Student Activity: What are the Effects of Various Mutations on Protein Synthesis?

INTRODUCTION: In this activity you will be translating strands of mRNA into small sequences of amino acids. You will also be experimenting with various types of mutations and trying to determine which mutations cause the greatest change in the polypeptide sequence.

STEP 1: Take your strand of mRNA and using a standard "dictionary" of mRNA codons, translate your mRNA into the correct sequence of amino acids.

Questions:

1. What did you discover about first codon in your sequence?

2. Check with some of the students near you. What is the first codon in their sequence?

3. What would you hypothesize about all strands of mRNA that code for proteins?

4. What did you discover about the last codon in your sequence?

5. Check with some of the students near you. What is their last codon and what does it do?

6. What would you hypothesize about the last codon for all strands of mRNA that code for proteins?

STEP 2: Take another copy of your strand of mRNA and change every **C** that is the third base in a codon to a **U**. Now translate the new mRNA into a polypeptide sequence.

Example: AUG/ACU/GU**C**/CAG/UCA/UC**C**/ACU (The underlined C's would be changed to U's.)

7. What did you discover about your new polypeptide strand (compared to the original)?

Collect some class data:

Number of strands with premature STOP codon _____

Number of strands with no new amino acids _____

Number of strands with 1 new amino acid _____

Number of strands with 2 new amino acids _____

Number of strands with 3 new amino acids _____

Number of strands with 4 or more new amino acids _____

8. How do you explain that some students had strands with no new amino acids?

STEP 3: Take another copy of your strand of mRNA and change every **C** that is the third base in a codon to an **A**. Now translate the new mRNA into a polypeptide sequence.

Example: AUG/UC**C**/CUU/AU**C**/ACU/GU**C** (The underlined C's would be changed to A's.)

9. What did you discover about your new polypeptide (compared to the original AND to the polypeptide from step 2)?

Collect some class data:

Number of strands with premature STOP codon _____

Number of strands with no new amino acids _____

Number of strands with 1 new amino acid _____

Number of strands with 2 new amino acids _____

Number of strands with 3 new amino acids _____

Number of strands with 4 or more new amino acids _____

10. How is the class data from Step 3 different from the class data from Step 2?

11. Which step seemed to result in the greatest number of changes in the polypeptide?

12. How do you explain the reason for your answer to question 11?

STEP 4: Take another copy of your mRNA strand. This time add one extra base (**A**) immediately after the START codon in your mRNA sequence. Translate this into a new amino acid sequence (polypeptide).

13. How does this polypeptide differ from the original and the ones you created in steps 2 and 3?

Collect some class data:

Number of strands with premature STOP codon _____

Number of strands with no new amino acids _____

Number of strands with 1 new amino acid _____

Number of strands with 2 new amino acids _____

Number of strands with 3 new amino acids _____

Number of strands with 4 or more new amino acids _____

13. What did you discover about the type of mutation where a single base is inserted into the mRNA sequence.

14. What would have happened to the polypeptide if you had deleted a single base instead of inserting a base at the same location in the mRNA sequence?

15. What would have been the results if the insertion or deletion of a base had happened near the end of the mRNA sequence?

GENERAL QUESTIONS:

16. What effect would these various mutations have on the trait that is controlled by the protein that is produced from the mRNA?

17. Summarize what you have learned about mutations and their effect on the resulting polypeptide.

1.
AUGCUCUCUGGAUACCGCAAGCGAAACGGCAAUGGGGUAUUGGCACAGG
ACAAAGCUUUGUAUGGUUAA

2.
AUGUUUGCUCCGUUUUACCCUUAUUCGAACACAGACUCCGAGUUGACAG
GGGGCUACAAAGAAUAUUAG

3.
AUGCCUCCGUUUAAGUAUCUAAUCCGGUUGAUACCAGACUACGAGAAGUU
AGCUAUAUCUACAGCGUAG

4.
AUGUCGACCCAAUGUCUGUGUAUUACGCAGUCUAUCCAAAACAUUACUCA
UGUAGAUUCUCUGCGGUGA

5.
AUGCUGUGGGGGCCGAUGCGGCAGUGGGAAGACUACGUGGGGCCACUG
GGGUACGAAUUGAUAACUUAA

6.
AUGAGCACUCCAUCACACUACGUUAGGGGGAGCAGGAGCCUUCGGUAUG
UGAUGGCCGCGAAGGGAUAA

7.
AUGGCACAGGAGAGCCAGCAGACGUUCCCCGUGACUGCCCUCCUAAGUAC
CCUCGCCGAGACGGAUUAG

8.
AUGCUGUACCCAGACAAAGAAUUCUUUUACGACAGAGCAGGACAGGGCAG
ACAGGCAUGGUUAGAUUAG

9.
AUGGAUGUUAUUCGUUACCCGAGUGAGACCAAUAGCCAGCAAAACUCUAC
UUUUAUGGAUUGGAACUGA

10.
AUGACGUGUACGUACUCGUACAUCCGCCCACGUCGAAACAGAAGUAGCAG
UCUGACGGGCGUACAAUAA

11.
AUGGUGUCCGCGUCACCUGUGGAUCGGACUCAUGAGUGGAUGGGUACCC
AACAACACUGGCUCACGUAG

12.
AUGGCUAGGCGGACGGCGCUUACAGUGCCUGUCCAUUACAAUGUGACGU
AUGUAGAACCCGUCAUUUAA

13.
AUGGGGGUGGACCUCAAGAAUUCUCGCAUCACUCAUGAUGGGGCGGCCC
UAAAAACGGGAGACAUUUGA

14.
AUGCCAUGUCCCCAGACGCUCGCCUUUUCGUUACUUAUGGUGUACUUAC
AUCAUUCCAUCUCACUCUAG

15.
AUGCACCGCAAAUACUACGCACGAGAUGCAAUGCGCAAAUCUUUGAUCUC
UACCGCUAUCUCUGGGUAG

16.
AUGUCCCGGUUACGUGGCAACGCGAACCCUCCGAACUCUUAUGCAGUGG
AGCCUAGUUCAGCUGUCUAA

17.
AUGGUAGGUCGCAUAGGGGACUUCAAAUAUGCCGGAGAUUCGUUACUGC
UGCACCGCGCCAUUGCUUGA

18.
AUGUCACGCAUUACCAAAGCCGUCCAGUCCAAGCGAGACAUCAUACGGAU
GCUUGCGCCAUAUCUUUAA

19.
AUGGAUAGCAUGCUGACCUUACAGCUGGAUACAUCGAACGCACGGAUUU
CUGCGACUCACUUAUUCUAG

20.
AUGCGACUUUACACCAAUGGCUUAAUGCCUGCGUAUAGUUGUAUUGCUG
UUGAGUAUCGCAAAACAUAA

21.
AUGUUCGCAUUCUGUGCCAACGAUGCAAUACCCUUAAGAGGCCACGGCUA
CUCGCCUCUGGUCGGAUGA

22.
AUGUCGAGGACCUUCCCUGUCACCUCAAAGAGUUACCCCCUCGAAGUCGU
GUCGAUCGUGAAUCGCUAG

23.
AUGGGUGGAUCGUCCAACAAUAGGACGAAAAACUUGCUCUUUCCCAAUGC
UUACACUCGGGGUGCGUAA

24.
AUGGAGGCGUUCCGGAAACACGCAACUAUGCCAUUAGUCUGCGAUCCGG
GUCCCAACAAUAGGAGUUGA

25.
AUGGGUAAUAACUUAUUGCAACAUCCCGUGUUGACUCUAAGGAGUCGUU
UGGCUUAUUCACUGCUCUAA

26.
AUGGGCUUAACAGGAGACUUUCAGCGCAGCUCAGGCGUCCCGUACAGGC
GUCCCCCUAAUAAAGCAUGA

27.
AUGGCGGGACGCAGUUUCAAAUUUAGGGCGAACCAGACGAGAAUUCGCA
CAGGCCGUUCACUGAUGUGA

28.
AUGGAACUGCGUGGGAUAGUCGCGGGGCACUUAGCCCACGUUCAGUGUA
CAUCGCACAAAUAUUUAUAA

29.
AUGUCCCGGCGGGCCCGAUGCAGGGCAUCGAAAGACACUAGACCGAAUU
UCGAGUCAAGUGCUGCCUGA

30.
AUGGAUUACAACUUUGAUACCCUGGUAUGGAUCGUACGGAGAUAUUUAG
CUCUCUUAGAUCCGUUAUGA

31.
AUGCUAGUGCCCAUCCCGUUUAUCAACGCCGACAUUCUCUGUGUAGCCCC
UCUUCGUGGCAUGCCAUGA

32.
AUGAACUUUAUCGACCAGGAUCAUUACACAGGCUCUGACAUAUUGCCAAG
AGGCGUUAGAAUAUUAUGA

33.
AUGUCUACCCACUUUUGGGAGAGAACUGGACCUGAGUUACAUCUUGAGG
CGCACGACCUUGGUCGGUAA

34.
AUGGGACAUUGUAAGGUAUUCUGUGACGGAAUCUGUGUCCUAGUCCAGG
CUAUCUUACAGUCCCACUAG

35.
AUGUGUCUCAAAAUCAAUACCAAGAGUAGAUGUAAGGCCGAGGCGAUGAA
UAUCACGUCUAGGACCUUAUAA

36.
AUGCCCACAGAGAUUUCGCACCGUAAGCGGGUGGUGAUCACUGAAGCUA
UAAGGAGAUGGAGUUAUUAG

37.
AUGGAGAUGGCAAAGGCUUACAGGAUACUUGAUACAUCCUUGGGAGCUA
CGCCGUCUGGUCACCCAUAA

38.
AUGCAAUACCUUCAGCGCUCCAUUGAUAUUCAAACGCGCACCGCAGUACG
GCAGAUAUCUCCCGUCUAG

39.
AUGCAAUACCUUCAGCGCUCCAUUGAUAUUCAAACGCGCACCGCAGUACG
GCAGAUAUCUCCCGUCUGA

40.
AUGUCGAGUCCCAAUUGCGGUAGUCGCGGUACACUUCAAUCUGAUAGCU
CGAUAAUCAUGCAUAGCUAA