Unit 6: Gene Expression and Regulation

Topic	Learning Objective(s)
6.1 DNA and RNA Structure	**IST-1.K** Describe the structures involved in passing hereditary information from one generation to the next.
	IST-1.L Describe the characteristics of DNA that allow it to be used as the hereditary material
6.2 Replication	**IST-1.M** Describe the mechanisms by which genetic information is copied for transmission between generations.
6.3 Transcription and RNA Processing	**IST-1.N** Describe the mechanisms by which genetic information flows from DNA to RNA to protein.
6.4 Translation	**IST-1.O** Explain how the phenotype of an organism is determined by its genotype
6.5 Regulation of Gene Expression	**IST-2.A** Describe the types of interactions that regulate gene expression.
	IST-2.B Explain how the location of regulatory sequences relates to their function.
6.6 Gene Expression and Cell Specialization	**IST-2.C** Explain how the binding of transcription factors to promoter regions affects gene expression and/or the phenotype of the organism.
	IST-2.D Explain the connection between the regulation of gene expression and phenotypic differences in cells and organisms.
6.7 Mutations	**IST-2.E** Describe the various types of mutation
	IST-4.A Explain how changes in genotype may result in changes in phenotype.
	IST-4.B Explain how alterations in DNA sequences contribute to variation that can be subject to natural selection.
6.8 Biotechnology	**IST-1.P** Explain the use of genetic engineering techniques in analyzing or manipulating DNA.

Free Response Practice

2022 #6

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 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 $\pm 2SE_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{x}}$ (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.

(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.

2021 #2

Geneticists investigated the mode of inheritance of a rare disorder that alters glucose metabolism and first shows symptoms in adulthood. The geneticists studied a family in which some individuals of generations II and III are known to have the disorder. Based on the pedigree (Figure 1), the geneticists concluded that the disorder arose in individuals II-2 and was caused by a mutation in mitochondrial DNA.

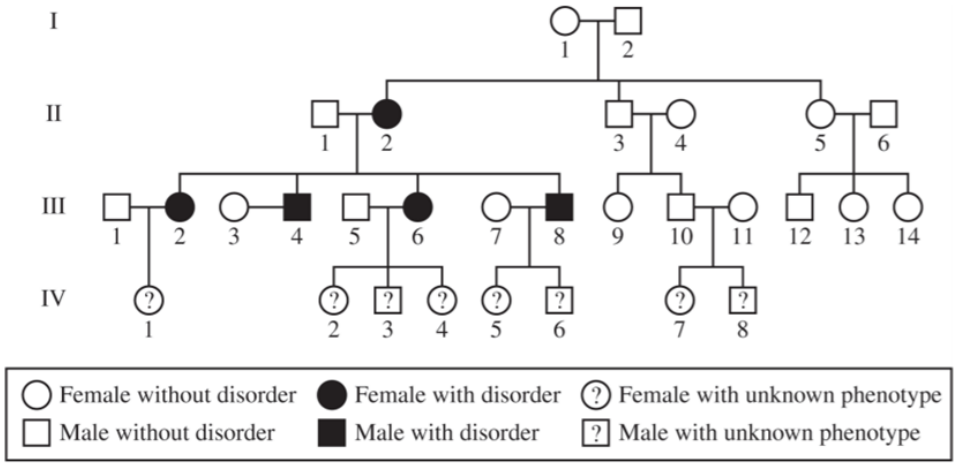


Figure 1. Pedigree of a family showing individuals with the glucose metabolism disorder. A question mark indicates that the phenotype is unknown.

TABLE 1. AVERAGE BLOOD GLUCOSE LEVELS OF INDIVIDUALS IN GENERATION IV

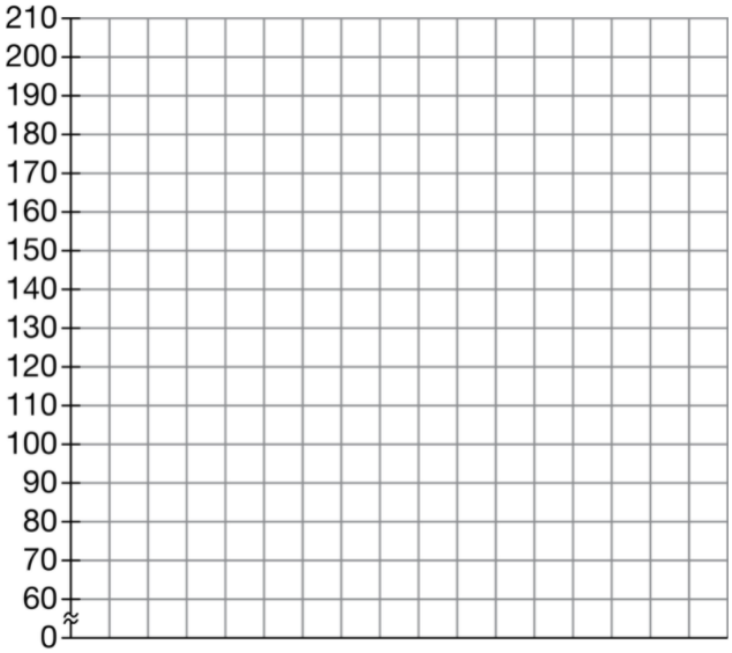
Individual	Average Blood Glucose Level (mg/dL ± $2SE_{\bar{x}}$)
IV–1	170 ± 15
IV–2	190 ± 10
IV–3	145 ± 5
IV–4	165 ± 15
IV–5	110 ± 15
IV–6	125 ± 5
IV–7	105 ± 15
IV–8	120 ± 10

TABLE 2. PHENOTYPIC CLASSIFICATIONS BASED ON BLOOD GLUCOSE LEVELS

Phenotype	Blood Glucose Level (mg/dL)
Normal	< 140 mg/dL
At risk	140 – 199 mg/dL
Affected	≥ 200 mg/dL

(a) The disorder alters glucose metabolism. **Describe** the atoms AND types of bonds in a glucose molecule.

(b) Using the template in the space provided for your response, **construct** an appropriately labeled graph based on the data in Table 1. **Determine** one individual who is both at risk of developing the disorder and has a significantly different blood glucose level from that of individual IV-1.



(c) Based on the pedigree, **identify** all individuals in generation IV who can pass on the mutation to their children.

(d) Based on the fact that individual II-2 is affected, a student claims that the disorder is inherited in an X-linked recessive pattern. Based on the student's claim, **predict** which individuals of generation III will be affected by the disorder. Based on the pedigree, **justify** why the data do NOT support the student's claim.

2021 #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 were detected throughout the test period (data not shown).

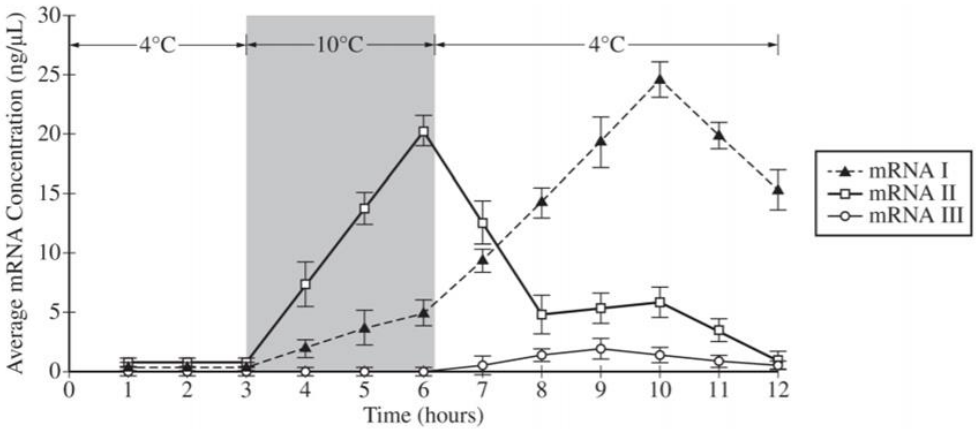


Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from *hsp* genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$.

(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.

2019 #6

	MEDIUM	STRAINS		
		Wild Type	Mutant 1	Mutant 2
Treatment I	All amino acids present	+	+	+
Treatment II	No amino acids present	+	–	–
Treatment III	All amino acids present EXCEPT methionine	+	–	+
Treatment IV	All amino acids present EXCEPT leucine	+	+	–

Table 1. The data show the growth of haploid *Saccharomyces cerevisiae* yeast strains on media that differ in amino acid content. A plus sign (+) indicates that the yeast strains grow, and a minus sign (–) indicates that the strains do not grow.

The yeast *Saccharomyces cerevisiae* is a single-celled organism. Amino acid synthesis in yeast cells occurs through metabolic pathways, and enzymes in the synthesis pathways are encoded by different genes. The synthesis of a particular amino acid can be prevented by mutation of a gene encoding an enzyme in the required pathway.

A researcher conducted an experiment to determine the ability of yeast to grow on media that differ in amino acid content. Yeast can grow as both haploid and diploid cells. The researcher tested two different haploid yeast strains (Mutant 1 and Mutant 2), each of which has a single recessive mutation, and a haploid wild-type strain. The resulting data are shown in Table 1.

(a) **Identify** the role of treatment I in the experiment.

(b) **Provide reasoning** to explain how Mutant 1 can grow on treatment I medium but cannot grow on treatment III medium.

(c) Yeast mate by fusing two haploid cells to make a diploid cell. In a second experiment, the researcher mates the Mutant 1 and Mutant 2 haploid strains to produce diploid cells. Using the table provided, **predict** whether the diploid cells will grow on each of the four media. Use a plus sign (+) to indicate growth and a minus sign (-) to indicate no growth.

	MEDIUM	STRAINS			
		Wild Type (haploid)	Mutant 1 (haploid)	Mutant 2 (haploid)	Diploid Cells Produced by Mating Mutant 1 and Mutant 2
Treatment I	All amino acids present	+	+	+	
Treatment II	No amino acids present	+	–	–	
Treatment III	All amino acids present EXCEPT methionine	+	–	+	
Treatment IV	All amino acids present EXCEPT leucine	+	+	–	

2019 #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.

mRNA EXPRESSION LEVELS

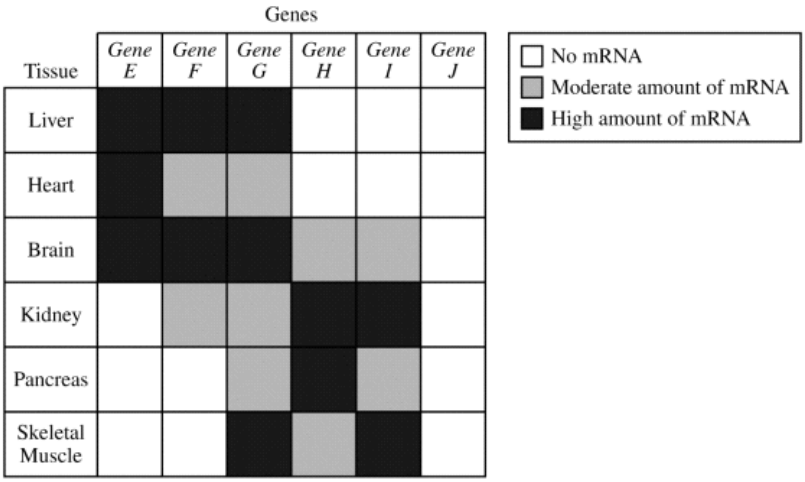


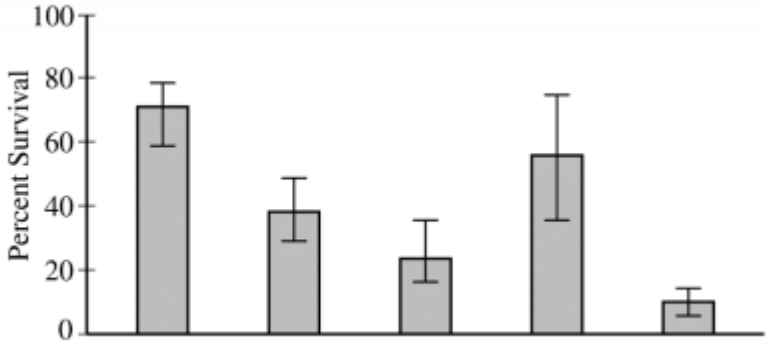
Figure 1. mRNA expression levels of six genes

(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.

2018 #4

The common bedbug (*Cimex lectularius*) is a species of insect that is becoming increasingly resistant to insecticides. Bedbugs possess several genes suspected of contributing to the resistance, including *P450*, *Abc8*, and *Cps*. To investigate the role of these genes in insecticide resistance, researchers deleted one or more of these genes in different strains of bedbugs, as indicated in Figure 1, and treated the strains with the insecticide beta-cyfluthrin. Each strain was genetically identical except for the deleted gene(s) and was equally fit in the absence of beta-cyfluthrin. The percent survival of each strain following beta-cyfluthrin treatment is shown in Figure 1.



Strain	I	II	III	IV	V
P450	+	–	+	+	–
Abc8	+	+	–	+	–
Cps	+	+	+	–	+

+ = Wildtype
– = Deletion

Figure 1. Percent survival of five strains of bedbugs treated with beta-cyfluthrin. A (+) indicates the gene is present; a (–) indicates the gene is deleted. Error bars represent the 95% confidence interval.

(a) **Identify** the control strain in the experiment. Use the means and confidence intervals in Figure 1 to **justify** the claim that *Abc8* is effective at providing resistance to beta-cyfluthrin.

(b) *P450* encodes an enzyme that detoxifies insecticide. *Abc8* encodes a transporter protein that pumps insecticides out of cells. *Cps* encodes external structural protein located in the exoskeleton that reduces the absorption of insecticides. Based on this information and the data in Figure 1, **explain** how a deletion of both *P450* and *Abc8* results in lower survival in bedbugs compared with a deletion of *Cps* only.

2017 #3

Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydrozylase (*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 Base in Codon	U	C	A	G	Third Base in Codon
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, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U C A G

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.

2017 #6

A comet assay is a technique used to determine the amount of double-stranded breaks in DNA (DNA damage) in cells. The nucleus of an individual cell is placed on a microscope slide coated with an agarose gel. An electric current is applied to the gel that causes DNA to move (electrophoresis), and the DNA is stained with a fluorescent dye. When viewed using a microscope, undamaged DNA from the nucleus appears as a round shape (the head), and the fragments of damaged DNA extend out from the head (the tail). The length of the tail corresponds to the amount of the damage in the DNA (see Figure 1).

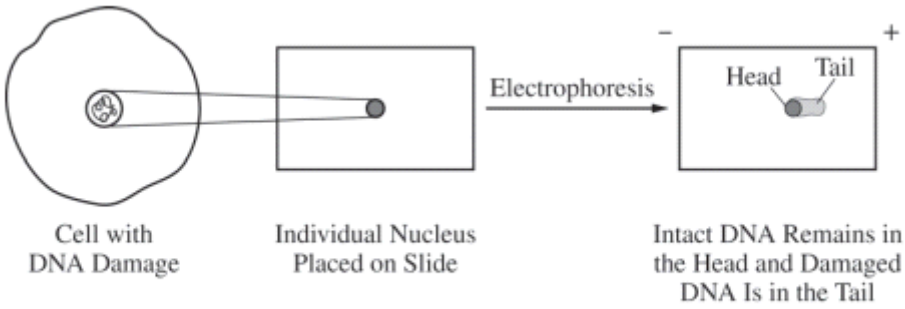


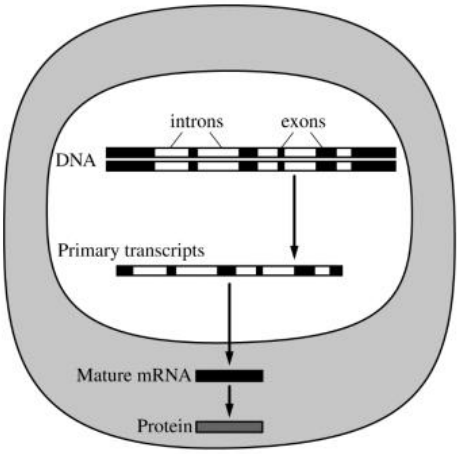
Figure 1. Comet assay to detect double-stranded breaks in DNA

(a) To explain the movement of DNA fragments in the comet assay, **identify** one property of DNA and **provide reasoning** to support how the property contributes to the movement during the comet assay technique.

(b) In a different experiment, cells are treated with a chemical mutagen that causes only nucleotide substitutions in DNA. **Predict** the likely results of a comet assay from this treatment.

2016 #4

The figure represents the process of expression of gene X in a eukaryotic cell.



(a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7kb in length. **Describe** the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs.

(b) **Predict** the length of the mature gene X mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction.

2016 #6

Living and dead organisms continuously shed DNA fragments, known as eDNA, into the environment. To detect eDNA fragments in the environment, the polymerase chain reaction (PCR) can be used to amplify specific eDNA fragments. eDNA fragments of different lengths persist in the environment for varying amounts of time before becoming undetectable (Figure 1).

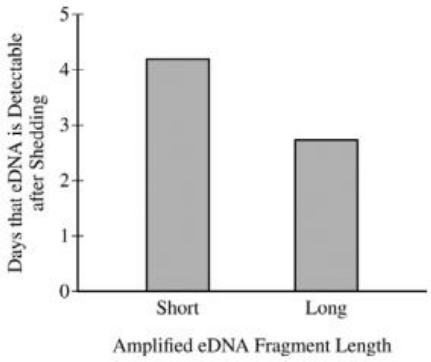


Figure 1. Detectability of eDNA fragments of varying lengths

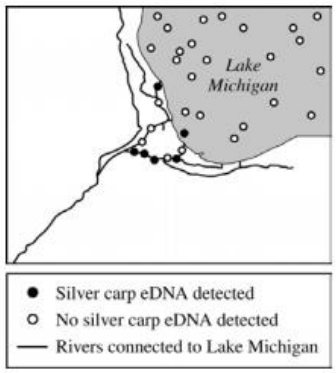


Figure 2. Map of the waterways that connect a nearby river system to Lake Michigan

To investigate whether silver carp, an invasive fish, have moved from a nearby river system into Lake Michigan, researchers tested water samples for the presence of eDNA specific to silver carp (Figure 2).

(a) **Justify** the use of eDNA sampling as an appropriate technique for detecting the presence of silver carp in an environment whether many different species of fish are found. **Propose** ONE advantage of identifying long eDNA fragments as opposed to short fragments for detecting silver carp.

(b) The researchers tested a large number of water samples from Lake Michigan and found eDNA specific to silver carp in a single sample in the lake, as indicated in Figure 2. The researchers concluded that the simple positive sample was a false positive and that no silver carp had entered Lake Michigan. **Provide reasoning** other than human error to support the researcher's claim.

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.

2013 #5

The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

	Relative Amino Acid Position									
Species	1	2	3	4	5	6	7	8	9	10
I	Val	His	Leu	Val	Glu	Glu	His	Val	Glu	His
II	Val	His	Leu	Lys	Glu	Glu	His	Val	Glu	His
III	Val	His	Leu	Val	Glu	Glu	His	Val		
IV	Val	His	Leu	Val	Arg	Trp	Ala	Cys	Met	Asp

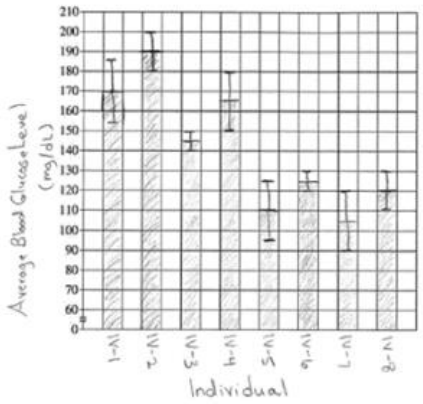
(a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.

(b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.

Free Response Scoring Guidelines

2022 #6		
Part	Scoring Guidelines	Topic
(a)	Based on the data, **identify** which cap structure is most likely to protect the end of the mRNAs from degradation. • Modified cap II	6.3
(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. Accept one of the following: • A longer mRNA half-life is associated with more protein. • There is a positive correlation/relationship.	6.4
(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. • The data support their hypothesis because the half-lives of the two mRNAs are the same, but the amount of protein produced from the mRNA with modified cap I is more than (four times as much as) that produced from the mRNA with the normal cap.	6.4
(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. Accept one of the following: • Protein production from the DNA requires (transcription) factors to initiate transcription. • Protein production from the mRNA does not depend on (correct posttranscriptional) processing of the pre-mRNA. • The cells may be unable to transcribe the DNA (while mRNA can be directly translated).	6.6

2021 #2		
Part	Scoring Guidelines	Topic
(a)	The disorder alters glucose metabolism. **Describe** the atoms AND types of bonds in a glucose molecule. • The atoms are carbon, hydrogen, and oxygen (C, H, and O) and are held together by covalent bonds.	

(b)	Use the template provided to **construct** an appropriately labeled graph based on the data in Table 1.  • Point distribution: Axis labels; plotting in a bar graph or modified bar graph; error bars **Determine** one individual who is both at risk of developing the disorder and has a significantly different blood glucose level from that of individual IV-1. • IV-3	
(c)	Based on the pedigree, **identify** all individuals in generation IV who can pass on the mutation to their children. • IV-1, IV-2, IV-4	
(d)	Based on the fact that individual II-2 is affected, a student claims that the disorder is inherited in an X-linked recessive pattern. Based on the student's claim, **predict** which individuals of generation III will be affected by the disorder. • III-4 and III-8 Based on the pedigree, **justify** why the data do NOT support the student's claim. Accept one of the following: • The data do not support the claim because females III-2 and III-6 have the disorder and, if inheritance is X-linked recessive, they could only do so if their father II-1 had the disorder, which he does not. • The data instead support mitochondrial inheritance, because all of the offspring of individual II-2 , not only the sons, have the disorder.	

2021 #6		
Part	Scoring Guidelines	Topic
(a)	**Identify** the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment. • (mRNA) III	6.3
(b)	**Describe** the trend in the average concentration of mRNA I throughout the experiment. • (No change in concentration from 1 to 3 hours) increased concentration (slightly) between 3 and 6 hours/during the heat shock, increased concentration at a greater rate from 6 to 10 hours/for 4 hours after the heat shock, and then decreased concentration after hour 10.	6.3

(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. • mRNA I is still expressed at a high level after the heat-shock period, while mRNA II levels decrease after the heat shock, when proteins would need to be refolded.	6.6
(d)	mRNAs I and II are transcribed from the same gene. **Explain** how a cell can produce two different mRNAs from the same gene. Accept one of the following: • The cell expresses different exons/performs alternative splicing. • The cell uses different transcription termination sites (poly(A) sites). • The cell uses different promoters.	6.6

2019 #6		
Part	Scoring Guidelines	Topic
(a)	**Identification (1 point)** • (Positive) control (for yeast growth). • To test the viability of all yeast strains. • Treatment I allows the researcher to be confident that changes in experimental outcome are due to differences in treatments.	5.2
(b)	**Reasoning (1 point)** • Mutant 1 can use methionine when it is present in the medium, but Mutant 1 cannot synthesize methionine.	6.7
(c)	**Prediction (1 Point)** • There will be growth (+) in all four cells of the fourth column.	5.2

2019 #7		
Part	Scoring Guidelines	Topic
(a)	**Identification (1 point)** • *Gene G* **Reasoning (1 point)** • (*Gene G*) is the only gene expressed in all (six) tissues, AND glycolysis occurs in all (six) tissues. • (*Gene G*) mRNA is the only mRNA present in all (six) tissues, AND glycolysis occurs in all (six) tissues.	3.6
(b)	**Reasoning (1 point)** • The mRNA is not exported from the nucleus. • *Gene H* mRNA is not translated/RNA interference prevent(s) translation. • Post-transcriptional modifications.	6.4

2018 #4		
Part	Scoring Guidelines	Topic
(a)	**Identification (1 point)** • Strain I **Justification (1 point)** • Error bars/CIs from strain I/control/WT do not overlap with strain III/*Abc8* deleted strain. • Mean % survival of strain III/*Abc8* deletion falls outside the 95% confidence interval of strain I/control/WT. • Strain III/*Abc8* deletion shows a statistically significant difference from strain I/control.	6.7

(b)	**Explanation (1 point per row; 2 points maximum)** 	Strain	*P450* and *Abc8*	*Cps* only	Explanation
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V	Deleted	Present	Bedbugs can neither detoxify nor pump out insecticide, which results in a lower chance of bedbug survival.
IV	Present	Deleted	Bedbugs can detoxify and pump out insecticide, which results in a higher chance of bedbug survival.		6.7

2017 #3

Part	Scoring Guidelines	Topic
(a)	**Description (1 point)**: The amino acid substitution changes the shape/structure/function of the protein. **Reasoning (1 point)**: The mutation decreases/eliminates gibberellin production.	6.7
(b)	**Prediction (1 point maximum)** • G ↔ A in the first position (of the codon) • 5′-GCN-3′ ↔ 5′-ACN-3′ • 5′-NGC-3′ ↔ 5′-NGT-3′ in the template strand of DNA	6.7
(c)	**Description (1 point)** • Enough active enzyme is produced from one wild-type/dominant allele. • Enough gibberellin is produced in the presence of one wild-type/dominant allele.	6.4

2017 #6

Part	Scoring Guidelines	Topic
(a)	**Identification (1 point)**: DNA has a (negative) charge. **Reasoning (1 point)**: DNA moves toward the positive/oppositely charged pole. DNA can be different sizes. (Different size DNA fragments) move at different rates.	6.8
(b)	**Prediction (1 point)** • Head (only) OR (head with) no tail. • Tail will be shorter than a cell with double-stranded breaks in DNA.	6.8

2016 #4

Part	Scoring Guidelines	Topic
(a)	**Describe process (1 point)** • Removal of introns • RNA processing **Identification (1 point)** • Nucleus	6.3
(b)	**Prediction (1 point)** • 15 kb • Longer than the mature mRNA in the eukaryote **Justification (1 point)** • mRNA processing typically does not occur in prokaryotes	6.3

2016 #6

Part	Scoring Guidelines	Topic
(a)	**Justify (1 point)** • eDNA allows detection of the fish without visual identification/catching the fish. **Proposed advantage (1 point)** • Longer fragments indicate more recent presence of fish. • Longer fragments are more likely to contain a sequence that is specific to silver carp. • Longer sequences/more base pairs may increase accuracy/specificity/confidence that the eDNA is from a silver carp and not a related species.	6.8
(b)	**Reasoning (1 point)** • eDNA entered the lake by means other than the fish (e.g., river flow, boats, waste from predators).	6.8

2015 #7

Part	Scoring Guidelines	Topic
(a)	**Description (1 point)** • Neurotransmitters are released from the olfactory neuron and bind to receptors in the postsynaptic neuron.	4.2
(b)	<table><tr><th></th><th>Explanation (1 point)</th><th>Support (1 point)</th></tr><tr><td>Molecular</td><td>• One odorant molecule can be recognized by more than one odorant receptor • One odorant receptor can bind to more than one odorant molecule</td><td>Mathematical combinations expand possible odors detected</td></tr><tr><td>CNS Control</td><td>Signals integrated in the brain</td><td>Multiple interactions among neurons in the brain</td></tr><tr><td>Genetic</td><td>Alternate processing/splicing (of pre-mRNA/primary transcript)</td><td>Multiple receptors can be produced from a gene</td></tr></table> *Note: The nervous system is no longer in scope*	6.3

2013 #5

Part	Scoring Guidelines	Topic
(a)	Explanation: **1 point per row** NOTE: Specific names of mutation types are not required. <table><tr><th>Species</th><th>Genetic Change in DNA / Bases</th><th>Result of Change to Polypeptide / Protein</th></tr><tr><td>II</td><td>mutation / substitution / point mutation / missense mutation</td><td>an amino acid change only at position 4 (Val to Lys)</td></tr><tr><td>III</td><td>mutation (e.g., substitution / insertion / deletion / point mutation / frameshift mutation / nonsense mutation) that introduces a stop codon after the codon for Val</td><td>termination of the polypeptide after the Val at position 8</td></tr></table>	6.7
(b)	<table><tr><th>Predicted Change (**1 point maximum**)</th><th>Justification of Prediction (**1 point maximum**)</th></tr><tr><td>Protein may have a different structure and a change in function.</td><td>Change in amino acid sequence of the protein starting at position 5 could alter the overall structure or local structural regions, interfering with function of the protein.</td></tr><tr><td>Protein may have a different structure and no change in function.</td><td>Change in amino acid sequence alters the shape / conformation / folding / binding region / regulatory region of the protein, but does not affect the critical functional region(s) of the protein.</td></tr><tr><td>Protein structure and function may not be affected.</td><td>Change in amino acid sequence does not alter the protein shape / conformation / folding and does not alter function.</td></tr></table>	6.7