

Transcription and RNA Processing

Learning objective 6.3.A Describe the mechanisms by which genetic information flows from DNA to RNA.

Name: _____

Date: _____

Period: _____

Use the tool **From Gene to Message**. Part 1 uses **Pick the strand**, Parts 2 and 3 use **Cut and paste** and Part 4 uses **Against replication**. Two things here are easy to say and worth actually computing: what happens if you read the **wrong strand**, and how many different proteins one gene can specify.

Part 1 • Which strand, and what comes out

For each coding strand below, write the template strand and then the mRNA. Remember that the mRNA matches the **coding** strand with U for T — so you have a built-in check on your own working.

Coding strand (5'→3')	Template strand (3'→5')	mRNA (5'→3')	Check: does the mRNA match the coding strand?
TACGGATC			
ATGCCGTA			
GGCATTAC			

1. Distinguish between the template strand and the coding strand, and explain why the coding strand has that name.

2. Open **Pick the strand** and select the coding strand by mistake. Record how many of the 18 bases are wrong, and explain why the answer is that number and not a smaller one.

Part 2 · Processing the transcript

Switch to **Cut and paste** with every exon included. Record the lengths, then work out what each processing step does to them.

Quantity	Length in bases	Where it comes from
Primary transcript		
Introns removed		
Exons kept		
Mature mRNA with tail		

3. The mature mRNA is longer than the exons it was assembled from, even though splicing only removes material. Explain how both of those can be true.

4. Calculate what percentage of the primary transcript is discarded as introns, and comment on what that means for the length of a gene compared with the mRNA it produces.

Part 3 · One gene, several messages

Stay on **Cut and paste** and use the buttons to include or remove each optional exon. Work through every combination and record the mature mRNA it gives.

Exon 2	Exon 3	Exons in the mRNA	Coding bases	Mature mRNA
In	In			
In	Out			
Out	In			
Out	Out			

5. State how many different mature mRNAs this gene can make, and write the general rule for a gene with n independently optional exons.

6. Explain why this is the same counting argument as independent assortment in Topic 5.2.

7. Explain why “exon” describes what happens to a sequence rather than what the sequence is.

Part 4 · Against replication

Switch to **Against replication**. Complete the comparison, then answer without the tool.

	Replication	Transcription
What is made		
How much of the DNA is used		
Enzyme		
Needs a primer?		
Product pairs with the template?		
Direction of synthesis		
Base used opposite adenine		
How often it happens		

8. One row of the table is the same in both columns. Identify it and explain why it is the same.

9. Transcription needs no primer and replication does. Explain what that one difference accounts for in replication.

10. Explain why gene expression can be regulated but replication essentially cannot, using two rows of your table as evidence.

What the model simplifies

The gene on the first tab is 18 bases long so that both strands and the RNA fit on one line. A real gene is thousands of bases, and only part of it is the sequence that ends up specifying the protein.

Exon and intron lengths are drawn to scale relative to one another and are typical in shape — introns much longer than exons — but the numbers are chosen so the arithmetic can be checked rather than taken from a particular gene.

Alternative splicing is modeled as each optional exon being independently included or excluded. Real splicing is more constrained: some combinations are never made, some exons are mutually exclusive, and which pattern is used depends on the cell type. The 2^n figure is an upper bound rather than a count.

Introns are shown being removed cleanly at exon boundaries. The actual splicing is done by a large complex of RNA and protein that recognizes sequences at the ends of each intron, and mutations in those sequences cause introns to be kept or exons to be skipped.

Prokaryotes are left out. Bacterial genes generally have no introns, no cap and no poly-A tail, and transcription and translation happen at the same time in the same compartment — the processing here is a eukaryotic story.