The following information applies to all parts.

1. Molecules known as dinucleoside polyphosphates, a type of nucleotide, are signaling molecules that accumulate in plant cells during dry or stressful conditions.

Part A

Describe the three structural components of a nucleotide.

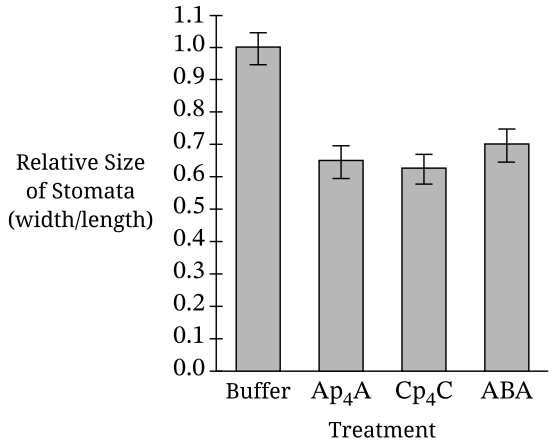
The following information applies to parts B, C, and D.

Stomata are pores on the surface of leaves that open when exposed to light and regulate the flow of carbon dioxide, oxygen, and water vapor in and out of a plant. In response to dry environmental conditions, many plants close their stomata, which reduces water loss.

Scientists hypothesized that the dinucleoside polyphosphates Ap_4A and Cp_4C bind to DORN1 receptors on the plasma membrane of plant cells and initiate signaling cascades that cause stomata to close. The scientists exposed plants to light to open the stomata and then placed samples of the leaves in buffer alone or in buffer containing one of three different compounds: Ap_4A, Cp_4C, or abscisic acid (ABA), a molecule that causes stomata to close.

The scientists measured the size of the stomata in each sample and calculated their sizes relative to the size of the stomata in the sample kept in buffer alone, as shown in Figure 1.

Figure 1. Effect of Ap_4A, Cp_4C, and ABA on Relative Stomatal Size (Error Bars Represent $\pm SE_{\bar{x}}$)



Part B

i. **Identify** the dependent variable in the scientists' first experiment.

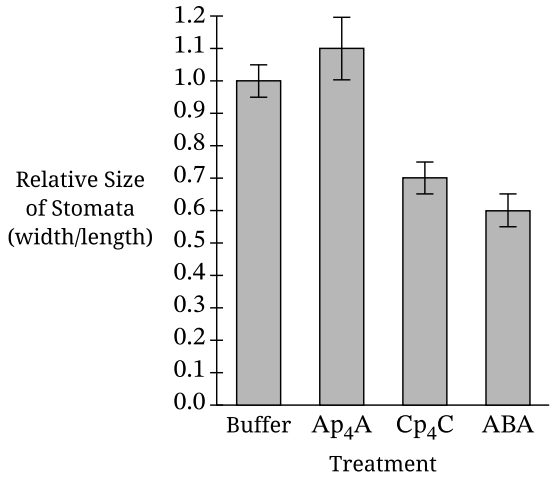
ii. Based on Figure 1, **describe** the relative size of the stomata in the Cp_4C treatment group as compared with the size of the stomata in the group treated with buffer alone.

iii. **Justify** the use of buffer alone as a control in the scientists' experiments.

Part C

In a second experiment, the scientists used plants that were identical to those in the first experiment except that the gene encoding the DORN1 receptor was mutated. The scientists repeated the procedure of the first experiment. Their results are shown in Figure 2.

Figure 2. Effect of Ap_4A, Cp_4C, and ABA on Relative Stomatal Size in DORN1 Mutants (Error Bars Represent $\pm SE_{\bar{x}}$)



i. **Justify** the scientists' treating one sample of leaves with ABA in the experiments.

ii. Based on Figure 2, **describe** the difference between the effects of Ap_4A and Cp_4C treatments on the size of stomata in plants with mutated DORN1 receptors.

iii. Activation of DORN1 receptors induces plant cells to produce certain molecules that cause the stomata to close. Based on the data in Figures 1 and 2 for cells treated with Ap_4A, **predict** the relative production of the molecules by DORN1-mutated cells in comparison to the production by nonmutated cells.

Part D

The DORN1 receptor transmits signals that result in an increase in the transcription of genes involved in plant defenses. The scientists then developed DORN1-mutant plants in which the DORN1 receptor lacked most of its intracellular domain.

i. In cells homozygous for this mutation, **predict** the effect of Ap_4A treatment on transcription of the genes involved in plant defenses relative to the effect of Ap_4A on nonmutated cells.

ii. **Justify** your prediction.

The following information applies to all parts.

2. 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.

Part A

Describe one location where ribosomes are found in eukaryotic cells.

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 ($AGO2^{-/-}$)

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 $\pm$ 0.1	0.9 $\pm$ 0.4	1.5 $\pm$ 0.5
Gene *H*	1.0 $\pm$ 0.1	2.0 $\pm$ 0.1	3.0 $\pm$ 0.4

Part 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.

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.

Part 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.

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.

Part D

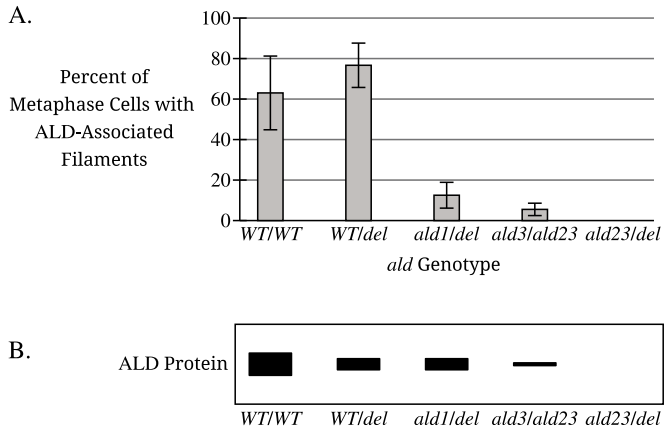
i. The scientists claim that siRNA binding and AGO2 cleavage of mRNAs play a greater role in the regulation of Gene *H* expression than in the regulation of Gene *G* expression. Based on the table, **support** the scientists' claim.

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.

6. The *ald* gene of fruit flies encodes the ALD protein, which is associated with both the centromeres of chromosomes and protein filaments produced during meiosis. In the absence of functional ALD proteins, gamete-producing cells enter anaphase I before homologous chromosomes are correctly aligned. As a result, the gametes produced do not contain the correct numbers of chromosomes.

Scientists generated four mutations in the *ald* gene: *ald1*, *ald3*, *ald23*, and *del*, which was a deletion of the gene. To study the role of the ALD protein in meiosis, scientists used gameteforming metaphase cells from groups of flies with different *ald* genotypes. Some of the flies were homozygous for the wild-type allele of *ald*: *WT/WT*. Other flies were heterozygous for different *ald* alleles: *WT/del*; *ald1/del*; *ald3/ald23*; *ald23/del*. The scientists measured the percent of metaphase cells that contained ALD-associated filaments (Figure 1A) and the amount of ALD protein produced by each of the cell types (Figure 1B).

Figure 1. (A) The average percent of gamete-forming metaphase cells that contained filaments associated with ALD and (B) the amount of ALD protein produced by each cell type. A thicker band indicates a greater amount of ALD protein.



A. Based on Figure 1A, **identify** the fly genotype in which the average percent of metaphase cells with ALD-associated filaments is close to 12%.

B. Based on Figure 1B, **describe** the difference in ALD protein production between gamete-forming metaphase cells of flies with the genotype *ald3/ald23* and flies with the genotype *ald23/del*.

C. Scientists hypothesize that gamete-forming metaphase cells can produce a normal amount of ALD-associated filaments even when they produce about half as much ALD protein as the wild-type cells produce. Use the data in Figures 1A and 1B to **support** the scientists' hypothesis.

D. For gamete-forming metaphase cells of the *WT/del* and *ald1/del* flies, **explain** why the phenotypes observed in Figure 1A differ even though the amount of ALD protein produced (Figure 1B) does not.

STOP

END OF EXAM

6. 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).

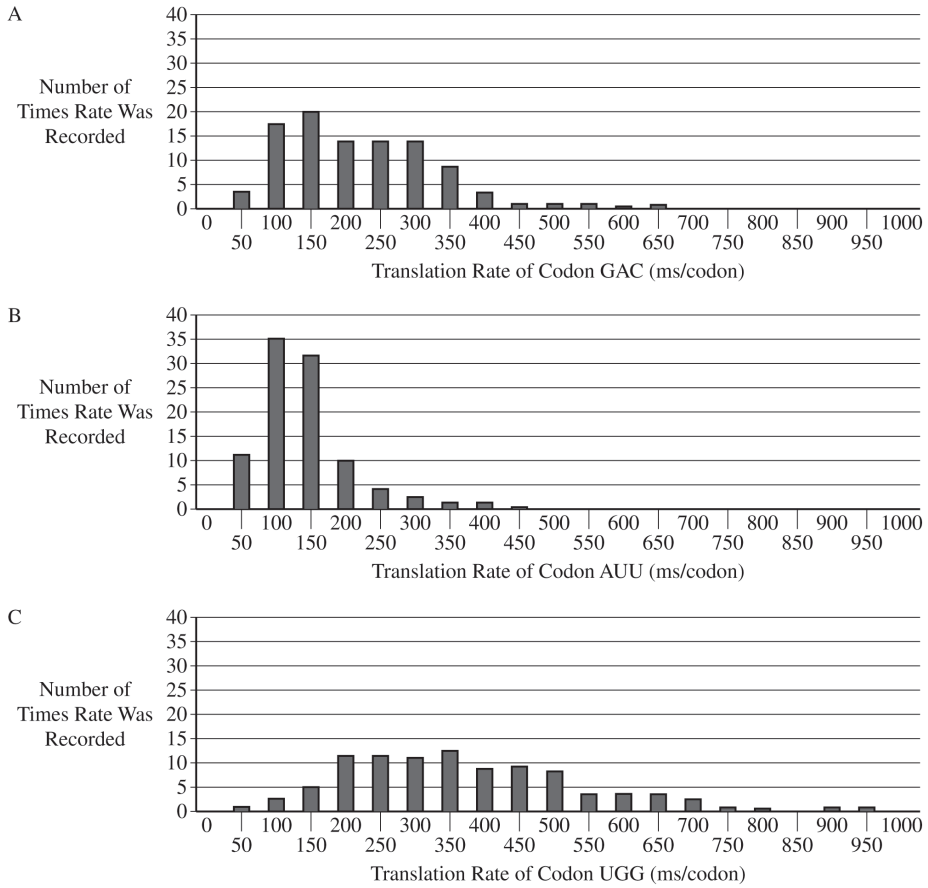


Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG

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

Write your responses to this question only on the designated pages in the separate Free Response booklet.

If there are multiple parts to this question, write the part letter with your response.

STOP

END OF EXAM

6. Housekeeping genes encode proteins involved in universally important processes such as transcription, translation, and glycolysis. Because these genes appear to be expressed in all cells at constant levels, the expression of housekeeping genes is often used as a control when comparing how the expression of other genes varies under different conditions.

   Researchers studying the effect of pesticides on declining bee populations wanted to determine whether the expression of four housekeeping genes (*GAPDH*, *RPL32*, *RPS5*, and *TBP-AF*) was in fact constant in bees across different variables. The researchers collected samples of mRNA for each of the four genes and compared how their expression varied across the developmental stage of the bee, the sex of the bee, and the cell type from which the sample was taken. The mRNA from the samples was reverse transcribed to produce DNA copies of each gene. PCR was then used to amplify the DNA, and the Cq value was determined. The Cq value is the number of PCR cycles needed to produce a specified number of DNA copies. A high Cq value for a sample indicates the gene was expressed at a low level.

   To analyze whether any of the examined variables affected expression of the housekeeping genes, researchers examined the range of Cq values for each gene in response to each variable. Genes with a wide range of Cq values were determined to be affected by the variable, while genes with a narrow range of Cq values were determined to be unaffected by the variable.

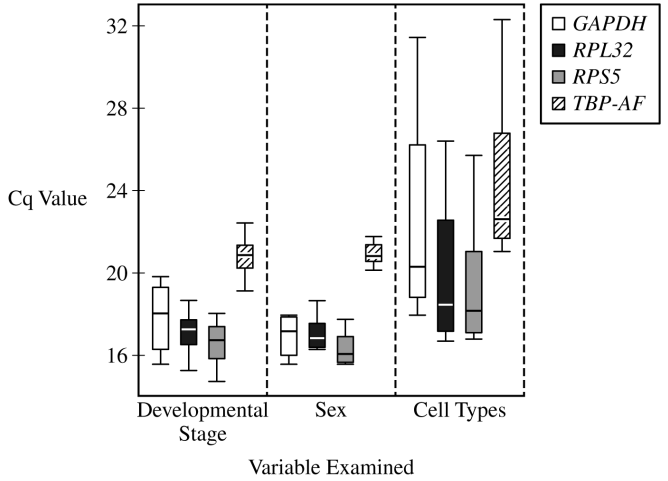


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

(a) Based on the data in Figure 1, **identify** the gene that had the lowest median Cq value when bees of different developmental stages were compared.

(b) The Cq value is inversely proportional to the amount of mRNA from that gene in the starting sample. Based on the data in Figure 1, **identify** the gene that has the lowest level of gene expression regardless of variable.

(c) The scientists investigated the effect of pesticides on the expression of other genes in one cell type of a group of bees containing males and females of the same developmental stage. They hypothesized that *TBP-AF* would serve as the best control gene for this experiment. Use the data to **evaluate** their hypothesis.

(d) **Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

STOP

END OF EXAM

6. The small invertebrate krill species *Thysanoessa inermis* is adapted to cold (4°C) seawater. Over the past ten years, there has been a gradual increase in the water temperature of the krill's habitat. A sustained increase in water temperature may ultimately affect the ability of the krill to survive.

One effect of higher temperatures is protein misfolding within cells. Krill have several *hsp* genes that code for heat-shock proteins (HSPs). These proteins help prevent protein misfolding or help to refold proteins to their normal shapes.

Scientists conducted experiments on *T. inermis* to detect changes in the expression of *hsp* genes when the krill were exposed to temperatures above 4°C. An experimental group of krill was maintained in tanks with 4°C seawater and then placed into tanks with 10°C seawater for approximately three hours. The krill were then given a six-hour recovery period in the 4°C seawater tanks. A control group of krill was moved from a tank of 4°C seawater to another tank of 4°C seawater for approximately three hours and then returned to the original tank. The scientists analyzed *hsp* gene expression by measuring the concentrations of three mRNAs (I, II, III) transcribed from certain *hsp* genes in both the heat-shocked krill (Figure 1) and the control krill. For the control krill, no transcription of the *hsp* genes was detected throughout the test period (data not shown).

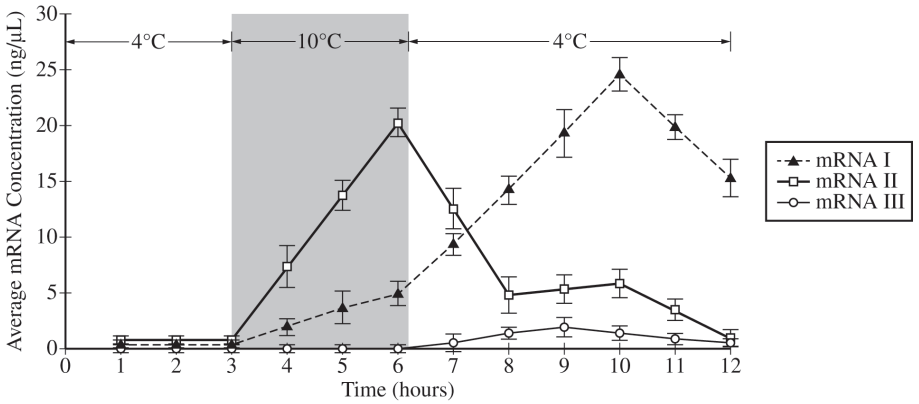


Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from *hsp* genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$.

(a) **Identify** the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment.

(b) **Describe** the trend in the average concentration of mRNA I throughout the experiment.

(c) The scientists hypothesized that the heat-shock protein (HSP) translated from mRNA I plays a greater role in refolding proteins than does the HSP translated from mRNA II. Use the data to **support** the hypothesis.

(d) mRNAs I and II are transcribed from the same gene. **Explain** how a cell can produce two different mRNAs from the same gene.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

STOP

END OF EXAM

7. A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

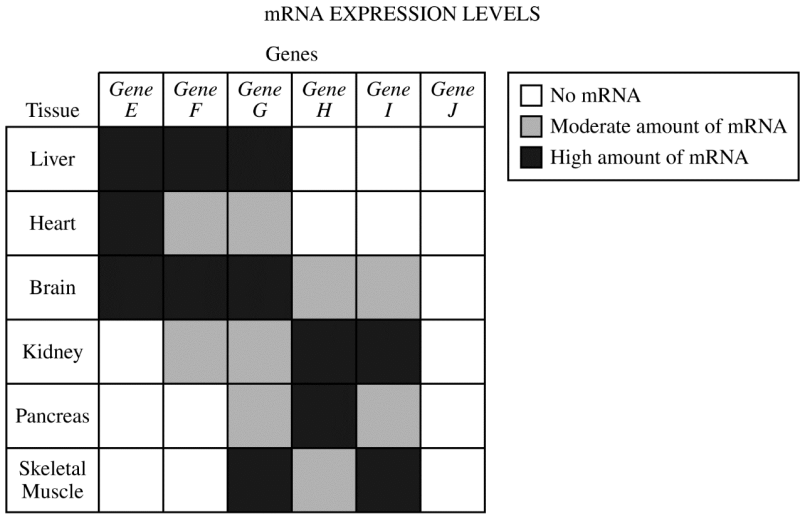


Figure 1. mRNA expression levels of six genes

(a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.

(b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.

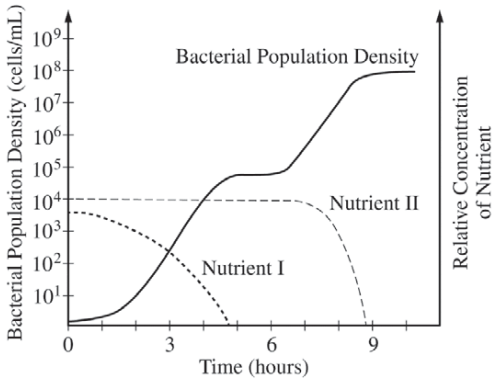


Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II)

2. Bacteria can be cultured in media with a carefully controlled nutrient composition. The graph above shows the growth of a bacterial population in a medium with limiting amounts of two nutrients, I and II.

   (a) **Estimate** the maximum population density in $\frac{\text{cells}}{\text{mL}}$ for the culture. Using the data, **describe** what prevents further growth of the bacterial population in the culture.

   (b) Using the data, **calculate** the growth rate in $\frac{\text{cells}}{\text{mL}\times\text{hour}}$ of the bacterial population between hours 2 and 4.

   (c) **Identify** the preferred nutrient source of the bacteria in the culture over the course of the experiment. Use the graph to **justify** your response. **Propose** ONE advantage of the nutrient preference for an individual bacterium.

   (d) **Describe** how nutrient I most likely regulates the genes for metabolism of nutrient I and the genes for metabolism of nutrient II. **Provide** TWO reasons that the population does not grow between hours 5 and 6.

AP Biology: **2015**

7. Smell perception in mammals involves the interactions of airborne odorant molecules from the environment with receptor proteins on the olfactory neurons in the nasal cavity. The binding of odorant molecules to the receptor proteins triggers action potentials in the olfactory neurons and results in transmission of information to the brain. Mammalian genomes typically have approximately 1,000 functional odorant-receptor genes, each encoding a unique odorant receptor.

   (a) **Describe** how the signal is transmitted across the synapse from an activated olfactory sensory neuron to the interneuron that transmits the information to the brain.

   (b) **Explain** how the expression of a limited number of odorant receptor genes can lead to the perception of thousands of odors. Use the evidence about the number of odorant receptor genes to **support** your answer.