AP BIOLOGY · UNIT 6 · TOPIC 6.4

Translation

Learning objective 6.4.A Explain how the sequence of an mRNA is translated into a polypeptide.

Name: Date: Period:

Use the tool **Three at a Time**. Part 2 uses **Read the message**, Parts 1 and 3 use **The whole code**, and Parts 4 and 5 use **Which base matters**. Part 4 measures how often a change at each base of a codon changes the amino acid.

Part 1 · Reading a message three bases at a time

Translate each mRNA below by hand, using the code table on The whole code tab. Give the codons, the anticodon of the **first** codon, and the polypeptide. Stop translating at a stop codon; if an mRNA has none, translate it to the end.

mRNA (5′→3′)	Codons	Anticodon of codon 1	Polypeptide
AUGUUUGGCUAA			
AUGCAUCACUGG			
AUGAGCUCAUAG			

1. (a) Describe what a codon is.

(b) Describe what an anticodon is.

(c) Describe the relationship between a codon and its anticodon.

2. Every polypeptide in the Part 1 table begins with the same amino acid.
(a) Identify the amino acid.

(b) Explain why every polypeptide begins with this amino acid.

Part 2 · The same bases, a different frame

On **Read the message**, the mRNA AUGGCAUUAGCCUGAAGU is translated in each of its three reading frames. Press Frame 0 (starts at AUG), Frame 1 and Frame 2 in turn, and record what each frame produces.

Frame	Codons	Polypeptide	Number of amino acids
0			
1			
2			

3. (a) Using the Part 2 table, identify the number of positions that hold the same amino acid in all three polypeptides.

(b) Explain how shifting the reading frame produces the result in part (a).

4. In frame 0, translation stops before the end of the mRNA. Explain what this observation shows about what a stop codon is.

5. A single extra base is inserted immediately after the start codon of this mRNA.
(a) Predict the effect of the insertion on the polypeptide.

(b) Justify your prediction using the Part 2 table.

Part 3 · Sixty-four codons, twenty amino acids

Switch to **The whole code** and use the amino-acid buttons, such as Leu (6), to complete the table.

Quantity	Number	Why it is that number
Codons in the table		
Codons that specify an amino acid		
Amino acids specified		
Amino acids with exactly one codon		
Amino acids with six codons		

6. Explain why the genetic code reads three bases at a time rather than two. In your answer, include the number of combinations that two bases would give.

7. (a) Explain what it means to say that the genetic code is redundant but not ambiguous.

(b) Describe one thing that the redundancy of the code makes impossible.

Part 4 · Measuring which base matters

Click the **Which base matters** tab. The tool has tried every possible single-base change at every one of the 61 sense codons. Record the results from the tool's table.

Position in the codon	Changes tried	Amino acid changed	Silent	% silent
1				
2				
3				

8. One position in the codon is never silent.
(a) Identify the position.

(b) Describe the effect on the amino acid of any substitution at this position.

9. A student claims that “mutations in the third base of a codon do not matter.” Using two numbers from the Part 4 table, evaluate the student’s claim.

Part 5 · One codon, every substitution

Use the Try it on one codon panel of **Which base matters** and press the codon UCA (Ser). Press First, Second and Third in turn, and record the three codons a single substitution could give and what each one specifies.

Position changed	Three possible new codons	What each specifies	How many are silent
First			
Second			
Third			

10. Two of the substitutions at the second position of UCA give a codon that does not specify an amino acid.
(a) Identify what these two substitutions produce.

(b) Explain why this outcome is usually more damaging to the protein than a change of one amino acid.

11. (a) Explain what the near-universality of the genetic code is evidence for.

(b) Describe the exceptions that make “nearly universal” more accurate than “universal.”

What the model simplifies

Anticodons are given as the exact complement of the codon. Real base pairing at the third position is looser than that (the “wobble” position), which is why one tRNA can serve more than one codon and why a cell needs fewer than 61 different tRNAs.

The ribosome is drawn as a single shape moving along the mRNA. It is two subunits with three tRNA binding sites, and the chemistry of forming each peptide bond is carried out by the ribosomal RNA itself rather than by a protein.

The percentages in Part 4 are properties of the standard code table with every single-base change weighted equally. Real mutation is not uniform: some base changes are commoner than others, and a change that alters an amino acid may still leave the protein working.

Initiation is shown as the ribosome finding an AUG. In eukaryotes it binds the 5′ cap first and scans along to the first AUG; in bacteria it binds a sequence just before the start codon instead. Both end up at an AUG.

The code is described as nearly universal because it is: some mitochondria and a few single-celled organisms read a handful of codons differently. Those exceptions are small and rare, which is why the shared code is still evidence of common ancestry.