Past-paper walk-through

Cell Compartmentalization ▪ 2.9

eXercise

Questions in this set

- 2026 Q2
- 2025 Q1
- 2023 Q2
- 2018 Q2
- 2018 Q6

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 2

2026 ▪ Q2

Eukaryotic cells use small interfering RNA (siRNA) molecules that regulate the expression of certain genes by binding to complementary sequences in target mRNAs. This binding causes the protein AGO2 to cleave the target mRNAs. As a result of the cleavage, the mRNAs are not translated.

The following information applies to parts B, C, and D.

To investigate the role of AGO2 in the cleavage of mRNA transcribed from two genes, Gene *G* and Gene *H*, scientists determined the amount of Gene *G* and Gene *H* mRNA produced in cells with three different *AGO2* genotypes:

- Homozygous for the wild-type AGO2 protein ($AGO2^{+/+}$) - Heterozygous for the allele encoding a nonfunctional AGO2 protein ($AGO2^{+/-}$) - Homozygous for the allele encoding a nonfunctional AGO2 protein ($AGO2^{-/-}$)

Question 2

The scientists then calculated the amount of Gene *G* and Gene *H* mRNA produced from cells of each genotype relative to that in $AGO2^{+/+}$ cells. These results are shown in the table.

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

	mRNA in $AGO2^{+/+}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{+/-}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{-/-}$ Cells $\pm SE_{\bar{x}}$
Gene *G*	1.0 ± 0.1	0.9 ± 0.4	1.5 ± 0.5
Gene *H*	1.0 ± 0.1	2.0 ± 0.1	3.0 ± 0.4

(a) Describe one location where ribosomes are found in eukaryotic cells.

Question 2

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

	mRNA in $AGO2^{+/+}$ Cells $\pm$ $SE_{\bar{x}}$	mRNA in $AGO2^{+/-}$ Cells $\pm$ $SE_{\bar{x}}$	mRNA in $AGO2^{-/-}$ Cells $\pm$ $SE_{\bar{x}}$
Gene *G*	1.0 $\pm$ 0.1	0.9 $\pm$ 0.4	1.5 $\pm$ 0.5
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Question 2

2026 ▪ Q2

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The scientists then calculated the amount of Gene *G* and Gene *H* mRNA produced from cells of each genotype relative to that in $AGO2^{+/+}$ cells. These results are shown in the table.

Question 2

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

	mRNA in $AGO2^{+/+}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{+/-}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{-/-}$ Cells $\pm SE_{\bar{x}}$
Gene *G*	1.0 ± 0.1	0.9 ± 0.4	1.5 ± 0.5
Gene *H*	1.0 ± 0.1	2.0 ± 0.1	3.0 ± 0.4

(b)(i) Using the template in the space provided for your response, **construct** a bar graph that represents the data in the table. Your graph should be appropriately plotted and labeled.

(b)(ii) Based on the table, **determine** all the cells in which the amount of Gene *G* mRNA produced is statistically the same as the amount in the cells with the $AGO2^{+/+}$ genotype.

Question 2

2026 ▪ Q2

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Question 2

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

	mRNA in $AGO2^{+/+}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{+/-}$ Cells $\pm SE_{\bar{x}}$	mRNA in $AGO2^{-/-}$ Cells $\pm SE_{\bar{x}}$
Gene *G*	1.0 ± 0.1	0.9 ± 0.4	1.5 ± 0.5
Gene *H*	1.0 ± 0.1	2.0 ± 0.1	3.0 ± 0.4

(c)(i) Based on the table, **describe** the relationship between the number of wild-type copies of the *AGO2* gene and the amount of Gene *H* mRNA in the cells.

(c)(ii) Based on the data in the table for Gene *H*, **calculate** the percent by which the average amount of mRNA in $AGO2^{-/-}$ cells increases compared with that in $AGO2^{+/-}$ cells.

Question 2

2026 ▪ Q2

Eukaryotic cells use small interfering RNA (siRNA) molecules that regulate the expression of certain genes by binding to complementary sequences in target mRNAs. This binding causes the protein AGO2 to cleave the target mRNAs. As a result of the cleavage, the mRNAs are not translated.

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The scientists then calculated the amount of Gene *G* and Gene *H* mRNA produced from cells of each genotype relative to that in $AGO2^{+/+}$ cells. These results are shown in the table.

Question 2

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

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Gene *G*	1.0 ± 0.1	0.9 ± 0.4	1.5 ± 0.5
Gene *H*	1.0 ± 0.1	2.0 ± 0.1	3.0 ± 0.4

(d)(i) The scientists claim that siRNA binding and AGO2 cleavage of mRNAs play a greater role in the regulation of Gene *H* expression than in the regulation of Gene *G* expression. Based on the table, **support** the scientists' claim.

(d)(ii) Anaphase I of meiosis is blocked in mice with the $AGO2^{-/-}$ genotype. Scientists hypothesize that the block in meiosis occurs because the continued presence of a spindle-fiber stabilizing protein prevents the chromosomes from separating. Based on the table, **explain** how the $AGO2^{-/-}$ genotype could cause this effect on the dividing cells.

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

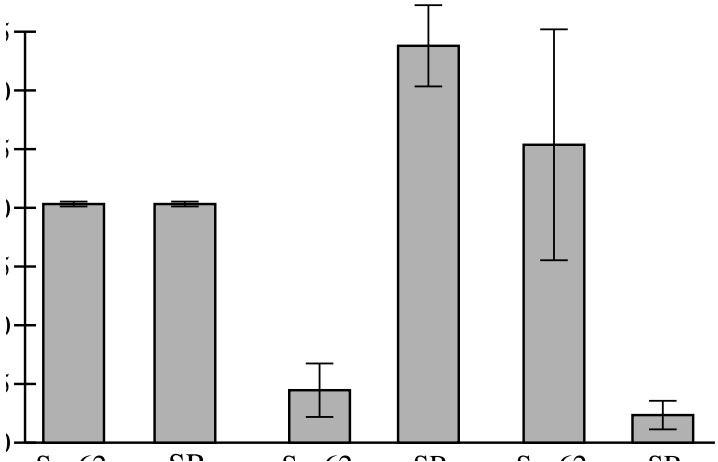
Question 1

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).

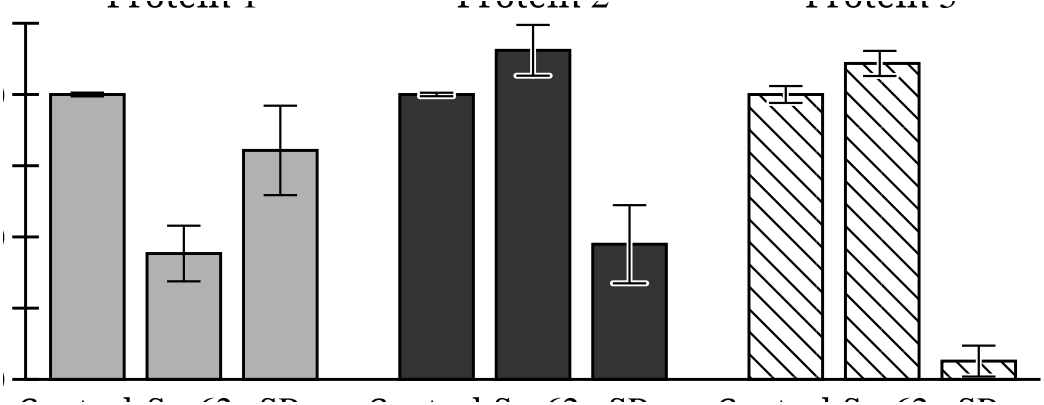
Figure 1. Average relative amounts of Sec62 and SR proteins in cells treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{x}}$.

[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 2

2023 ▪ Q2

Elevated levels of CO_2 increase the rate of photosynthesis and growth in plants. Scientists studying the mechanisms involved in these increases examined a variety of species and found that when plants are exposed to elevated levels of CO_2, there is an increase in the number of chloroplasts per cell. To investigate whether the elevated levels of CO_2 have a similar effect on the number of mitochondria in plant cells, the scientists then selected six of these species to quantify the number of mitochondria per cell when the plants were exposed to both normal and elevated levels of CO_2 (Table 1).
TABLE 1. AVERAGE NUMBER OF MITOCHONDRIA IN PLANTS EXPOSED TO NORMAL AND ELEVATED LEVELS OF CO_2
| Species | Mitochondria at Normal CO_2 (per 100 μm^2 of cell area) $\pm 2SE_{\bar{x}}$ | Mitochondria at Elevated CO_2 (per 100 μm^2 of cell area) $\pm 2SE_{\bar{x}}$ | |—|—|—| | 1 |

Question 2

1.0 ± 0.10 | 1.6 ± 0.10 | | 2 | 0.4 ± 0.05 | 0.9 ± 0.08 | | 3 | 0.5 ± 0.07 | 0.9 ± 0.10 | | 4 | 0.3 ± 0.03 | 0.6 ± 0.06 | | 5 | 0.7 ± 0.06 | 1.5 ± 0.22 | | 6 | 1.3 ± 0.15 | 2.4 ± 0.22 |

(a) Describe the role of the inner mitochondrial membrane in cellular respiration.

Question 2

2023 ▪ Q2

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Question 2

(b) Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1. **Determine** which species show(s) a difference in the number of mitochondria between normal and elevated levels of CO_2.

Question 2

2023 ▪ Q2

Elevated levels of CO_2 increase the rate of photosynthesis and growth in plants. Scientists studying the mechanisms involved in these increases examined a variety of species and found that when plants are exposed to elevated levels of CO_2, there is an increase in the number of chloroplasts per cell. To investigate whether the elevated levels of CO_2 have a similar effect on the number of mitochondria in plant cells, the scientists then selected six of these species to quantify the number of mitochondria per cell when the plants were exposed to both normal and elevated levels of CO_2 (Table 1).

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Question 2

(c) Based on the data in Table 1, **describe** the relationship between the level of CO_2 and the average number of mitochondria per unit area of a cell.

Question 2

2023 ▪ Q2

Elevated levels of CO_2 increase the rate of photosynthesis and growth in plants. Scientists studying the mechanisms involved in these increases examined a variety of species and found that when plants are exposed to elevated levels of CO_2, there is an increase in the number of chloroplasts per cell. To investigate whether the elevated levels of CO_2 have a similar effect on the number of mitochondria in plant cells, the scientists then selected six of these species to quantify the number of mitochondria per cell when the plants were exposed to both normal and elevated levels of CO_2 (Table 1).

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Question 2

(d) The leaves of a particular plant species are typically green, but scientists notice a plant in which the leaves have white stripes. They determine that the stripes result from a mutation in mitochondrial DNA that interferes with the development of chloroplasts. The scientists crossed plants using pollen from the plant with white-striped leaves and ovules from a plant with green leaves. **Predict** the phenotype(s) of the leaves of offspring produced from this cross. Provide reasoning to **justify** your prediction. **Explain** why plants with the same genotype are able to differ in the structure and/or number of certain organelles in response to changes in atmospheric levels of CO_2.

Solution 2

(a)

Mark scheme

- The inner mitochondrial membrane houses the electron transport chain components and ATP synthase, i.e., it is the site of oxidative phosphorylation. By separating the intermembrane space from the matrix, it allows a proton ($H+$) gradient to be established across it as electrons move through the ETC; this gradient then drives ATP synthesis via chemiosmosis through ATP synthase.

Solution 2

(b) Mark scheme

- Construct a bar graph (or modified/grouped bar graph) with the six plant species (1–6) on the x-axis and average number of mitochondria (per 100 μm^2 of cell area) on the y-axis, with appropriate axis labels/units and a legend distinguishing normal-CO2 bars from elevated-CO2 bars. Plot each species' two data points (normal and elevated CO2) at the values given in Table 1, each with error bars representing $\pm 2SE(\bar{x})$ as listed in the table (e.g., species 1: 1.0 ± 0.10 normal, 1.6 ± 0.10 elevated; species 6: 1.3 ± 0.15 normal, 2.4 ± 0.22 elevated). Points earned for: appropriate labeling; using a bar/modified bar graph format; correctly plotting the data points and error bars. Determine which species show a difference in mitochondria number between normal and elevated CO2: all six species (1

Solution 2

through 6) show a difference — every species has a higher (non-overlapping, given the error bars) mitochondria count under elevated CO2 than under normal CO2.

Solution 2

(c)

Mark scheme

- There is a positive relationship between CO2 level and the average number of mitochondria per unit cell area: the number of mitochondria is greater under elevated CO2 conditions than under normal CO2 conditions (across the species examined).

Solution 2

(d) Mark scheme

- Prediction: the offspring from this cross (pollen from the white-striped-leaf plant $\times$ ovules from the green-leaf plant) will all have green leaves (will not have white stripes). Justification: mitochondria (and mitochondrial DNA) are maternally inherited — they are transferred to offspring through the ovule/egg cytoplasm, not through the pollen — so all offspring inherit the mitochondrial genotype of the green (ovule-producing) parent, whose mitochondria are functional for chloroplast development. Separately, explain why plants with the same (nuclear) genotype can still differ in the structure and/or number of certain organelles in response to CO2: because changes in CO2 levels (the environment) affect the expression of certain genes — i.e., environmentally-induced differences in gene expression (not

Solution 2

differences in genotype) drive differences in organelle structure/number, such as the increase in mitochondria number seen at elevated CO2.

Question 2

2018 ▪ Q2

Question 2

[Figure 1: Diagram of cellular response to infection by pathogenic bacteria. At the top is a double-line "Cell Membrane" with two small vertical channel/pore segments embedded in it, arrows converging up into the pore from below (labeled with circled "3"), and one arrow pointing up and out through the membrane at the far left (from the Active Interleukin). Below the membrane, left region: "Inactive Interleukin" (drawn as a triangle attached to an oval) is converted via a step labeled circled "2" into "Active Interleukin" (an oval with a triangle nearby, arrow pointing up out of the membrane, showing the active portion is released from the cell). Middle-right region: "N-terminal Gasdermin" (a small rectangle/bracket shape) sits just below the membrane pore; "Gasdermin" (a rectangle attached to a filled black square) is converted via a step labeled circled "3" into N-terminal Gasdermin, which is shown assembling into the membrane pore. Bottom-left region: "Inactive Caspase-1" (a filled circle attached to an oval) is converted via a step labeled circled "1", triggered by "Bacterial Infection" (arrow pointing up into step 1), into "Active Caspase-1" (an oval with a filled circle nearby); Active

Question 2

Caspase-1 then has arrows pointing to both step 2 (activating Interleukin) and step 3 (activating Gasdermin). Caption: "Figure 1. Cellular response to infection by pathogenic bacteria."]

Question 2

Some pathogenic bacteria enter cells, replicate, and spread to other cells, causing illness in the host organism. Host cells respond to these infections in a number of ways, one of which involves activating particular enzymatic pathways (Figure 1). Cells normally produce a steady supply of inactive caspase-1 protein. In response to intracellular pathogens, the inactive caspase-1 is cleaved and forms an active caspase-1 (step 1). Active caspase-1 can cleave two other proteins. When caspase-1 cleaves an inactive interleukin (step 2), the active portion of the interleukin is released from the cell. An interleukin is a signaling molecule that can activate the immune response. When caspase-1 cleaves gasdermin (step 3), the N-terminal portions of several gasdermin proteins associate in the cell membrane to form large, nonspecific pores.

Question 2

Researchers created the model in Figure 1 using data from cell fractionation studies. In the experiments, various parts of the cell were separated into fractions by mechanical and chemical methods. Specific proteins known to be located in different parts of the cell were used as markers to determine the location of other proteins. The table below shows the presence of known proteins in specific cellular fractions.

CELL FRACTIONS CONTAINING DIFFERENT CELLULAR PROTEINS

	Aconitase (Krebs cycle protein)	**DNA poly-merase**	**GAPDH (glycolytic protein)**	**Sodium-potassium pump**	**NF-κB (Immune response protein)**
Whole cell sample	+	+	+	+	+
Fraction 1	+				
Fraction 2		+			+
Fraction 3			+		+
Fraction 4				+	

Question 2

- = presence of protein

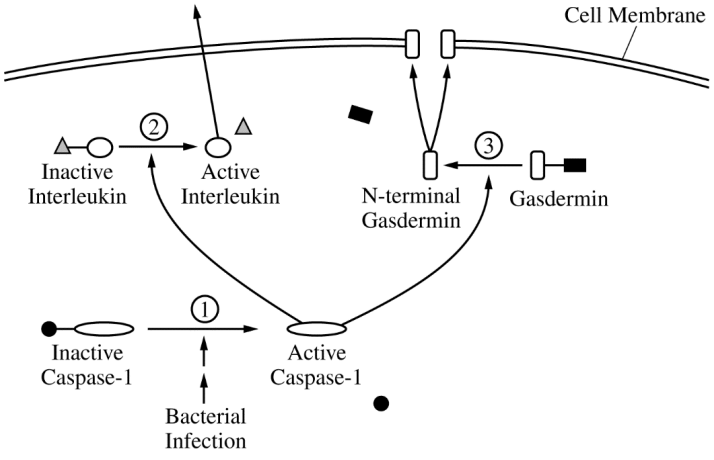
(a) Describe the effect of inhibiting step 3 on the formation of pores AND on the release of interleukin from the cell.

Question 2

CELL FRACTIONS CONTAINING DIFFERENT CELLULAR PROTEINS

	Aconitase (Krebs cycle protein)	DNA polymerase	GAPDH (glycolytic protein)	Sodium-potassium pump	NF-κB (Immune response protein)
Whole cell sample	+	+	+	+	+
Fraction 1	+				
Fraction 2		+			+
Fraction 3			+		+
Fraction 4				+	
+ = presence of protein					

Question 2


Cell Membrane
2
Inactive
Interleukin
Active
Interleukin
3
N-terminal
Gasdermin
Gasdermin
1
Inactive
Caspase-1
Active
Caspase-1
Bacterial
Infection

Question 2

2018 ▪ Q2

Question 2

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Question 2

then has arrows pointing to both step 2 (activating Interleukin) and step 3 (activating Gasdermin). Caption: “Figure 1. Cellular response to infection by pathogenic bacteria.”]

Question 2

Some pathogenic bacteria enter cells, replicate, and spread to other cells, causing illness in the host organism. Host cells respond to these infections in a number of ways, one of which involves activating particular enzymatic pathways (Figure 1). Cells normally produce a steady supply of inactive caspase-1 protein. In response to intracellular pathogens, the inactive caspase-1 is cleaved and forms an active caspase-1 (step 1). Active caspase-1 can cleave two other proteins. When caspase-1 cleaves an inactive interleukin (step 2), the active portion of the interleukin is released from the cell. An interleukin is a signaling molecule that can activate the immune response. When caspase-1 cleaves gasdermin (step 3), the N-terminal portions of several gasdermin proteins associate in the cell membrane to form large, nonspecific pores.

Question 2

Researchers created the model in Figure 1 using data from cell fractionation studies. In the experiments, various parts of the cell were separated into fractions by mechanical and chemical methods. Specific proteins known to be located in different parts of the cell were used as markers to determine the location of other proteins. The table below shows the presence of known proteins in specific cellular fractions.

CELL FRACTIONS CONTAINING DIFFERENT CELLULAR PROTEINS

	Aconitase (Krebs cycle protein)	**DNA poly-merase**	**GAPDH (glycolytic protein)**	**Sodium-potassium pump**	**NF-κB (Immune response protein)**
Whole cell sample	+	+	+	+	+
Fraction 1	+				
Fraction 2		+			+
Fraction 3			+		+
Fraction 4				+	