
- e. Gel Pair E
- $\bigcirc$  f. None of these

Platelet-derived growth factor (PDGF) is a small molecule signal that binds to the surface of cells and subsequently promotes cell growth and division. To respond to the PDGF signal, cells must express a PDGF receptor on their cell surface in a specific orientation. The diagram below shows the process of protein trafficking in the endomembrane system. The PDGF receptor is shown on the cell surface, with its receptor domain facing outward and its signaling domain facing inward. Use this information to answer the following questions.



Question 27	
Complete	
Not graded	
T/F: A ribosome initially became bound to the mRNA encoding PDGF Receptor on the rough endoplasmic reticulum.	
Select one:	
🔿 a. True	
b. False	
Question 28	
Complete	
Not graded	

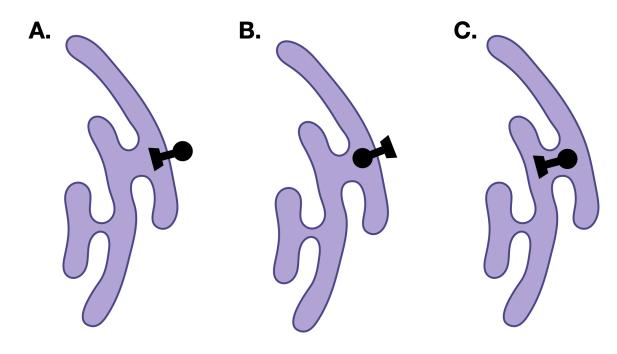
You are testing out a new drug in the laboratory, and add the drug to some cells expressing PDGF. Your drug supposedly prevents SRP from binding to signal peptides. Where would you expect to find PDGF in the cell if your drug treatment is successful?

- a. In the cytosol
- b. In the nucleus
- o c. In the rough ER
- Od. In vesicles
- e. In the golgi

Complete

Not graded

Which of the following images correctly depicts the configuration of the PDGF Receptor protein in relation to the endoplasmic reticulum following translation?



- Image A
- Image B
- Image C
- None of these

	Question	30	
--	----------	----	--

Complete

Not graded

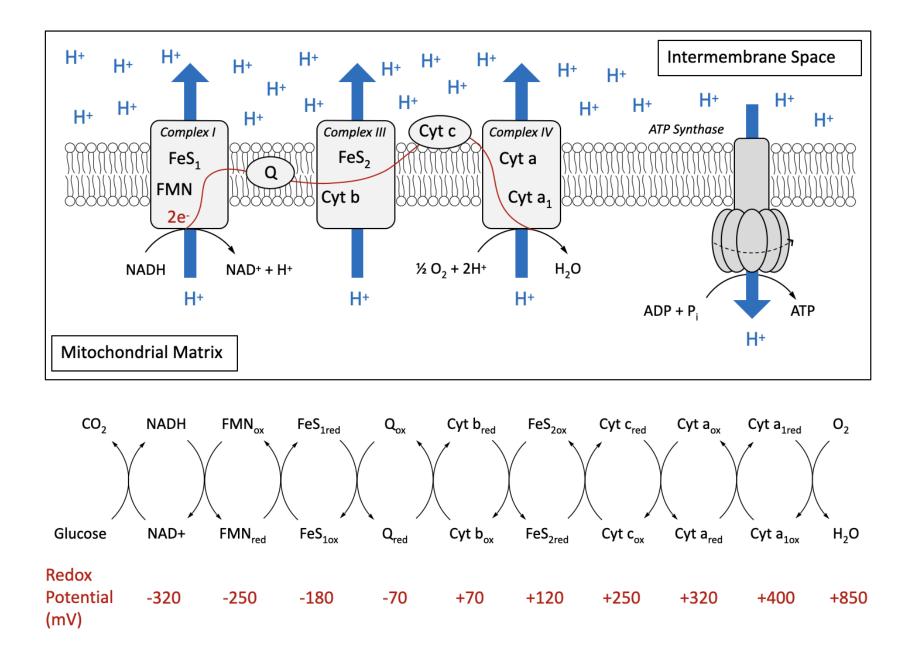
You are working on producing a vaccine by expressing the SARS-CoV-2 S Protein in a plant cell. However, you are becoming frustrated because your experiments aren't working. Your lab mate tells you that your experiments aren't working because the plant cells that you are working with have a mutation that prevents them from forming any vesicles. Where would you expect to find accumulation of S Protein in these plant cells?

#### Select one:

#### a. In the cytosol

- b. In the endoplasmic reticulum
- c. In vesicles
- Od. In the golgi

The following image depicts the electron transport chain and oxidative phosphorylation in a eukaryotic cell. Use this diagram to help you answer the following questions.



Question <b>31</b>				
Complete				
lot graded				
$FMN_{ox}$ is an example of an oxidizing	agent.			
Select one:				
🔵 a. True				
b. False				
Question <b>32</b>				
Complete				
lot graded				
At the same time the total amount o	f ATD increases in a col	l the total amount of Al	D in the call will increase	

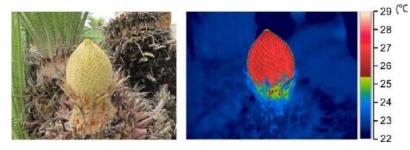
Select one:

🔵 a. True

b. False

Question 33 Complete Not graded
Adding a drug that decreases the pH in the intermembrane space of the mitochondrion will cause ATP production to decrease.
Select one:
🔿 a. True
b. False
Information

Many plants rely on the release of odors into the environment to attract pollinators. To aid in the spread of these odors, these plants often engage in a process called thermogenesis, where they produce heat in the flower (see the image below for one example).



Plants that engage in thermogenesis do so by "decoupling" electron transport from ATP synthesis. Under certain conditions, they produce a protein called alternative oxidase (AOX) that has a redox potential of +90 and acts as an alternate electron acceptor during electron transport. This prevents the normal movement of electrons through the electron transport chain, so fewer H+ ions are pumped and less ATP is made. The end result is that these plants speed up their metabolism by an enormous amount to make up for the lowered ATP production, producing a great deal of heat in the process.

Use this information to answer the following questions.

### Question 34

Complete

Not graded

You determine that the redox potential of AOX is +90. Which molecule in the electron transport chain could AOX be accepting electrons from?

Select one:

- a. FeS1
- ob. FeS2
- 🔵 c. Cyt a
- 🔘 d. Cyt a1
- e. More than one of these

## Question 35

Complete

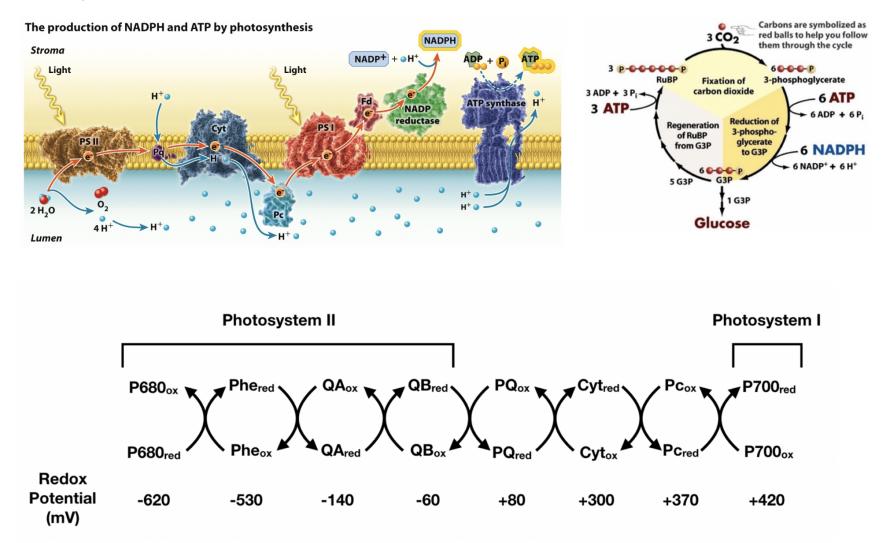
Not graded

If a plant cell begins producing AOX, the amount of Cyt c<sub>red</sub> will \_\_\_\_\_ compared to before AOX was present.

Select one:

- a. Increase
- b. Decrease
- c. Stay the same

The figures below show the light harvesting reactions of photosynthesis and the Calvin Cycle. Beneath the figures is a partial diagram of the redox reactions involved in the light harvesting reactions of photosynthesis, going from photosystem II to photosystem I. Note that photosystem II is made up of multiple smaller components indicated on the redox reaction diagram.



3-(3,4-dichlorophenyl)-1,1-dimethylurea (DCMU) is a chemical used in the laboratory to block the binding of QB to QA in Photosystem II (PSII). Use this information to answer the following questions.

Question <b>36</b>	
Complete	
Not graded	
T/F: When a plant is treated with DCMU, NADP+ accumulates in its reduced form.	
Select one:	
🔘 a. True	
b. False	
Question 37	
Complete	
Not graded	

T/F: When a plant is treated with DCMU, Pc accumulates in its oxidized form.

Select one:

a. True

🔵 b. False

Question <b>38</b>	
Complete	
Not graded	
T/F <sup>.</sup> When a plant is treated wi	th DCMU, light energy will no longer be absorbed by chlorophyll molecules in photosystem I.
	and beine, light energy will no longer be abcorbed by enerophyll molecules in photosystem i.
Select one:	
🔵 a. True	
💿 b. False	
Question <b>39</b>	
Complete	
Not graded	

Select one:

🔵 a. True

Question <b>40</b>	
Complete	
Not graded	
T/F: When a plant is treated	with DCMU, 3-phosphoglycerate will accumulate in the chloroplast.
Select one:	
🖲 a. True	
🔵 b. False	
Question <b>41</b>	
Complete	

a. True

🔵 b. False

Question	42
----------	----

Complete

Not graded

Adding a particular drug changes the redox potential of P700 from +420 to +310. Which of the following would you expect to observe in plant cells treated with this drug?

- a. Phe would accumulate in its reduced form.
- b. ATP would continue to be produced.
- c. Pc would accumulate in its oxidized form.
- O d. Levels of 3-phosphoglycerate would decrease.
- e. More than one of the above

Question	43
----------	----

Complete

Not graded

Prometryn is an herbicide that acts as a photosystem II inhibitor (it prevents photosystem II from splitting water). If a plant were treated with prometryn, which of the following effects would you NOT expect to observe?

- a. Pc would accumulate in its oxidized form
- b. NADPH would accumulate in the chloroplast
- C. ATP production would decrease in the chloroplast
- O d. 3-phosphoglycerate would accumulate in the chloroplast
- e. G3P production would decrease

The figure below represents a ribosome in the process of translating an mRNA molecule (only part of the mRNA molecule is shown - the mRNA can be assumed to extend to the right and left of your screen). What will happen as the ribosome continues to translate the mRNA molecule shown in the diagram? You may find the codon chart below useful.

Met Leu His F P A U G C U C U G C U A C A U A C C G A G C C G U A A A C C U A G G U A A C 5'

# **Second letter**

		U	С	Α	G		
	U	UUU UUC UUA UUG Leu	UCU UCC UCA UCG	UAU UAC UAA Stop UAG Stop	UGU UGC UGA Stop UGG Trp	UCAG	
etter	c	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC CAA CAG Gln	CGU CGC CGA CGG	U C A G	Third
First letter	A	AUU AUC AUA AUG Met	ACU ACC ACA ACG	AAU AAC AAA AAG Lys	AGU AGC } Ser AGA AGG } Arg	UCAG	letter
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAA GAG Glu	GGU GGC GGA GGG	UCAG	

### Question 44

Complete

Not graded

The growing polypeptide chain will be transferred to the tRNA in the E site of the ribosome.

Select one:

🔵 a. True

Question 45	
Complete	
Not graded	
The tRNA that is shown in the diagra	m with the anticodon 3'-CUC-5' will move to the A site of the ribosome.
Select one:	
🔾 a. True	
b. False	
Question <b>46</b>	
Complete	

The same aminoacyl tRNA synthetase can charge the tRNA molecule with the anticodon 3'-UGG-5' and the tRNA molecule with the anticodon 3'-CUC-5'.

Select one:

🔵 a. True

Question <b>47</b>	
Complete	
Not graded	
The amino acid encoded by	the codon 5'-CCG-3' will be covalently bonded to the tRNA currently shown in the P site.
Select one:	
🔵 a. True	
b. False	
Question <b>48</b>	
Complete	

Select one:

🔵 a. True

Questic	n <b>49</b>
Comple	te
Not gra	ded

Refer to the diagram of translation above. What is the anticodon of the tRNA that brought leucine into the growing polypeptide chain?

Select one:

- a. 3'-GAU-5'
- o b. 3'-GUA-5'
- oc. 3'-AUC-5'
- od. 3'-CAU-5'
- e. None of the above

Question 50	
Complete	
Not graded	

What amino acid will be attached to a tRNA with the anticodon sequence 3'-GUA-5'?

Select one:

- a. Arginine (Arg)
- b. Threonine (Thr)
- oc. Methionine (Met)
- d. Serine (Ser)
- e. None of the above

Question 51	
Complete	
Not graded	
Which of the follow	ing describes where the ribosome began translating this mRNA molecule?
<ul> <li>a. At the pror</li> </ul>	noter

○ b. At the +1 transcription start site

## $\bigcirc$ c. At the 5' cap

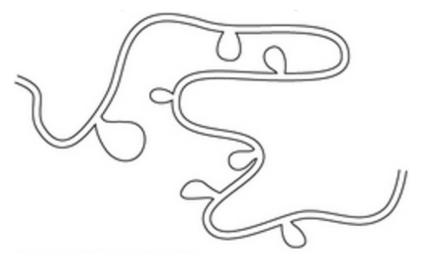
- $\odot$  d. At the AUG nearest to the 5' cap
- $\bigcirc$  e. At the beginning of exon 1

Question 52

Complete

Not graded

You are studying a eukaryotic gene (Gene Z) and want to know how many introns and exons it has. To do this, you hybridize denatured Gene Z DNA with mature Gene Z mRNA. (You may assume that Gene Z only has one possible mature mRNA product.) You look in the microscope and see this result:

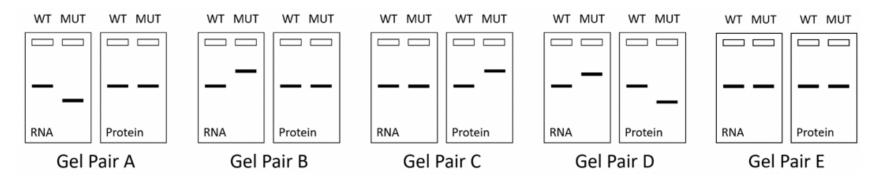


What can you conclude from this result?

- a. Gene Z has seven exons
- b. Gene Z has seven introns
- c. Both of the above are true
- d. Neither of the above are true

#### Information

[Questions 54-57] Each of the questions below describes a different mutation that could occur in a eukaryotic gene. Each gel pair contains an RNA gel showing the mature mRNA product of a eukaryotic gene and a Protein gel showing the protein product of the same gene. On each gel, "WT" is the normal wild type version and "MUT" is the mutated version. Use the answer choices [A, B, C, D, or E] to determine which pair of gels you would be most likely to observe as a consequence of each mutation. Answer choices may be used more than once or not at all.



Question 53	
Complete	
Not graded	

A mutation that causes the polyA tail to be half the length of the WT polyA tail.

Select one:

- a. Gel pair A
- b. Gel pair B
- C. Gel pair C
- 🔘 d. Gel pair D
- 🔵 e. Gel pair E

Question 54	
Complete	
Not graded	

A missense mutation in an exon of this gene that changes the codon for serine to the codon for threonine.

Select one:

- 🔘 a. Gel pair A
- 🔘 b. Gel pair B
- 🔘 c. Gel pair C
- 🔵 d. Gel pair D
- e. Gel pair E

### Question 55

Complete

Not graded

A mutation that adds 50 nucleotides to the 5' untranslated region (UTR) of this gene (assume that these nucleotides do not contain a start codon).

Select one:

- 🔵 a. Gel pair A
- b. Gel pair B
- 🔘 c. Gel pair C
- 🔘 d. Gel pair D
- 🔘 e. Gel pair E

Question 56	
Complete	
Not graded	

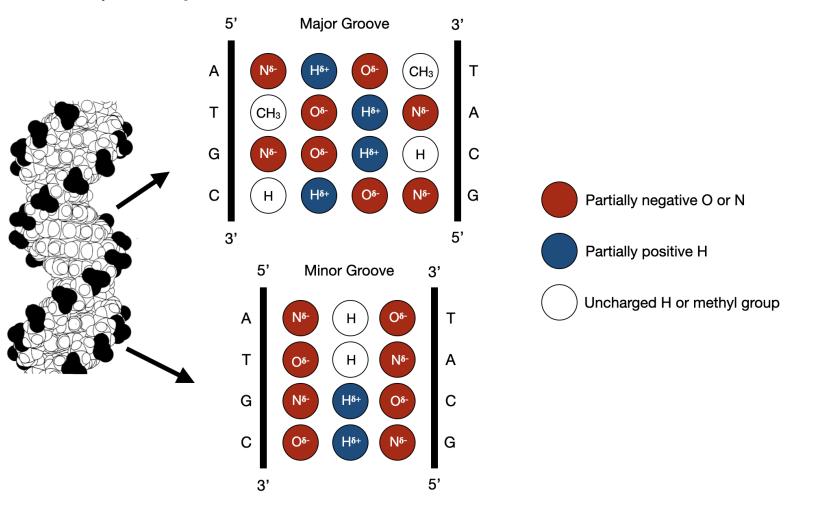
A mutation changing the stop codon into the codon for methionine.

Select one:

- 🔘 a. Gel pair A
- 🔵 b. Gel pair B
- C. Gel pair C
- 🔘 d. Gel pair D
- 🔘 e. Gel pair E

#### Information

As we discussed in class, transcription factors often bind to specific nucleotide sequences by recognizing features of base pairs that are accessible via the major or minor groove of DNA. Specifically, transcription factors often look for specific combinations of hydrogen bond acceptors (partially negative O or N), hydrogen bond donors (partially positive H), and uncharged hydrogen atoms or methyl groups. The images below show what various base pairs would look like to a transcription factor if it were to approach the DNA from the major or minor groove.



Consider two promoter sequences to answer the following questions (note that for each promoter, only the top strand is shown, but you can assume that these represent double stranded DNA sequences):

Promoter 1: 5' – TAATAA – 3'

Promoter 2: 5' – AAATTT – 3'

Question 57		
Complete		
Not graded		

T/F: A transcription factor that binds in the major groove could distinguish between these promoter sequences.

Select one:

True

False

Question 58			
Complete			
Not graded			

T/F: A transcription factor that binds in the minor groove could distinguish between these promoter sequences.

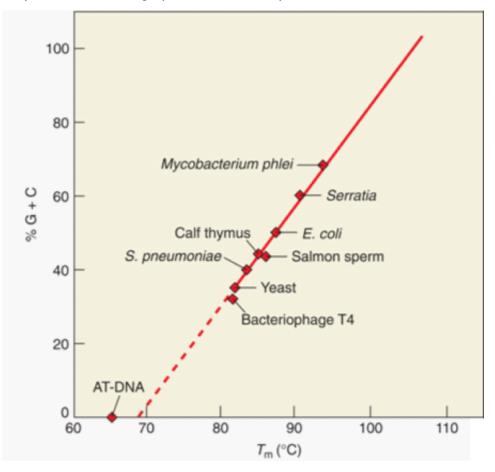
Select one:

True

False

#### Information

Consider the graph below, which shows the melting temperature of different organism's genomes as a function of nucleotide composition. Use this graph to answer the questions below.



Question	59
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Complete

Not graded

The organisms *Mycobacterium phlei* and *E. coli* both have genomes with approximately 5 million base pairs. The number of hydrogen bonds between base pairs in the *Mycobacterium phlei* genome is \_\_\_\_\_\_ in the *E. coli* genome.

- a. Greater than
- O b. Fewer than
- c. The same as

Question 60 Complete
Not graded
The percentage of adenine in the <i>E. coli</i> genome is in the yeast genome.
<ul> <li>a. Greater than</li> </ul>
b. Less than
<ul> <li>c. The same as</li> </ul>

## ◀ LS 7A Fall 2021 Midterm 2 ...

Jump to...