

AP[®] Biology
Scoring Statistics
2018 Free-Response Questions

Question	Mean	Standard Deviation	Number of Possible Points
1	4.73	2.42	10
2	2.68	2.33	10
3	2.38	1.23	4
4	1.41	1.03	4
5	2.66	1.19	4
6	0.89	0.88	3
7	1.10	1.15	3
8	0.95	1.00	3

2018

AP

CollegeBoard

AP Biology

Sample Student Responses and Scoring Commentary

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- Scoring Commentary**

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AP[®] BIOLOGY
2018 SCORING GUIDELINES

Question 1

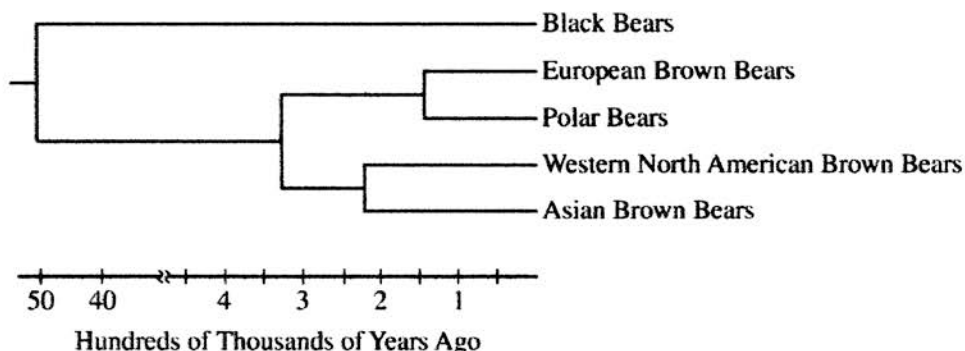


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their evolutionary relatedness (Figure 1).

A researcher studying adaptation in bears sequenced the nuclear gene encoding a lysosomal trafficking protein (LYST) in polar bears, brown bears, black bears, and panda bears. There are seven inferred amino acid substitutions that are found only in polar bears. Mutations that cause similar substitutions in the human LYST protein are associated with Chediak-Higashi syndrome, an autosomal recessive condition in which pigment is absent from the hair and eyes. The researcher used the inferred amino acid sequences to build the distance matrix shown in Table 1.

TABLE 1. AMINO ACID DIFFERENCES IN THE
 LYST PROTEIN AMONG BEAR SPECIES

	Panda	Black	Brown	Polar
Panda	–			
Black	33	–		
Brown	34	1	–	
Polar	40	7	8	–

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Question 1 (continued)

- (a) Use the phylogenetic tree in Figure 1 to **estimate** the age in hundreds of thousands of years of the most recent common ancestor of all brown bears. **Identify** the population of brown bears to which polar bears are most closely related based on the mitochondrial DNA sequence comparison. **Identify** two populations whose positions could be switched without affecting the relationships illustrated in the phylogenetic tree.

Estimate (1 point)

- First two digits of the answer must be between 30 and 35.

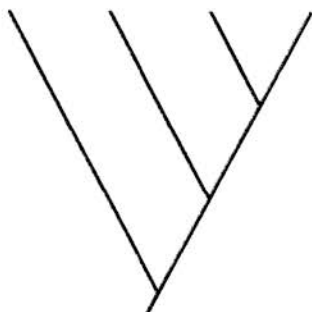
Identification (1 point)

- European

Identification (1 point)

- European/Polar OR Asian/Western (North American)

- (b) **Construct** a cladogram on the template to represent a model of the evolutionary relatedness among the bear species based on the differences in LYST protein sequences (Table 1). **Circle** the position on the cladogram that represents the out-group.



Construction (1 point)

- Correctly illustrated evolutionary relationship among the four species

Circling (1 point)

- Correctly circled out-group based on orientation of cladogram

- (c) A student claims that mitochondrial DNA sequence comparisons provide a more accurate phylogeny of bear species than do LYST protein sequence comparisons. **Provide ONE piece of reasoning** to support the student's claim.

Reasoning (1 point)

- Genes show more variability (in nucleotide sequence) than proteins do (in amino acid sequences).
- mtDNA genome contains multiple genes vs. one *lyst* gene.
- The phenotype associated with the *lyst* gene is under strong selection.

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Question 1 (continued)

- (d) A researcher genetically engineers a mouse strain by deleting the mouse *lyst* gene and replacing it with the polar bear *lyst* gene. **Predict** the most likely difference in phenotype of the transgenic mouse strain compared to the wild-type mouse strain. **Justify** your prediction.

Prediction (1 point)

- Mouse fur and/or eyes will not have pigment/will have reduced pigment.
- Mouse (fur) will be white/lighter.

Justification (1 point)

- Polar bear *lyst* gene/LYST protein is associated with a lack of pigment/white hair.
- Mutated human *lyst* gene/ LYST protein is associated with a lack of pigment in hair and eyes.

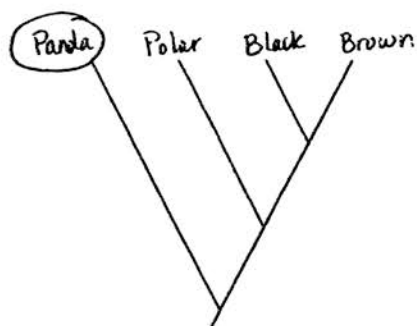
- (e) **Describe** how the mutation in the *lyst* gene became common in the polar bear population. If the *lyst* gene were the only determinant of fur color, **predict** the percent of white offspring produced by a mating between a polar bear and a brown bear.

Description (1 point)

- Natural selection for the white fur phenotype

Prediction (1 point)

- 0%



a) The age is around 325,000 years old. Based off mitochondrial DNA, polar bears are closest to European brown bears. Western North American brown bears + Asian brown bears could switch position w/o changing any relationships.

c) Mitochondrial DNA has a wider array of genes, therefore amino acids, to study + compare from species to species than the LYST gene does - there are only seven amino acids. With fewer comparisons, LYST has fewer opportunities + is less accurate than mitochondrial DNA.

d) The most likely change is that the mouse will appear white due to a lack of pigment in its fur. This seems likely because ~~for~~ polar bears are normally only white; humans who have similar LYST mutations (Chediak-Higashi Syndrome) also display a lack of pigment in hair + eyes. Overall, the mutations appear to cause the

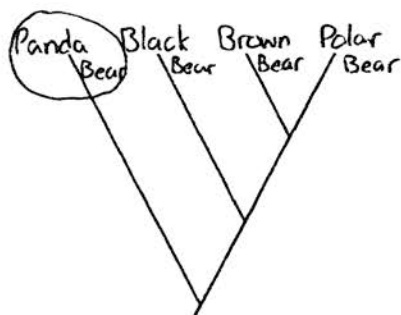
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lack of pigment.

e) The *LYST* gene became common through the process of natural selection. After the mutation appeared, white individuals gained an advantage in their environment — hunting became easier ~~and~~ since they were blending in with the snow + ice. Because these individuals were more successful in eating, therefore surviving more, they were able to reproduce + ~~spread~~ carry on the mutation. The mutation was so advantageous it eventually became commonplace.

The percent of white offspring (assuming the offspring survived/could be conceived) ~~is~~ should be zero, since the similar mutation of *LYST* in humans is recessive. Therefore, brown coats would be dominant + pass the dominant coloring to all offspring.

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a) The most recent common ancestor of all brown bears is 325 hundred thousand years old. Based on DNA sequence comparison, Polar Bears are most closely related to European Brown Bears. Two populations that could be switched would be Polar Bears and European Brown Bears.

b) Mitochondrial DNA sequences show evolutionary differences of over time, whereas LYST comparisons do not.

d) The mouse would begin growing pigment-less hair, and its eyes, if previously colored, would lose pigment as well. This would occur because the LYST gene in a polar bear encodes for lack of pigment in hair and eyes.

e) Mutation of the LYST gene became popular in Polar Bears most likely due to natural selection. Polar Bears live in a snowy, white climate, and the lack of pigment in their fur allows them to blend in.

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1B2

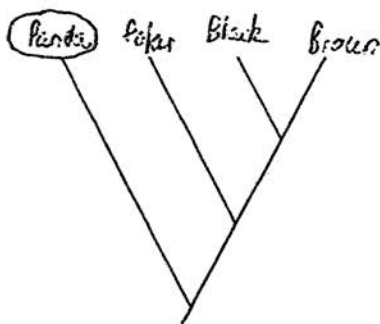
ADDITIONAL PAGE FOR ANSWERING QUESTION 1

If a ~~+~~ Polar Bear and a Brown Bear were bred, there would probably be no white offspring.

Lined area for writing an answer.

GO ON TO THE NEXT PAGE.

B)



- A) The most common recent ancestor of all brown bears appears to be around 325 hundreds of thousands years old. Based on the DNA sequence comparison polar bears are most closely related to European Brown Bears. The polar bear's & the European Brown Bear's positions on the cladogram can be switched without affecting the relationships.
- C) More errors can be made during the synthesizing of a protein than the replication of DNA, therefore using mitochondrial DNA is more accurate.
- D) The transgenic mouse strain are more likely to have Chedhak-Higashi syndrome because the new Lyst gene is able to cause it at higher rates.
- E) In the polar bear population white fur is advantageous because it allows the bear to use the snow as camouflage. This made the mutation more common overtime because those without it had a lower survival rate. The percent of offspring with white coloration would be 0% between this cross because the polar bear would be homozygous recessive.

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2018 SCORING COMMENTARY

Question 1

Overview

This question is based on recent investigations into the evolutionary history of polar bears. Students were presented with a phylogenetic tree created from mitochondrial DNA (mtDNA) data for five populations of bears. Using this phylogenetic tree, students were asked to estimate the age of the most recent common ancestor of all brown bears, to identify what population of brown bears was most closely related to polar bears, and to identify two populations of bears whose positions on the phylogenetic tree could be switched without altering the proposed relationships. Students were presented with a data table indicating the number of amino acid differences in the lysosomal trafficking protein *LYST* among four species of bears. Using these data, the students were asked to construct a cladogram on a provided template and circle the outgroup position on that cladogram. Students then were asked to provide one piece of reasoning to support a claim that mtDNA sequence comparisons provide a more accurate prediction of bear phylogeny. The students were then asked to predict the most likely difference in the phenotype of a mouse that was genetically altered to contain the polar bear-specific *lyst* allele. The students were asked to justify their prediction. Finally, students were asked to describe how the *lyst* allele became common in the polar bear population and to predict what percentage of the offspring resulting from a mating between a brown bear and a polar bear would be white.

The key understandings and skills students were expected to demonstrate included the following:

- Basic concepts of evolution were used to evaluate and interpret data and to describe evolutionary relationships and processes.
- Knowledge of Mendelian and molecular genetics was used to predict the outcomes of a genetic alteration and a mating based on experimental design.

Sample: 1A

Score: 10

The response earned 1 point in part (a) for estimating that the most recent common ancestor of all brown bears existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that Western North American Brown Bear and Asian Brown Bear positions could be switched on the phylogenetic tree. The response earned 1 point in part (b) for constructing a cladogram that correctly orders the taxa, from left to right, Panda, Polar, Black, and Brown. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (c) for supporting the student's claim by reasoning that mtDNA would include more genes that code for more proteins that could be compared in contrast to one gene coding for a single *LYST* protein. The response earned 1 point in part (d) for predicting that the mouse's fur would lack pigment. The response earned 1 point in part (d) for justifying that humans having the mutant form of the *LYST* protein lack pigment in hair. The response earned 1 point in part (e) for describing that the *lyst* gene became common when white individuals had a selective advantage. The response earned 1 point in part (e) for predicting that zero percent of offspring should be white.

Sample: 1B

Score: 8

The response earned 1 point in part (a) for estimating that the most recent common ancestor existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that Polar Bear and European Brown Bear positions could be switched on the phylogenetic tree. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (d) for predicting that the mouse would be growing pigmentless hair. The

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Question 1 (continued)

response earned 1 point in part (d) for the justification that because the *lyst* gene in Polar Bears encodes for a lack of pigment in hair, the mouse would begin growing pigmentless hair. The response earned 1 point in part (e) for describing that the *lyst* gene became common as a result of natural selection for white Polar Bears that were able to blend into a snowy white environment. The response earned 1 point in part (e) for predicting that no offspring should be white.

Sample: 1C

Score: 6

The response earned 1 point in part (a) for estimating that the most recent common ancestor existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that the position of the Polar Bear and the position of the European Brown Bear could be switched on the phylogenetic tree. The response earned 1 point in part (b) for constructing a cladogram that correctly orders the taxa, from left to right, Panda, Polar, Black, and Brown. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (e) for predicting that zero percent of offspring should be white.

Chief Reader Report on Student Responses: 2018 AP[®] Biology Free-Response Questions

• Number of Students Scored	259,663			
• Number of Readers	712			
• Score Distribution		Exam Score	N	%At
		5	18,594	7.2
		4	55,964	21.6
		3	85,175	32.8
		2	73,544	28.3
		1	26,386	10.2
• Global Mean	2.87			

The following comments on the 2018 free-response questions for AP[®] Biology were written by the Chief Reader, Nancy Morvillo, Ph.D., Professor and Chair of Biology, Florida Southern College. They give an overview of each free-response question and of how students performed on the question, including typical student errors. General comments regarding the skills and content that students frequently have the most problems with are included. Some suggestions for improving student preparation in these areas are also provided. Teachers are encouraged to attend a College Board workshop to learn strategies for improving student performance in specific areas.

Question #1 **Task:** Interpret data; identify evolutionary relationships; predict the effects of natural selection and genetic manipulation

Topic: Investigating the evolution of polar bears

Max. Points: 10

Mean Score: 4.73

What were the responses to this question expected to demonstrate?

This question is based on recent investigations into the evolutionary history of polar bears. Students were presented with a phylogenetic tree created from mitochondrial DNA (mtDNA) data for five populations of bears. Using this phylogenetic tree, students were asked to estimate the age of the most recent common ancestor of all brown bears, to identify what population of brown bears was most closely related to polar bears, and to identify two populations of bears whose positions on the phylogenetic tree could be switched without altering the proposed relationships. Students were presented with a data table indicating the number of amino acid differences in the lysosomal trafficking protein *LYST* among four species of bears. Using these data, the students were asked to construct a cladogram on a provided template and circle the outgroup position on that cladogram. Students then were asked to provide one piece of reasoning to support a claim that mtDNA sequence comparisons provide a more accurate prediction of bear phylogeny. The students were then asked to predict the most likely difference in the phenotype of a mouse that was genetically altered to contain the polar bear-specific *hyst* allele. The students were asked to justify their prediction. Finally, students were asked to describe how the *hyst* allele became common in the polar bear population and to predict what percentage of the offspring resulting from a mating between a brown bear and a polar bear would be white.

The key understandings and skills students were expected to demonstrate included the following:

- Basic concepts of evolution were used to evaluate and interpret data and to describe evolutionary relationships and processes.
- Knowledge of Mendelian and molecular genetics was used to predict the outcomes of a genetic alteration and a mating based on experimental design.

How well did the response address the course content related to this question? How well did the responses integrate the skills required on this question?

In part (a), most students correctly estimated the age of the most recent common ancestor of all brown bears to be between 310 and 350 thousand years ago, and correctly identified European brown bears to be most closely related to polar bears based on the mtDNA sequence data. Most students were also able to correctly identify that either the European brown bear and polar bear positions could be switched or the Asian and Western (North American) brown bears positions could be switched on the phylogenetic tree without affecting their relationships.

Course content highlighted in this part included a basic understanding of evolutionary relationships among taxa. Skills highlighted in this part included extrapolating a data point from a graphical representation and interpreting the representation to determine evolutionary relationships.

In part (b), many students were able to correctly construct the cladogram and to identify the position of the outgroup.

Course content highlighted in this part included a basic understanding of evolutionary relationships among taxa. Skills highlighted in this part included drawing a cladogram from the data provided and identifying where on the cladogram the outgroup is located.

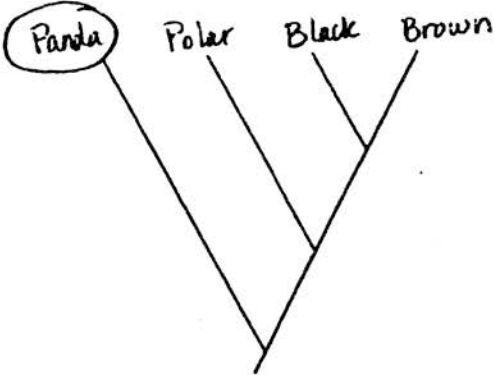
In part (c), it was difficult for students to provide reasoning to support that the mtDNA sequence comparisons were more accurate than the *LYST* protein sequence comparisons to construct a phylogenetic tree. Responses did not often articulate that there was more variability in DNA sequences than in protein sequences or that there is more information from multiple mitochondrial genes than from only one *hyst* gene, or that phenotypes associated with the *hyst* gene might be under selection and less likely to show variation.

Course content highlighted in this part included an understanding of the structure of macromolecules (DNA and proteins) and fundamental understandings of the central dogma (notably that genes can contain different DNA sequences that could result in proteins of the same amino acid sequence). Skills highlighted in this part included applying fundamental knowledge of basic biology to provide reasoning for the choice of the type of data that would be most accurate to answer a question.

In part (d), students were often able to predict that the phenotype of the transgenic mice with the polar bear *hyst*-specific allele would be white or produce less pigment. Students were often able to predict that 0% of the offspring from a mating between a brown bear and a polar bear would be white.

Course content highlighted in this part included a basic understanding that a transgene will be expressed and can confer a new phenotype to the organism. Mendelian genetics were also highlighted. Skills highlighted in this part included predicting the phenotype that would be produced in a transgenic organism, and calculating the percentage of a specific phenotype that would be predicted from a given cross between bears.

What common student misconceptions or gaps in knowledge were seen in the responses to this question?

Common Misconceptions/Knowledge Gaps	Responses that Demonstrate Understanding
<p>Incorrectly constructing a cladogram and identifying the outgroup (part b)</p> <ul style="list-style-type: none"> • Student responses often demonstrated a misinterpretation of the data table, causing incorrect placement of the species on the cladogram. • Students were asked to identify (circle) the <i>position</i> of the outgroup, not the species. Some responses had a circle around the panda even though the panda was incorrectly placed on the cladogram. • Some responses had not just the outgroup, but also the entire branch, including the common ancestor, circled. 	

<p>Misunderstanding of the use of types of genetic data (part c)</p> <p>Some student responses incorrectly used the following as lines of reasoning to support that mtDNA was more accurate to determine evolutionary relatedness:</p> <ul style="list-style-type: none"> • mtDNA is only inherited from the maternal line • mtDNA inheritance is highly conserved • protein (amino acid) sequence data cannot be used to determine evolutionary relatedness • mtDNA was used to construct the phylogenetic tree and was able to separate three types of brown bears, but the amino acid data only grouped the brown bears into one clade 	<ul style="list-style-type: none"> • “The student’s reasoning is valid because multiple codons can code for the same amino acid. Thus, simply comparing the differences in the amino acids on the LYST protein could indicate that two species are equally similar to another where one could actually be less similar due to a different base sequence.”
<p>Lack of or irrelevant specificity (part d)</p> <ul style="list-style-type: none"> • Predictions did not include a specific phenotype (e.g., “The mice would be like polar bears”) • Predictions included traits associated with polar bears (e.g., thick fur) that were not provided by the question • Justifications included genes other than the <i>lyst</i> gene 	<ul style="list-style-type: none"> • “The most likely change is that the mouse will appear white due to a lack of pigment in its fur.”
<p>Misunderstanding of natural selection (part e)</p> <ul style="list-style-type: none"> • Some responses included descriptions of natural selection acting on a genotype rather than a phenotype • Some responses included descriptions of the phenotype conferring a specific advantage for 	<ul style="list-style-type: none"> • “The LYST gene became common through the process of natural selection. After the mutation appeared, white individuals gained an advantage in their environment-hunting became easier since they were blending in with the snow and ice. Because these individuals were more successful in eating, therefore surviving more, they were able to reproduce and carry on the mutation. The mutation was so advantageous it eventually became commonplace.”

<p>survival without connecting survival to reproduction</p>	
<p>Misreading (part e)</p> <ul style="list-style-type: none"> • Some responses indicated that the <i>lyst</i> allele causing white fur would be present in heterozygous brown bears when the information in the question indicated that the allele was ONLY present in polar bears • Some responses indicated the percentage of brown offspring, not the percentage of white offspring from the cross 	<ul style="list-style-type: none"> • “The percent of white offspring (assuming the offspring survive/could be conceived) should be zero, since the similar mutation of <i>LYST</i> in humans is recessive.”

Based on your experience at the AP® Reading with student responses, what advice would you offer to teachers to help them improve the student performance on the exam?

- Help students with reading and addressing the prompt. Encourage them to underline key words and phrases, and to re-read the information.
- Interpreting and constructing models (including phylogenetic trees and cladograms) are different skills. Be sure to practice both with students, and do not assume that if students are proficient in one skill they are proficient in the other.
- Help students understand that natural selection has two components: survival and reproduction. Students do not often extend the notion of survival to reproductive fitness. Provide practice with different scenarios.
- Help students develop their reasoning skills with “explain” questions. Students can follow the popular model of “claim-evidence-reasoning” with these types of questions. Have students break down an argument into these three components, to help them articulate their ideas. Have students write their responses to practice clear communication of their ideas.

What resources would you recommend to teachers to better prepare their students for the content and skill(s) required on this question?

AP Central, Visualizing Information, Lessons Two and Three: Modeling Evolution;
<https://apcentral.collegeboard.org/pdf/biology-visualizinginformation.pdf?course=ap-biology>

AP Central, Investigative Labs: Comprehensive Links: <https://apcentral.collegeboard.org/courses/ap-biology/classroom-resources/investigative-labs-comprehensive-links?course=ap-biology>, Investigation 3