

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 1 uses **Read the message**, Part 2 uses **The whole code**, and Part 3 uses **Which base matters**. The point of Part 3 is that the claim “the third base matters least” is usually asserted and almost never measured. In this topic you measure it.

Part 1 • Reading a message three bases at a time

Translate each mRNA below by hand, using the code table on the tool's second tab. Give the codons, the anticodon of the **first** codon, and the polypeptide. Stop where the message tells you to stop.

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

1. Define a codon and an anticodon, and state the relationship between them.

2. Every polypeptide in the table above begins with the same amino acid. State which one, and explain why that is not a coincidence.

Part 2 · The same bases, a different frame

On **Read the message**, the mRNA AUGGCAUUAGCCUGAAGU is translated in each of its three reading frames. Record what each frame produces, then compare them.

Frame	Codons	Polypeptide	Number of amino acids
0			
1			
2			

3. Compare the three polypeptides position by position. State how many positions hold the same amino acid in all three, and explain why that number is what it is.

4. In frame 0, translation stops before the mRNA runs out. Explain what that shows about what a stop codon actually is.

5. Predict what would happen to the polypeptide if a single extra base were inserted immediately after the start codon, and justify your prediction using this table.

Part 3 · Sixty-four codons, twenty amino acids

Switch to **The whole code** and use the amino-acid buttons to fill this in.

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, using a number in your answer.

7. Explain what it means to say the code is redundant but not ambiguous, and state one thing that redundancy makes impossible.

Part 4 · Measuring which base matters

Go to **Which base matters**. The tool has tried every possible single-base change at every one of the 61 sense codons. Record the measurement, then explain it.

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

8. One position is never silent — not merely rarely. Identify it and state what that means for a mutation landing there.

9. A student says “mutations in the third base don't matter.” Correct this statement using two numbers from your table.

Part 5 · One codon, every substitution

Use the second panel of **Which base matters** with the codon UCA (Ser). For each position, list the three codons a single substitution could give and what each one now 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 turn this codon into something that is not an amino acid at all. Identify what they produce and explain why that outcome is worse than a change of amino acid.

11. Explain what the near-universality of the genetic code is evidence for, and state the caveat that keeps the claim accurate.

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” the third tab is named after — 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.