

11. Use the following mRNA codon key as needed to answer the next two questions:

GCC	Alanine
AAU	Asparagine
CCU	Proline
GGA	Glycine
UGG	Tryptophan
UGA	"Stop" (no amino acid)
GAA	Glutamic acid
GAG	Glutamic acid
AGG	Arginine
CCC	Proline
CAU	Histidine

The following DNA sequence (coding strand) occurs near the middle of the coding region of a gene.

DNA
 5'—AATGAATGGGAGCCTGAAGGAG—3'

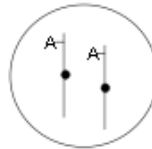
The corresponding mRNA sequence is shown below. Note that the coding strand of DNA has the same sequence as the mRNA, except that there are U's in the mRNA where there are T's in the DNA. The first triplet of nucleotides AAU (underlined) is in frame for coding, and encodes Asparagine as the codon table above indicates.

mRNA
 5'—AAUGAAUGGGAGCCUGAAGGAG—3'

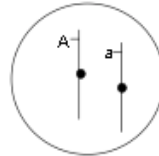
Which of the following DNA mutations is almost certain to result in a shorter than normal mRNA?

- a) A→G at position 50
- b) G→A at position 53
- c) C→A at position 58
- d) None of the above

20. Sue's chromosome #18 pair looks like this:

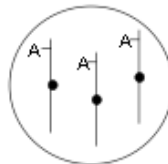


Bob's chromosome #18 pair looks like this:



Bob and Sue have a stillborn son with three

copies of chromosome #18 that look like this:



In which parent did the chromosome separation problem occur?

- a) Sue
- b) Bob
- c) You need additional information to determine which parent.

Figure S1 Complete versions of abbreviated GCA questions shown in Table 3.

Supplemental Figure 2. Examples of formative and summative questions used to discuss the difficult concept of mutation. The correct answer is highlighted in bold.

Clicker question:

A type of human dwarfism results from the production of mutant SHR-1 protein. You look at the length of the mutant SHR-1 and the normal (wild-type) SHR-1 protein, and discover that the mutant SHR-1 protein has fewer amino acids. What do you expect to find when you examine the DNA sequence?

- A. nucleotides were deleted
- B. additional nucleotides were added
- C. one nucleotide was changed
- D. without additional information, any of the above are possible**

Homework question:

Mutations in the adenomatous polyposis of the colon (*APC*) gene predisposes a person to colorectal cancer. Below is the DNA nucleotide sequence of the *APC* gene on the non-template strand from a normal individual and an individual who was diagnosed with colorectal cancer.

What type of mutation occurred in the individual that has colon cancer?

Note this sequence is from the middle of the *APC* gene, so use the first 3 nucleotides for the first codon of this part of the *APC* gene.

Coding strand of a normal individual:

5'-GAG GCG GGT TCA CGA GAG -3'

Coding strand of an individual with colorectal cancer:

5'-GAG GCG GGT TGA CGA GAG -3'

- A. Missense
- B. Nonsense**
- C. Silent
- D. Frameshift

Exam questions:

One form of cystic fibrosis is caused by a mutation in the middle of the DNA sequence of the *CFTR* gene. If you look at the protein produced from this mutated sequence, and the protein is the normal length, what type of mutation is most likely?

- A. Frame shift
- B. Silent
- C. Missense**
- D. Nonsense
- E. Either answer B or C could be true

A mutation has been found in the DNA sequence below, indicated with the box. Comparing this sequence to the normal sequence, what effect will this mutation have on the protein ultimately produced from this gene, and why?

Normal:

5'GGGTATAAT3' template

3'CCCATATTA5' coding

Mutation:

5' GGGTAG **G**AT 3' template

3' CCCATC **C**TA 5' coding

Answer: *AUU and AUC both code for leucine. This is a silent mutation, and will not affect the structure or function of the protein.*

Figure S2 Examples of formative and summative questions used to discuss the difficult concept of mutation. The correct answer is highlighted in bold.

TABLE S1 Chi-square values comparing the proportion of students who answered a question correctly on the pretest to the proportion of students who answered a question correctly on the posttest (n=751 students).

Question Number	χ^2	p value
1	70.04	<0.001
2	90.23	<0.001
3	150.52	<0.001
4	131.70	<0.001
5	189.87	<0.001
6	290.82	<0.001
7	238.01	<0.001
8	139.60	<0.001
9	78.89	<0.001
10	235.48	<0.001
11	86.31	<0.001
12	163.23	<0.001
13	193.83	<0.001
14	339.96	<0.001
15	82.25	<0.001
16	482.22	<0.001
17	111.33	<0.001
18	315.96	<0.001
19	2.31	0.146
20	110.71	<0.001
21	123.29	<0.001
22	269.49	<0.001
23	405.96	<0.001
24	432.76	<0.001
25	466.99	<0.001