Past-paper walk-through

Regulation of Gene Expression ▪ 6.5

eXercise

Questions in this set

- 2026 Q1
- 2026 Q2
- 2025 Q6
- 2024 Q6
- 2023 Q6
- 2021 Q6
- 2019 Q7
- 2016 Q2
- 2015 Q7

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

2026 ▪ Q1

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

Question 1

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 $\pm SE_{\bar{x}}$)
[Bar graph; y-axis "Relative Size of Stomata (width/length)" from 0.0 to 1.1 in increments of 0.1; x-axis "Treatment" with four bars: Buffer, Ap_4A, Cp_4C, ABA. Approximate bar heights with error bars: Buffer $\approx 1.0 \pm 0.05$; $Ap_4A \approx 0.65 \pm 0.05$; $Cp_4C \approx 0.62 \pm 0.05$; ABA $\approx 0.70 \pm 0.05$.]
(a) Describe the three structural components of a nucleotide.

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2026 ▪ Q1

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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.

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(b)(i) Identify the dependent variable in the scientists' first experiment.

(b)(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.

(b)(iii) Justify the use of buffer alone as a control in the scientists' experiments.

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2026 ▪ Q1

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Question 1

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(c)(i) 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 $\pm SE_{\bar{x}}$)

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[Bar graph; y-axis "Relative Size of Stomata (width/length)" from 0.0 to 1.2 in increments of 0.1; x-axis "Treatment" with four bars: Buffer, Ap_4A, Cp_4C, ABA. Approximate bar heights with error bars: Buffer $\approx 1.0 \pm 0.05$; $Ap_4A \approx 1.1 \pm 0.1$; $Cp_4C \approx 0.70 \pm 0.05$; ABA $\approx 0.60 \pm 0.05$.]

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

(c)(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.

(c)(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.

Question 1

2026 ▪ Q1

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Question 1

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(d)(i) 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.

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.

Question 1

(d)(ii) Justify your prediction.

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

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	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

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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

(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.

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2026 ▪ Q2

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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 6

2025 ▪ Q6

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

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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.
[Panel A: Bar graph; y-axis "Percent of Metaphase Cells with ALD-Associated Filaments" from 0 to 100 in increments of 20. x-axis "*ald* Genotype" with five bars labeled "WT/WT", "WT/del", "ald1/del", "ald3/ald23", "ald23/del". Approximate values with error bars: WT/WT ≈ 63 (error bar roughly 45-80), WT/del ≈ 77 (error bar roughly 65-88), ald1/del ≈ 13 (error bar roughly 5-20), ald3/ald23 ≈ 6 (small error bar), ald23/del ≈ 1 (negligible, near 0).
Panel B: Gel-blot style diagram labeled "ALD Protein" showing bands of varying thickness for the same five genotypes in the same order (WT/WT, WT/del, ald1/del,

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ald3/ald23, ald23/del): WT/WT shows a thick solid band; WT/del shows a medium-thick band; ald1/del shows a medium-thick band similar to WT/del; ald3/ald23 shows a thin band; no band is shown for ald23/del (or an extremely faint/absent line).]

(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.

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(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.

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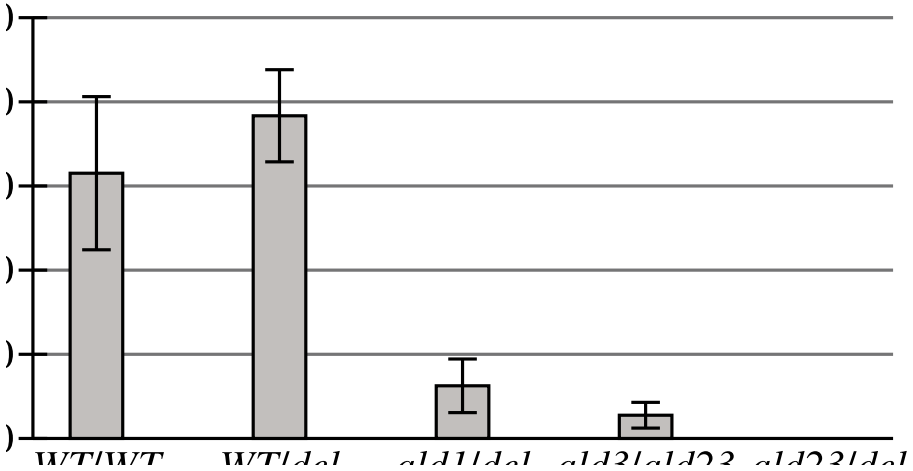

Solution 6

(a)

Mark scheme

- The genotype ald1/del has an average of about 12% of metaphase cells with ALD-associated filaments, based on Figure 1A.

Solution 6

(b)

Mark scheme

- More ALD protein is produced by ald3/ald23 cells than by ald23/del cells (Figure 1B shows a thin but visible band for ald3/ald23, while ald23/del shows little to no detectable band) — equivalently, ald23/del cells produce little to no ALD protein compared with ald3/ald23 cells.

Solution 6

(c)

Mark scheme

- The WT/del cells produce about half as much ALD protein as WT/WT cells (Figure 1B, a thinner band), yet show no substantial difference from WT/WT in the percent of metaphase cells with ALD-associated filaments (Figure 1A, roughly 76% vs 63%, with overlapping error bars) — this comparison supports the hypothesis that gamete-forming metaphase cells can produce a normal amount of ALD-associated filaments with about half the normal ALD protein.

Solution 6

(d)

Mark scheme

- The phenotypes differ because it is protein function, not quantity, that differs: WT/del flies produce ALD protein from their functional WT allele, which is enough to generate a wild-type phenotype (~76% of cells with filaments), whereas ald1/del flies produce a similar total amount of ALD protein (Figure 1B) but it comes from the nonfunctional/impaired ald1 allele, so it cannot properly support filament formation, giving a much lower percentage of cells with ALD-associated filaments (~12%, Figure 1A).

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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

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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

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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

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

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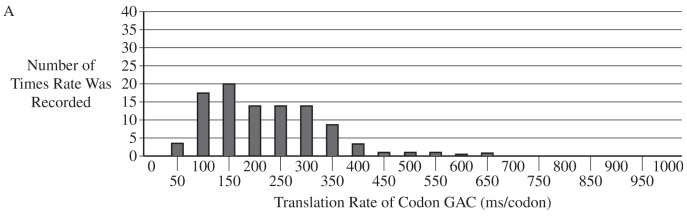
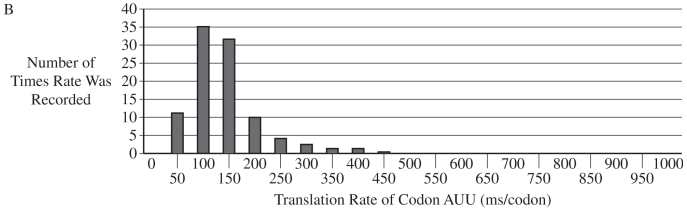

A
Number of Times Rate Was Recorded
40
35
30
25
20
15
10
5
0
0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1000
Translation Rate of Codon GAC (ms/codon)


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

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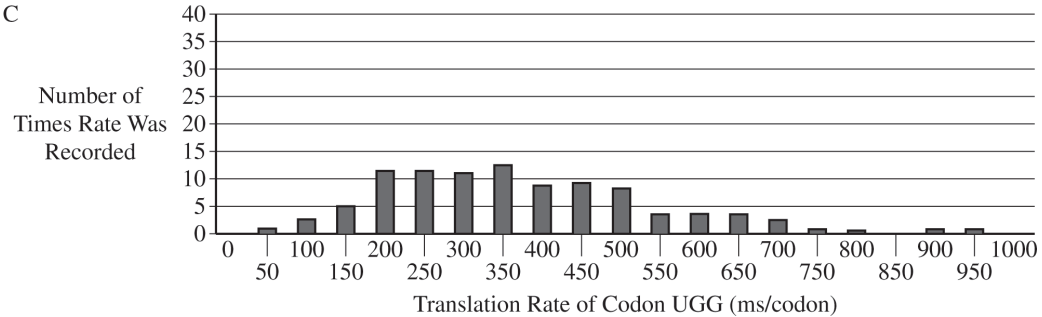
C


Number of Times Rate Was Recorded
40
35
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20
15
10
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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 6

2023 ▪ Q6

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

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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, a box-and-whisker plot with the y-axis labeled "Cq Value" ranging from 16 to 32 (gridlines at 16, 20, 24, 28, 32) and the x-axis labeled "Variable Examined", divided by dashed vertical lines into three groups: "Developmental Stage", "Sex", and "Cell Types". Each group contains four box plots, one per gene, per the legend: open square = *GAPDH*, filled black square = *RPL32*, gray square = *RPS5*,

Question 6

hatched/crosshatched square = *TBP-AF*. Developmental Stage group: *GAPDH* box spans roughly 15.5-19.5 (median ~17.5); *RPL32* box spans roughly 16.5-18.5 (median ~17.5); *RPS5* box spans roughly 15.5-18 (median ~16.5); *TBP-AF* box spans roughly 19.5-22 (median ~20.5). Sex group: *GAPDH* box spans roughly 17-18.5 (median ~17.5); *RPL32* box spans roughly 16.5-18.5 (median ~17.5); *RPS5* box spans roughly 15.5-17 (median ~16); *TBP-AF* box spans roughly 19.5-21.5 (median ~20.5). Cell Types group: *GAPDH* box spans roughly 17.5-31.5 (median ~20.5), the widest range of all boxes shown; *RPL32* box spans roughly 16.5-26 (median ~18.5); *RPS5* box spans roughly 16.5-25.5 (median ~18); *TBP-AF* box spans roughly 21-32 (median ~23).]

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.

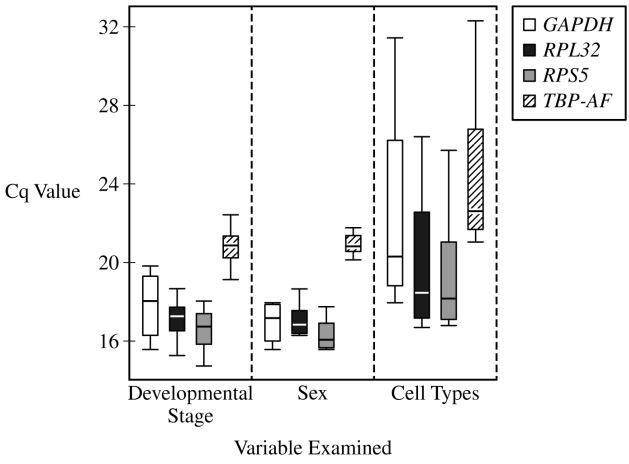
Question 6

(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.

Question 6


32
28
24
20
16
Cq Value
GAPDH
RPL32
RPS5
TBP-AF
Developmental Stage
Sex
Cell Types
Variable Examined

Solution 6

(a)

Mark scheme

- RPS5 had the lowest median Cq value when bees of different developmental stages were compared (per the box plot in Figure 1).

Solution 6

(b)

Mark scheme

- TBP-AF has the lowest level of gene expression regardless of variable. Because Cq value is inversely proportional to the amount of starting mRNA, and TBP-AF shows the highest Cq values across all three variables examined (developmental stage, sex, and cell type) in Figure 1, it corresponds to the lowest mRNA/expression level overall.

Solution 6

(c)

Mark scheme

- The hypothesis that TBP-AF is the best control gene for this experiment (comparing males vs. females within one cell type/developmental stage) is supported: in the "Sex" panel of Figure 1, TBP-AF has the smallest (narrowest) range of Cq values / most constant expression when comparing sexes, meaning its expression is unaffected by the sex variable — the property required of a good control gene.

Solution 6

(d)

Mark scheme

- Expression of a gene such as GAPDH can differ between cell types within the same bee because different cell types contain different levels/types of transcription factors, which bind regulatory DNA sequences differently in each cell type and therefore regulate (activate or repress) the expression of genes like GAPDH differently from one cell type to another, even though all cells share the same genome.

Question 6

2021 ▪ Q6

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

Question 6

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: Line graph, "Average mRNA Concentration (ng/μL)" (y-axis, 0 to 30) vs. "Time (hours)" (x-axis, 0 to 12), with a shaded region from hour 3 to hour 6 marking the 10°C exposure period (labeled "4°C" from 0-3, "10°C" from 3-6 shaded grey, "4°C" from 6-12). Three curves: mRNA I (filled triangles, dashed line) stays near 0 from hours 0-3, rises slowly to ~2 at hour 4, ~3.5 at hour 5, ~5 at hour 6, then rises steeply to ~9.5 at hour 7, ~14.5 at hour 8, ~19.5 at hour 9, peaks at ~25 at hour 10, declines to ~20 at hour 11, ~15.5 at hour 12; mRNA II (open squares, solid line) stays

Question 6

near 0 from hours 0-2, rises to ~2 at hour 3, ~7.5 at hour 4, ~13.5 at hour 5, peaks at ~20 at hour 6, then declines to ~12.5 at hour 7, ~5 at hour 8, ~5.5 at hour 9, ~6 at hour 10, ~3.5 at hour 11, ~1 at hour 12; mRNA III (open circles, solid line) stays near 0 throughout hours 0-7, rises slightly to ~1 at hour 8, ~2 at hour 9, ~1.5 at hour 10, ~1 at hour 11, back to ~0 at hour 12. Error bars represent $\pm 2SE_{\bar{x}}$ on all curves. Caption: "Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from hsp genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$."]

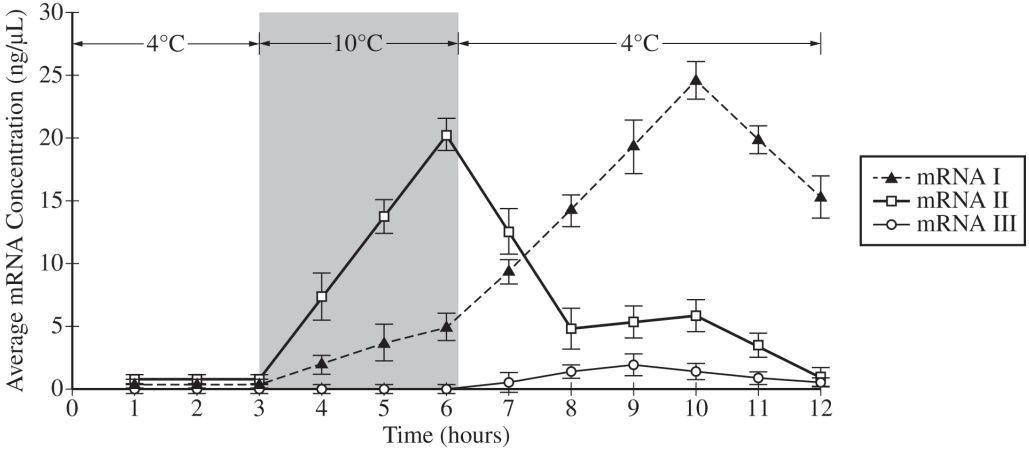
(a) Identify the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment.

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

Question 6

(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.

Question 6


4°C
10°C
4°C
Average mRNA Concentration (ng/μL)
Time (hours)
0
1
2
3
4
5
6
7
8
9
10
11
12
0
5
10
15
20
25
30
mRNA I
mRNA II
mRNA III

Solution 6

(a)

Mark scheme

- The hsp mRNA with the slowest rate of concentration increase in response to heat-shock treatment is mRNA III.

Solution 6

(b)

Mark scheme

- Trend in average concentration of mRNA I throughout the experiment: no change in concentration from hour 1 to 3; concentration increased (slightly) between hours 3 and 6 (during the heat shock); concentration increased at a greater rate from hours 6 to 10 (for about 4 hours after the heat shock ended); concentration then decreased after hour 10.

Solution 6

(c)

Mark scheme

- Data supporting the hypothesis that the HSP from mRNA I plays a greater role in refolding proteins than the HSP from mRNA II: mRNA I is still expressed at a high level after the heat-shock period (peaking around hour 10, well after the 10°C exposure ends at hour 6), while mRNA II levels decrease after the heat shock — i.e., right when misfolded proteins would need to be refolded, mRNA I (and its protein) remains elevated while mRNA II does not.

Solution 6

(d)

Mark scheme

- How a cell can produce two different mRNAs (I and II) from the same gene (accept any): the cell expresses different exons/performs alternative splicing; the cell uses different transcription termination sites (poly(A) sites); or the cell uses different promoters.

Question 7

2019 ▪ Q7

mRNA EXPRESSION LEVELS

[Figure 1. mRNA expression levels of six genes — a table with rows Liver, Heart, Brain, Kidney, Pancreas, Skeletal Muscle and columns Gene E, Gene F, Gene G, Gene H, Gene I, Gene J; each cell is shaded white (No mRNA), gray (Moderate amount of mRNA), or black (High amount of mRNA), as follows:

Tissue	**Gene E**	**Gene F**	**Gene G**	**Gene H**	**Gene I**	**Gene J**
Liver	High	High	High	No	No	No
Heart	High	Moderate	Moderate	No	No	No
Brain	High	High	High	Moderate	Moderate	No
Kidney	No	Moderate	Moderate	High	High	No
Pancreas	No	No	Moderate	High	Moderate	No
Skeletal Muscle	No	No	High	Moderate	High	No

]

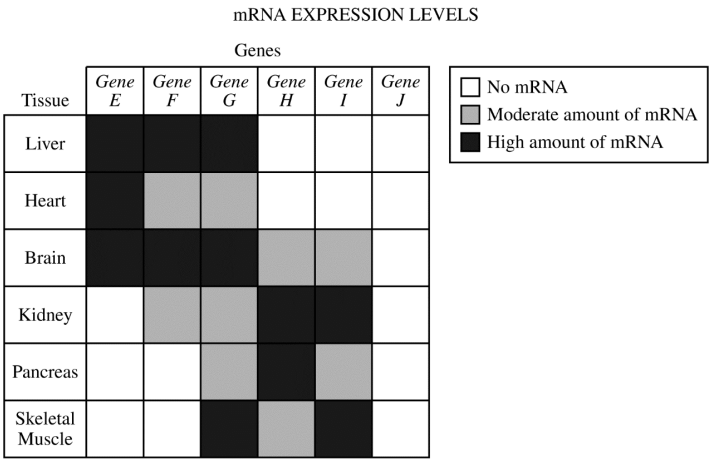
Question 7

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.

(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.

Question 7


mRNA EXPRESSION LEVELS
Genes
Tissue
Gene E
Gene F
Gene G
Gene H
Gene I
Gene J
Liver
Heart
Brain
Kidney
Pancreas
Skeletal Muscle
No mRNA
Moderate amount of mRNA
High amount of mRNA

Solution 7

(a)

Mark scheme

- Identification: Gene G is most likely to encode a protein that is an essential component of glycolysis. [1 point] Reasoning: Gene G's mRNA is the only one of the six genes expressed (present, whether moderate or high) in all six tissues examined (liver, heart, brain, kidney, pancreas, skeletal muscle); since glycolysis is a metabolic pathway that occurs in essentially all cells/tissues (all six tissues), a gene essential for glycolysis would be expected to be expressed everywhere, matching Gene G's universal expression pattern. [1 point]

Solution 7

(b)

Mark scheme

- A tissue can have high gene H mRNA levels but no gene H protein because gene expression is regulated beyond transcription — for example: the mRNA may fail to be exported from the nucleus into the cytoplasm where translation occurs; the mRNA may not be translated at all (e.g., translation is blocked by RNA interference/a regulatory microRNA); or the protein could undergo post-transcriptional/post-translational regulation (e.g., rapid degradation) that prevents functional, detectable protein from accumulating even though the mRNA is present.

Question 2

2016 ▪ Q2

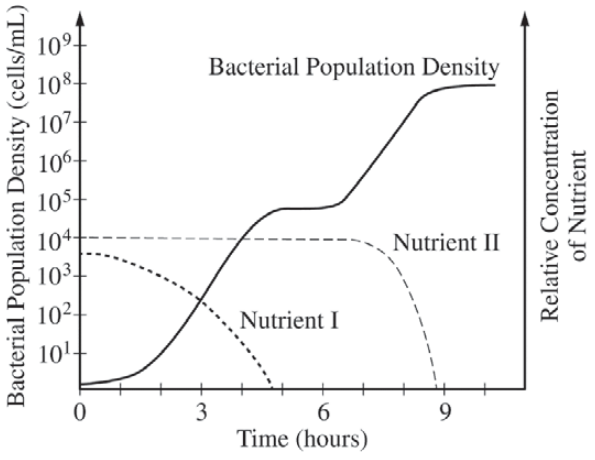
[Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II). Graph with left y-axis "Bacterial Population Density (cells/mL)" on a log scale from 10^1 to 10^9, right y-axis "Relative Concentration of Nutrient" (unlabeled scale), and x-axis "Time (hours)" from 0 to 9 (gridlines at 3, 6, 9). A solid curve labeled "Bacterial Population Density" starts near 10^1 at $t = 0$, rises steeply to about 10^4 by $t \approx 3$–4, plateaus around $10^{4.5}$–10^5 from about $t = 4$ to $t = 6$, then rises again to about 10^8 by $t = 9$. A dotted curve labeled "Nutrient I" starts high (around $10^{3.7}$ on the relative-concentration scale) at $t = 0$ and declines steadily to near zero by about $t = 5$. A dashed curve labeled "Nutrient II" starts at a high, roughly constant relative concentration (around 10^4 on the same scale) from $t = 0$ to about $t = 6$–7, then declines steeply to near zero by $t = 9$.]

Question 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.

Question 2


Bacterial Population Density (cells/mL)
10^9
10^8
10^7
10^6
10^5
10^4
10^3
10^2
10^1
Bacterial Population Density
Nutrient II
Nutrient I
Relative Concentration of Nutrient
0
3
6
9
Time (hours)

Question 2

2016 ▪ Q2

[Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II). Graph with left y-axis "Bacterial Population Density (cells/mL)" on a log scale from 10^1 to 10^9, right y-axis "Relative Concentration of Nutrient" (unlabeled scale), and x-axis "Time (hours)" from 0 to 9 (gridlines at 3, 6, 9). A solid curve labeled "Bacterial Population Density" starts near 10^1 at $t = 0$, rises steeply to about 10^4 by $t \approx 3$–4, plateaus around $10^{4.5}$–10^5 from about $t = 4$ to $t = 6$, then rises again to about 10^8 by $t = 9$. A dotted curve labeled "Nutrient I" starts high (around $10^{3.7}$ on the relative-concentration scale) at $t = 0$ and declines steadily to near zero by about $t = 5$. A dashed curve labeled "Nutrient II" starts at a high, roughly constant relative concentration (around 10^4 on the same scale) from $t = 0$ to about $t = 6$–7, then declines steeply to near zero by $t = 9$.]

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.

Question 2

(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.

Question 2

2016 ▪ Q2

[Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II). Graph with left y-axis "Bacterial Population Density (cells/mL)" on a log scale from 10^1 to 10^9, right y-axis "Relative Concentration of Nutrient" (unlabeled scale), and x-axis "Time (hours)" from 0 to 9 (gridlines at 3, 6, 9). A solid curve labeled "Bacterial Population Density" starts near 10^1 at $t = 0$, rises steeply to about 10^4 by $t \approx 3$–4, plateaus around $10^{4.5}$–10^5 from about $t = 4$ to $t = 6$, then rises again to about 10^8 by $t = 9$. A dotted curve labeled "Nutrient I" starts high (around $10^{3.7}$ on the relative-concentration scale) at $t = 0$ and declines steadily to near zero by about $t = 5$. A dashed curve labeled "Nutrient II" starts at a high, roughly constant relative concentration (around 10^4 on the same scale) from $t = 0$ to about $t = 6$–7, then declines steeply to near zero by $t = 9$.]

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.

Question 2

(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.

Question 2

2016 ▪ Q2

[Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II). Graph with left y-axis "Bacterial Population Density (cells/mL)" on a log scale from 10^1 to 10^9, right y-axis "Relative Concentration of Nutrient" (unlabeled scale), and x-axis "Time (hours)" from 0 to 9 (gridlines at 3, 6, 9). A solid curve labeled "Bacterial Population Density" starts near 10^1 at $t = 0$, rises steeply to about 10^4 by $t \approx 3$–4, plateaus around $10^{4.5}$–10^5 from about $t = 4$ to $t = 6$, then rises again to about 10^8 by $t = 9$. A dotted curve labeled "Nutrient I" starts high (around $10^{3.7}$ on the relative-concentration scale) at $t = 0$ and declines steadily to near zero by about $t = 5$. A dashed curve labeled "Nutrient II" starts at a high, roughly constant relative concentration (around 10^4 on the same scale) from $t = 0$ to about $t = 6$–7, then declines steeply to near zero by $t = 9$.]

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.

Question 2

(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.

Solution 2

(a)

Mark scheme

- Estimate (1 point): the maximum bacterial population density is approximately 10^8 cells/mL (read from the plateau of the growth curve). Description (1 point): further growth is prevented when both nutrients (nutrient I and nutrient II) are depleted from the medium.

Solution 2

(b)

Mark scheme

- Calculation (1 point): the growth rate of the bacterial population between hours 2 and 4 is 4,995 cells/(mL · hour), obtained from the change in population density (read off the log-scale graph, e.g. roughly from $\sim 10^4$ down toward $\sim 10^{3.6}$ then up past hour 3, College Board's accepted value) divided by the 2-hour time interval; the SG-accepted numeric answer is 4,995 cells/(mL · hour).

Solution 2

(c)

Mark scheme

- Identification (1 point): Nutrient I is the preferred nutrient source. Justification (1 point): when both nutrients are present in the growth medium, only nutrient I is consumed/depleted first; nutrient II is only used after nutrient I is depleted (diauxic growth pattern). Proposed advantage (1 point, any one): the bacterium does not spend energy making enzymes/proteins that the cell doesn't need; it does not have to express all metabolic genes at once; OR the preferred nutrient provides more energy.

Solution 2

(d) Mark scheme

- Description (2 points - both required for full credit): Nutrient I promotes expression of the genes required for metabolism of nutrient I; AND nutrient I represses expression of the genes required for metabolism of nutrient II (catabolite-repression-style regulation, similar to the lac operon). Reasoning (2 points - provide TWO distinct reasons the population does not grow between hours 5 and 6): (1) nutrient I is depleted from the growth medium OR neither nutrient is being consumed at that time; (2) it takes time to produce the proteins/enzymes required to metabolize nutrient II (a lag phase for new gene expression), so growth pauses before resuming once those enzymes are made.

Question 7

2015 ▪ Q7

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.

Solution 7

(a)

Mark scheme

- 1 point. Neurotransmitters are released from the (presynaptic) olfactory sensory neuron and bind to receptors on the (postsynaptic) interneuron, which transmits the signal onward toward the brain.

Solution 7

(b) Mark scheme

- 2 points maximum, credited from only ONE of the following rows (explanation 1 pt + matching support 1 pt). Molecular: Explanation — one odorant molecule can be recognized by more than one odorant receptor, and/or one odorant receptor can bind more than one odorant molecule; Support — the resulting mathematical combinations of receptor activation greatly expand the number of distinguishable odors despite a limited number of receptor genes. CNS Control: Explanation — signals from different receptors are integrated in the brain; Support — multiple interactions among neurons in the brain. Genetic: Explanation — alternate processing/splicing of the pre-mRNA/primary transcript; Support — multiple different receptor proteins can be produced from a single gene.