Past-paper walk-through

Translation ▪ 6.4

eXercise

Questions in this set

- 2025 Q1
- 2024 Q6
- 2023 Q1
- 2022 Q6
- 2019 Q1
- 2017 Q3

Reading the mark scheme

- **B1** a mark that stands on its own – the point is either made or not.
- **M1** a *method* mark: the right approach, even if the number is wrong.
- **A1** an *answer* mark, and it usually needs its M mark first.
- **C1** a working mark on the way to the answer.
- // separates answers the examiner accepts equally.
- **ecf** = error carried forward: a later part is marked on your own earlier answer.
- **owtte** = "or words to that effect" – the wording need not match.

Question 1

2025 ▪ Q1

Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

(a) Describe the function of ribosomes.

For proteins transported during translation, this process begins in the cytosol and pauses when a specific sequence of amino acids is translated. The translation complex is then transported to the surface of the ER where translation continues. Proteins that are transported after translation are translated entirely in the cytosol and then transported to the ER. In both instances, the translated proteins enter the ER through a protein channel in the membrane of the ER.

Researchers studying the two types of protein transport identified that the ER membrane protein SR is necessary for transport during translation, while the ER membrane protein Sec62 is necessary for transport after translation. To investigate

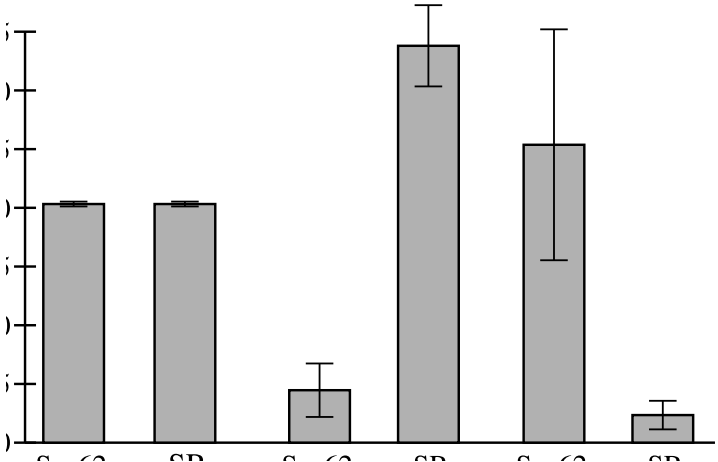
Question 1

which transport mechanism is used for different proteins, researchers first created small interfering RNAs (siRNAs) that reduce expression of either SR or Sec62. They then treated groups of cells with either the SR siRNA or the Sec62 siRNA and determined the relative amount of SR and Sec62 protein in each group of cells compared with cells treated with a control siRNA (Figure 1).

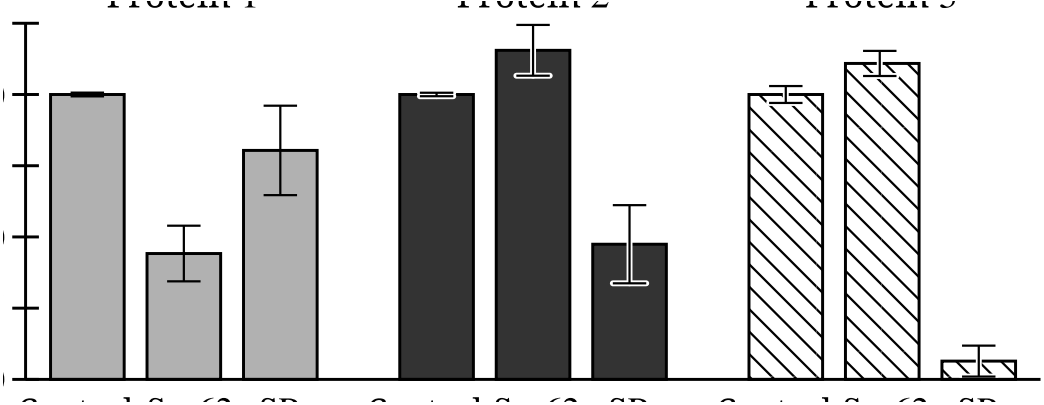
Figure 1. Average relative amounts of Sec62 and SR proteins in cells treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{x}}$.

[Bar graph; y-axis "Relative Protein Content (

Question 1



Question 1



Question 1

2025 ▪ Q1

Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

(b)(i) Identify the dependent variable in the experiments shown in Figure 1.

(b)(ii) Justify why the researchers included the control of measuring the relative amounts of both Sec62 and SR proteins in cells that were treated with Sec62 siRNA only (data shown in Figure 1).

(b)(iii) Based on Figure 1, describe the effect on the production of SR protein when cells are treated with Sec62 siRNA.

Question 1

2025 ▪ Q1

Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

(c)(i) The researchers then measured the amount of each of three different proteins that was transported to the ER in cells treated with Sec62 siRNA or SR siRNA. The researchers calculated the percent transported relative to the cells treated with control siRNA (Figure 2).

Figure 2. Average relative amounts of three proteins that were transported to the ER when treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{x}}$.

[Bar graph; y-axis "Relative Amount of Protein Transported to the ER (

Identify the independent variable in the researchers' second experiment (data shown in Figure 2).

Question 1

(c)(ii) Based on Figure 2, identify the protein(s) that when treated with Sec62 siRNA showed an increase in percent transport to the ER compared with the control.
(c)(iii) Protein 1 is encoded by 234 nucleotides, while protein 2 is encoded by 495 nucleotides. Assuming all nucleotides for both proteins encode amino acids, calculate the difference in the number of amino acids between the two proteins.

Question 1

2025 ▪ Q1

Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

(d)(i) Researchers claim that protein 1 is the only tested protein that is transported to the ER following its complete translation in the cytosol. Using data from Figure 2, support the researchers' claim.

(d)(ii) For any protein that enters the ER, researchers claim that amino acids close to the protein's amino terminus determine how likely the protein is to pass through the protein channel within the ER membrane. Justify the researchers' claim based on your understanding of factors that affect the transport of proteins across membranes.

Solution 1

(a)

Mark scheme

- Ribosomes synthesize polypeptides/proteins by carrying out translation; ribosomes are the sites of polypeptide/protein synthesis.

Solution 1

(b)(i)

Mark scheme

- The dependent variable is the (relative) amount of protein / protein content — i.e., the relative amounts of Sec62 protein and SR protein measured in each treatment group in Figure 1.

Solution 1

(b)(ii)

Mark scheme

- Measuring both Sec62 and SR protein levels in cells treated with Sec62 siRNA only let researchers determine whether the Sec62 siRNA reduced/affected the content of both proteins (i.e., acted nonspecifically), or reduced/affected only Sec62 protein content (i.e., acted specifically on its target), relative to protein content in cells treated with the control siRNA.

Solution 1

(b)(iii)

Mark scheme

- SR protein production increased when cells were treated with Sec62 siRNA (Figure 1 shows SR protein content rising to roughly 170% of control, an increase of about 65%; accept any answer describing an increase in the 50–80% range).

Solution 1

(c)(i)

Mark scheme

- The independent variable in the second experiment (Figure 2) is the type of siRNA added to the cells (control siRNA, Sec62 siRNA, or SR siRNA) — equivalently, which protein pathway (Sec62-dependent vs SR-dependent) was being disrupted for each of the three tested proteins.

Solution 1

(c)(ii)

Mark scheme

- Protein 2 and/or Protein 3 showed an increase in percent transport to the ER when cells were treated with Sec62 siRNA, compared with the control (Protein 1 instead showed a decrease).

Solution 1

(c)(iii)

Mark scheme

- 87 amino acids. Protein 1: $234/3 = 78$ amino acids. Protein 2: $495/3 = 165$ amino acids. Difference $= 165 - 78 = 87$ amino acids. Full credit requires the numeric answer 87 with a correct division-by-3 (codon-to-amino-acid) setup shown.

Solution 1

(d)(i)

Mark scheme

- Only protein 1 showed a reduced amount/percentage of transport to the ER when cells were treated with Sec62 siRNA (Figure 2); proteins 2 and 3 did not show a comparable reduction with Sec62 siRNA, but did drop sharply with SR siRNA — supporting that protein 1 alone depends on the post-translational (Sec62) pathway after complete cytosolic translation, while proteins 2 and 3 depend on the co-translational (SR) pathway.

Solution 1

(d)(ii)

Mark scheme

- Amino acids near the amino terminus that have similar polarity to — or opposite charge to — the R groups lining the ER protein channel are more likely to pass through the channel, compared with an amino terminus whose amino acids have dissimilar polarity or similar (like) charge to the channel lining, since like charges repel and dissimilar polarity resists favorable interactions needed to move through the channel.

Question 6

2024 ▪ Q6

Scientists can quantify the rate of translation as ribosomes move along an mRNA from one codon to the next. Using a procedure called ribosome profiling, the scientists measured how long a ribosome remains stationary at each codon of each mRNA. They determined the average translation rate across all codons is 5.2 amino acids per second but that the average translation rate for specific codons in different mRNA sequences can vary widely. These variations in translation rates are thought to facilitate correct folding of the protein being produced. The rate at which three different codons were translated was measured in 100 different mRNAs. The scientists determined the distribution of rate (number of times each rate was recorded) for each of the three codons: GAC (Figure 1A), AUU (Figure 1B), and UGG (Figure 1C).

[Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG. Each panel is a histogram with y-axis “Number of Times Rate

Question 6

Was Recorded" from 0 to 40 (gridlines every 5) and x-axis "Translation Rate of Codon [X] (ms/codon)" from 0 to 1000 (major gridlines every 100, minor labels every 50).
Panel A (codon GAC): bars rise sharply from ~3 (at ~50) to a peak of ~20 (at ~150), then ~14 (at ~200-250), ~14 (at ~250-300), drops to ~9 (at ~300-350), then ~3 (at ~350-400), and small bars of 1-2 continuing in a long low tail out past 700.
Panel B (codon AUU): bars start at ~11 (at ~50), peak sharply at ~35 (at ~100-150), then ~31 (at ~150-200), dropping to ~10 (at ~200-250), ~4 (at ~250-300), ~2-3 (at ~300-350), and near 0-1 beyond 400 — a narrow, sharply peaked distribution concentrated below 250 ms/codon.
Panel C (codon UGG): bars start near 0-1 (at ~50), rise gradually to ~3 (at ~100-150), ~5 (at ~150-200), ~11 (at ~200-250), ~11 (at ~250-300), ~11 (at ~300-350), ~12 (at ~350-400), ~9 (at ~400-450), ~9 (at ~450-500), ~8 (at ~500-550), then declining

Question 6

through ~3-4 (at ~550-700), ~1-2 out to 900, with a long tail extending to 1000 — a broad, flatter, right-shifted distribution compared with panels A and B.]

(a) Using the data in Figure 1, graph A, **identify** the rate (in ms/codon) that was recorded the greatest number of times for the GAC codon.

(b) Using the data in Figure 1, graphs B and C, **describe** the variation in translation rate of the AUU codon compared with that of the UGG codon.

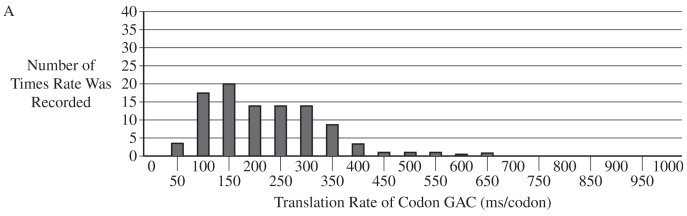
(c) Scientists hypothesize that tRNA molecules that bind to UGG codons are available in lower abundance than are tRNAs that bind to AUU codons. **Support** the scientists' hypothesis using the data in Figure 1.

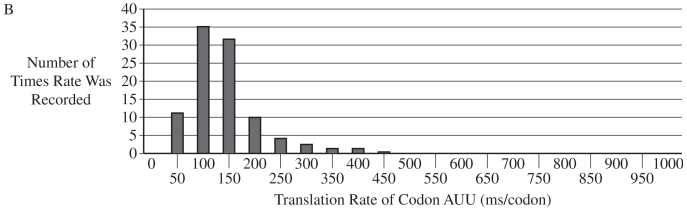
(d) Amino acids can be encoded by multiple codons. In many organisms, certain codons for the same amino acid occur more frequently in an mRNA than do other codons. Based on the data provided, **explain** why the use of one codon over another

Question 6

for the same amino acid might result in increased levels of protein production from a particular mRNA.

Question 6

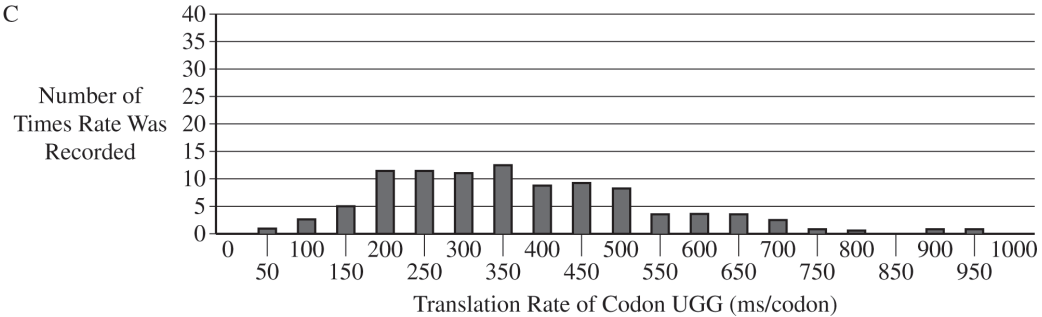

A
Number of Times Rate Was Recorded
40
35
30
25
20
15
10
5
0
0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1000
Translation Rate of Codon GAC (ms/codon)


B
Number of Times Rate Was Recorded
40
35
30
25
20
15
10
5
0
0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1000
Translation Rate of Codon AUU (ms/codon)


C
40

Question 6

C


Number of Times Rate Was Recorded
40
35
30
25
20
15
10
5
0
0
50
100
150
200
250
300
350
400
450
500
550
600
650
700
750
800
850
900
950
1000
Translation Rate of Codon UGG (ms/codon)

Solution 6

(a)

Mark scheme

- 150 ms/codon — this is the rate with the tallest bar (~20 occurrences) in graph A for the GAC codon.

Solution 6

(b)

Mark scheme

- There is greater variation in the translation rate of UGG codons than of AUU codons: the translation rate of UGG ranges from about 50 to 950 ms/codon (graph C, spread across many rate bins), while the translation rate of AUU ranges from only about 50 to 450 ms/codon (graph B, tightly clustered near 100–150).

Solution 6

(c)

Mark scheme

- The data support the hypothesis: the average translation rate of UGG is slower than that of AUU (translation of UGG takes longer per codon), and more of the UGG codons were translated at slower rates than AUU codons were (graph C is shifted toward higher ms/codon values than graph B) — consistent with UGG-binding tRNAs being less abundant, since a scarcer tRNA makes the ribosome wait longer at that codon.

Solution 6

(d)

Mark scheme

- Certain codons are translated at faster rates than others (as shown by the different rate distributions for GAC/AUU/UGG); using the faster-translated codon(s) for a given amino acid lets ribosomes move along the mRNA more quickly, so more protein can be synthesized per unit time from that mRNA, resulting in increased levels of protein production.

Question 1

2023 ▪ Q1

In eukaryotic microorganisms, the PHO signaling pathway regulates the expression of certain genes. These genes, *Pho* target genes, encode proteins involved in regulating phosphate homeostasis. When the level of extracellular inorganic phosphate (Pi) is high, a transcriptional activator Pho4 is phosphorylated by a complex of two proteins, Pho80-Pho85. As a result, the *Pho* target genes are not expressed. When the level of extracellular Pi is low, the activity of the Pho80-Pho85 complex is inhibited by another protein, Pho81, enabling Pho4 to induce the expression of these target genes. A simplified model of this pathway is shown in Figure 1.

[Figure 1, two panels side by side, showing a simplified model of the regulation of expression of *Pho* target genes. Panel A - "High-Phosphate Environment": An oval labeled "Pho81" sits above and unconnected to the rest of the diagram. A rectangle divided into two boxes labeled "Pho80" and "Pho85" sits above a horizontal arrow.

Question 1

The arrow points from a triangle labeled "Pho4" to another triangle labeled "Pho4" with a circled "P" attached (phosphorylated Pho4). Below the arrow, a curved arrow goes from "ATP" to "ADP", indicating ATP is consumed to phosphorylate Pho4. Below that, a DNA double helix is drawn (labeled "DNA") leading into an X-shaped region labeled "*Pho* Target Genes" (genes not being transcribed). Panel B - "Low-Phosphate Environment": An oval labeled "Pho81" sits above a "T"-shaped inhibition symbol (flat bar) pointing down to the "Pho80 | Pho85" rectangle, indicating Pho81 inhibits the Pho80-Pho85 complex. Below that, a triangle labeled "Pho4" (unphosphorylated) has a downward arrow to a bent arrow ("promoter" symbol) pointing into the DNA/"*Pho* Target Genes" region, indicating Pho4 activates transcription. From the *Pho* Target Genes region, a diagonal arrow labeled "*Pho* Target Gene mRNAs" points up and to the right to another diagonal arrow labeled "Proteins Encoded by *Pho* Target Genes".]

Question 1

Figure 1. A simplified model of the regulation of expression of *Pho* target genes in (A) a high-phosphate (high-Pi) environment and (B) a low-phosphate (low-Pi) environment

To study the role of the different proteins in the PHO pathway, researchers used a wild-type strain of yeast to create a strain with a mutant form of Pho81 (*pho81mt*) and a strain with a mutant form of Pho4 (*pho4mt*). In each of these mutant strains, researchers measured the activity of a particular enzyme, APase, which removes phosphates from its substrates and is encoded by *PHO1*, a *Pho* target gene (Table 1). They then determined the level of *PHO1* mRNA relative to that of the wild-type yeast strain, which was set to 10.

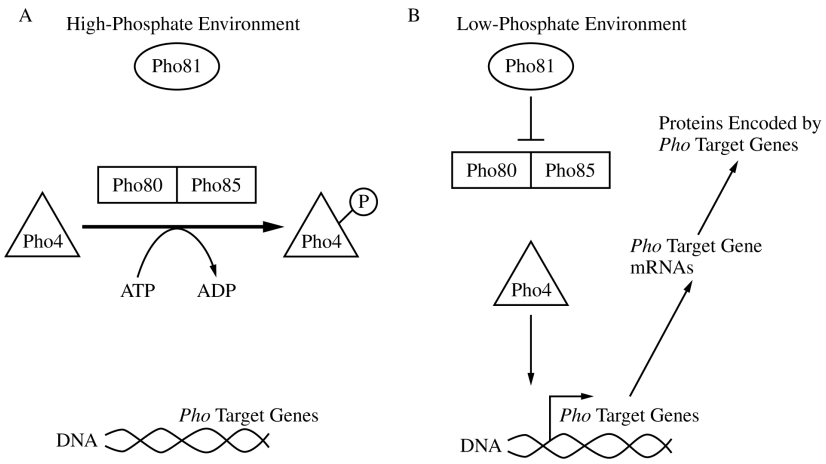
TABLE 1. APase ACTIVITY AND RELATIVE AMOUNTS OF *PHO1* mRNA IN WILD-TYPE AND MUTANT STRAINS OF YEAST IN HIGH- AND LOW-PHOSPHATE ENVIRONMENTS

Question 1

| Yeast Strain | Mutation | APase Activity in High-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$ | APase Activity in Low-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$ | Relative Amounts of *PHO1* mRNA in High-Pi Environment $\pm 2SE_{\bar{x}}$ | Relative Amounts of *PHO1* mRNA in Low-Pi Environment $\pm 2SE_{\bar{x}}$ | |—|—|—|—|—|—| | Wild-type | None | 0.5 ± 0.1 | 17.3 ± 0.9 | 0.1 ± 0.0 | 10 ± 2.0 | | *pho81mt* | Nonfunctional Pho81 | 0.4 ± 0.1 | 0.6 ± 0.1 | 0.7 ± 0.2 | 0.9 ± 0.8 | | *pho4mt* | Nonfunctional Pho4 | 0.5 ± 0.0 | 0.8 ± 0.2 | 0.6 ± 0.4 | 0.3 ± 0.1 |

(a) Describe the effect that the addition of a charged phosphate group can have on a protein that would cause the protein to become inactive. **Explain** how a signal can be amplified during signal transduction in a pathway such as the PHO signaling pathway.

Question 1


A
High-Phosphate Environment
Pho81
Pho80
Pho85
Pho4
P
Pho4
ATP
ADP
DNA
Pho Target Genes
B
Low-Phosphate Environment
Pho81
Pho80
Pho85
Proteins Encoded by
Pho Target Genes
Pho Target Gene
mRNAs
Pho4
Pho Target Genes
DNA

Question 1

2023 ▪ Q1

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Question 1

(b) Based on Table 1, **identify** a dependent variable in the researchers' experiment. **Justify** the researchers' using the wild-type strain for the creation of the mutant strains. **Justify** the researchers' using mutant strains in which only a single component of the pathway was mutated in each strain.

Question 1

2023 ▪ Q1

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Question 1

(c) Based on the data in Table 1, **identify** the yeast strain and growth conditions that lead to the highest relative amount of *PHO1* mRNA. **Calculate** the percent change in APase activity in wild-type yeast cells in a high-Pi environment compared with that of wild-type cells in a low-Pi environment.

Question 1

2023 ▪ Q1

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Yeast Strain	Mutation	APase Activity in High-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$	APase Activity in Low-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$	Relative Amounts of *PHO1* mRNA in High-Pi Environment $\pm 2SE_{\bar{x}}$	Relative Amounts of *PHO1* mRNA in Low-Pi Environment $\pm 2SE_{\bar{x}}$
Wild-type	None	0.5 ± 0.1	17.3 ± 0.9	0.1 ± 0.0	10 ± 2.0
pho81mt	Nonfunctional Pho81	0.4 ± 0.1	0.6 ± 0.1	0.7 ± 0.2	0.9 ± 0.8
pho4mt	Nonfunctional Pho4	0.5 ± 0.0	0.8 ± 0.2	0.6 ± 0.4	0.3 ± 0.1

Question 1

(d) In a follow-up experiment, researchers created a strain of yeast with a mutation that resulted in a nonfunctional Pho85 protein. Based on Figure 1, **predict** the effects of this mutation on *PHO1* expression in the mutant strain in a high-Pi environment. Provide reasoning to **justify** your prediction.

Solution 1

(a)

Mark scheme

- Effect of a charged phosphate group on a protein: adding the charged phosphate changes the structure/shape (conformation) of the protein, which is what causes it to become inactive. Signal amplification: in a signal-transduction pathway such as PHO signaling, each enzyme (e.g., a kinase) in the pathway can act on many copies of the next protein/substrate, so a single upstream signaling event is converted into activation of many downstream molecules — this stepwise, one-to-many catalysis at each relay step is how the signal is amplified.

Solution 1

(b) Mark scheme

- Dependent variable: APase activity, or the relative amount of PHO1 mRNA (either is acceptable). Justify using the wild-type strain as the source for creating the mutant strains: this ensures any observed differences in experimental results between strains are due to the introduced mutation itself and not to other, pre-existing genetic differences — i.e., the strains are genetically identical except for the one introduced mutation, giving a valid comparison. Justify using strains in which only a single pathway component was mutated in each strain: this allows the researchers to test the effect of each mutation separately, so they can determine which specific pathway component is responsible for any observed differences (avoids confounding effects of multiple simultaneous mutations).

Solution 1

(c)

Mark scheme

- Strain/conditions with highest relative PHO1 mRNA: wild-type yeast grown in a low-Pi environment (value of 10, per Table 1). Percent change in APase activity in wild-type cells, high-Pi vs. low-Pi: using the values 0.5 (high-Pi) and 17.3 (low-Pi) mU/mL/OD600, percent change $= (17.3 - 0.5)/0.5 \times 100\% \approx 3{,}360\%$ increase going from high-Pi to low-Pi (equivalently, a change of about -97% going from low-Pi to high-Pi: $(0.5 - 17.3)/17.3 \times 100\% \approx -97\%$). Credit either direction of calculation provided the arithmetic and setup are correct.

Solution 1

(d)

Mark scheme

- Prediction: in a high-Pi environment, a strain with nonfunctional Pho85 will still express PHO1 (Pho target genes will be expressed), unlike wild type where they are normally off in high-Pi. Justification: Pho85 is part of the Pho80–Pho85 complex that normally phosphorylates and inactivates Pho4 when Pi is high; a nonfunctional Pho85 cannot phosphorylate/inhibit Pho4, so Pho4 remains active and continues to induce transcription of PHO1 and other Pho target genes even when extracellular Pi is high.

Question 6

2022 ▪ Q6

Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the

Question 6

normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

5' Cap Structure	mRNA Half-Life $\pm 2\text{SE}_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2\text{SE}_{\bar{x}}$ (relative to amount in normal cap)
No cap	1.41 ± 0.02	0.011 ± 0.000
Normal GTP cap	16.10 ± 1.83	1.000 ± 0.007
Modified cap I	15.50 ± 1.57	4.777 ± 0.042
Modified cap II	27.00 ± 2.85	13.094 ± 0.307
Modified cap III	18.09 ± 0.81	6.570 ± 0.075

(a) Based on the data, identify which cap structure is most likely to protect the end of the mRNAs from degradation.

Question 6

(b) Based on the data for the mRNAs with modified caps, describe the relationship between the mRNA half-life and the total amount of protein produced.
(c) After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. Evaluate their hypothesis by comparing the data in Table 1.
(d) Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. Explain why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells.

Solution 6

(a)

Mark scheme

- Modified cap II is most likely to protect the end of the mRNAs from degradation, since it has the longest mRNA half-life in Table 1 (27.00 +/- 2.85 hours).

Solution 6

(b)

Mark scheme

- For the mRNAs with modified caps, a longer mRNA half-life is associated with a greater total amount of protein produced - i.e. there is a positive correlation/relationship between mRNA half-life and the amount of protein produced.

Solution 6

(c)

Mark scheme

- The data support the researchers' hypothesis: the half-lives of the modified-cap-I mRNA (15.50 hours) and the normal-GTP-cap mRNA (16.10 hours) are essentially the same, but the amount of protein produced from the modified-cap-I mRNA (4.777, relative units) is more than four times that produced from the normal-cap mRNA (1.000) - so, with roughly equal amounts of mRNA available for translation over a similar timeframe, each modified-cap-I mRNA molecule must have been translated more frequently than each normal-cap mRNA molecule.

Solution 6

(d)

Mark scheme

- Production of a foreign protein is more likely from introduced mRNA than DNA because protein production from DNA first requires transcription (and transcription factors to initiate it), whereas an introduced mRNA can be translated directly; also, protein production from mRNA does not depend on correct posttranscriptional processing of a pre-mRNA, and the cell may be unable to transcribe the foreign DNA at all, whereas the mRNA can still be directly translated.

Question 1

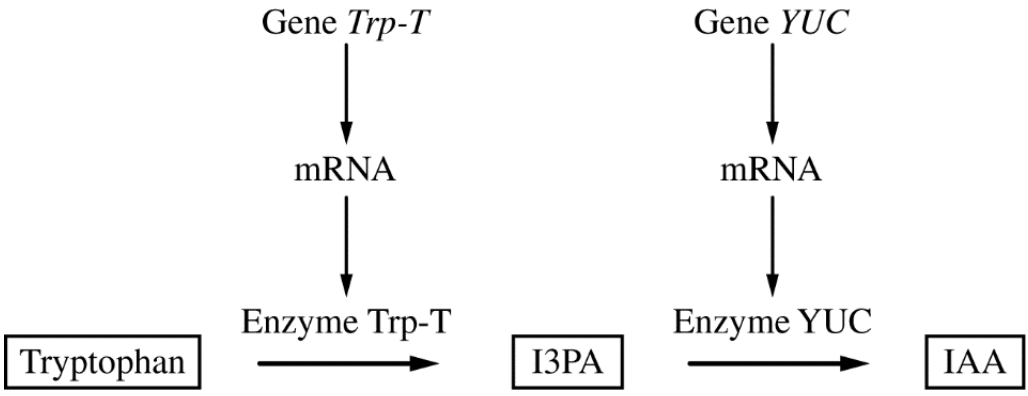
2019 ▪ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(Enzyme YUC)–> IAA.]

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*.

(a) Circle ONE arrow that represents transcription on the template pathway. **Identify** the molecule that would be absent if enzyme YUC is nonfunctional.

Question 1


Gene *Trp-T*
mRNA
Enzyme Trp-T
Tryptophan
I3PA
Gene *YUC*
mRNA
Enzyme YUC
IAA

Question 1

2019 ▪ Q1

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(b) Predict how the deletion of one base pair in the fourth codon of the coding region of gene *Trp-T* would most likely affect the production of IAA. **Justify** your prediction.

Question 1

2019 ▪ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(Enzyme YUC)–> IAA.]

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(c) Explain one feedback mechanism by which a cell could prevent production of too much IAA without limiting I3PA production.

Question 1

2019 ▪ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(Enzyme YUC)–> IAA.]

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(d) Rhizobacteria are a group of bacteria that live in nodules on plant roots. Rhizobacteria can produce IAA and convert atmospheric nitrogen into forms that can be used by plants. Plants release carbon-containing molecules into the nodules. Based

Question 1

on this information, **identify** the most likely ecological relationship between plants and rhizobacteria. **Describe** ONE advantage to the bacteria of producing IAA.

Question 1

2019 ▪ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(Enzyme YUC)–> IAA.]

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(e) A researcher removed a plant nodule and identified several "cheater" rhizobacteria that do not produce IAA or fix nitrogen. **Describe** the evolutionary advantage of being a bacterial cheater in a population composed predominantly of noncheater bacteria.

Question 1

Plants can adjust the amount of carbon-containing molecules released into nodules in response to the amount of nitrogen fixed in the nodule. **Predict** the change in the bacterial population that would cause the plant to reduce the amount of carbon-containing molecules provided to the nodule.

Solution 1

(a)

Mark scheme

- Circle: Circle either arrow that points from a gene (Trp-T or YUC) to its mRNA — this represents transcription. [1 point] Identify: If enzyme YUC is nonfunctional, the molecule IAA would be absent, because YUC catalyzes the conversion of I3PA to IAA (the final step of the pathway); with no functional YUC, I3PA cannot be converted to IAA. [1 point]

Solution 1

(b)

Mark scheme

- Prediction: Deletion of one base pair in the fourth codon of the Trp-T coding region would most likely reduce IAA production, or result in no IAA production. [1 point] Justification (any one): the frameshift mutation results in translation of an inactive/nonfunctional Trp-T enzyme; OR the mutation results in no translation of the Trp-T enzyme (e.g., a premature stop codon); OR the mutation results in no/reduced production of I3PA (since Trp-T is needed to convert tryptophan to I3PA, and I3PA is the precursor for IAA). [1 point]

Solution 1

(c)

Mark scheme

- This is a negative feedback (feedback inhibition) mechanism: as IAA accumulates, increasing amounts of IAA inhibit the pathway that produces it. [1 point] Specifically, the rising IAA level inhibits production of the YUC enzyme, or inhibits YUC enzyme activity — this blocks only the second step (I3PA $\rightarrow$ IAA), so I3PA production (via Trp-T, the first step) is not limited. [1 point]

Solution 1

(d)

Mark scheme

- Identification: The relationship between plants and rhizobacteria is mutualism — both organisms benefit. [1 point] Description: One advantage to the bacteria of producing IAA is that IAA promotes root growth, which increases the plant's habitat/number of nodules available to house the rhizobacteria; in exchange, the bacteria receive carbon-containing molecules released by the plant (as a result of the increased plant growth). [1 point]

Solution 1

(e)

Mark scheme

- Description: 'Cheater' bacteria that benefit from nodule resources without expending energy to produce IAA or fix nitrogen have more energy available for their own reproduction, giving them a reproductive/evolutionary advantage over noncheater bacteria as long as cheaters remain a minority. [1 point]
  Prediction: A decrease in the nitrogen-fixing/noncheater bacteria (or a decrease in the total amount of nitrogen fixed in the nodule) would cause the plant to reduce the amount of carbon-containing molecules it releases into that nodule. [1 point]

Question 3

2017 ▪ Q3

Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydroxylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the *GA3H* gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F_1 generation are tall. When the F_1 plants are crossed with each other, 75 percent of the plants in the F_2 generation are tall and 25 percent of the plants are short.

Second Base in Codon

First \ Second	U	C	A	G	Third
U	UUU, UUC = Phe; UUA, UUG = Leu	UCU, UCC, UCA, UCG = Ser	UAU, UAC = Tyr; UAA = Stop; UAG = Stop	UGU, UGC = Cys; UGA = Stop; UGG = Trp	U, C, A, G
C	CUU, CUC, CUA, CUG = Leu	CCU, CCC, CCA, CCG = Pro	CAU, CAC = His; CAA, CAG = Gln	CGU, CGC, CGA, CGG = Arg	U, C, A, G
A	AUU, AUC, AUA = Ile; AUG = Met or Start	ACU, ACC, ACA, ACG = Thr	AAU, AAC = Asn; AAA, AAG = Lys	AGU, AGC = Ser; AGA, AGG = Arg	U, C, A, G
G	GUU, GUC,	GCU, GCC, GCA, GCG =	GAU, GAC	GGU, GGC,	U, C, A, G

Question 3

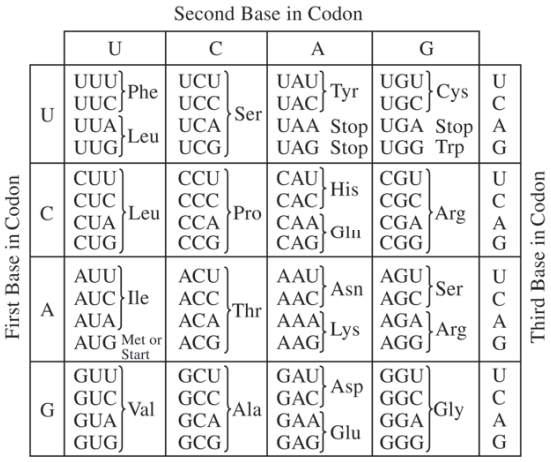
Figure 1. The universal genetic code

(a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.

(b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.

(c) Describe how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype.

Question 3


Second Base in Codon
U
C
A
G
First Base in Codon
Third Base in Codon
U
UUU Phe
UUC Phe
UUA Leu
UUG Leu
UCU Ser
UCC Ser
UCA Ser
UCG Ser
UAU Tyr
UAC Tyr
UAA Stop
UAG Stop
UGU Cys
UGC Cys
UGA Stop
UGG Trp
C
CUU Leu
CUC Leu
CUA Leu
CUG Leu
CCU Pro
CCC Pro
CCA Pro
CCG Pro
CAU His
CAC His
CAA Gln
CAG Gln
CGU Arg
CGC Arg
CGA Arg
CGG Arg
A
AUU Ile
AUC Ile
AUA Ile
AUG Met or Start
ACU Thr
ACC Thr
ACA Thr
ACG Thr
AAU Asn
AAC Asn
AAA Lys
AAG Lys
AGU Ser
AGC Ser
AGA Arg
AGG Arg
G
GUU Val
GUC Val
GUA Val
GUG Val
GCU Ala
GCC Ala
GCA Ala
GCG Ala
GAU Asp
GAC Asp
GAA Glu
GAG Glu
GGU Gly
GGC Gly
GGA Gly
GGG Gly

Solution 3

(a)

Mark scheme

- Description (1 point): the amino acid substitution (Ala→Thr, nonpolar→polar) changes the shape/structure/function of the GA3H protein. Reasoning (1 point): the altered/less-functional enzyme decreases or eliminates gibberellin production, and because gibberellin promotes stem elongation, low gibberellin in homozygous recessive plants results in the short phenotype.

Solution 3

(b)

Mark scheme

- Any one correctly stated codon-change representation earns the point: G↔A in the first position of the second base of the codon, i.e., 5'-GCN-3' (Ala) ↔ 5'-ACN-3' (Thr); equivalently on the DNA template strand, 5'-NGC-3' ↔ 5'-NGT-3'.

Solution 3

(c)

Mark scheme

- Enough active GA3H enzyme is produced from just one wild-type/dominant allele (the wild-type allele is dominant), so enough gibberellin is produced in both heterozygotes and homozygous-dominant plants, giving them the same (tall) phenotype.