AP BIOLOGY · UNIT 6 · TOPIC 6.3

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 parts of this handout ask for a calculation: what happens if RNA polymerase reads the **wrong strand**, and how many different mature mRNAs one gene can produce.

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 in place of T. Use the last column to check your work.

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

1. (a) Describe the difference between the template strand and the coding strand of a gene.

(b) Explain why the coding strand has that name.

2. On the Pick the strand tab, press Read the coding strand (a mistake).
(a) Identify how many of the 18 bases in the RNA are wrong.

(b) Explain why every base is wrong, rather than only some of the bases.

Part 2 · Processing the transcript

Switch to **Cut and paste** with every exon included, as the tool opens. Record each length from the readouts, and describe where it comes from.

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 the mature mRNA can be longer than its exons.

4. (a) Calculate the percentage of the primary transcript that is removed as introns. Show your work.

(b) Describe what this percentage indicates about the length of a gene compared with the length of the exons it keeps.

Part 3 · One gene, several messages

Stay on **Cut and paste** and use the Exon 2 and Exon 3 buttons to include or remove each optional exon. Set each combination in the table 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. (a) Identify the number of different mature mRNAs this gene can make.

(b) Determine the number of different mature mRNAs that a gene with n independently optional exons can make.

6. Explain why the number of mature mRNAs is calculated in the same way as the number of different gametes produced by independent assortment in Topic 5.2.

7. In this gene, Exon 2 is kept in some mature mRNAs and removed in others. Explain why “exon” describes what happens to a sequence rather than a fixed property of the sequence.

Part 4 · Against replication

Switch to **Against replication**. Complete the comparison, then answer questions 8 to 10.

	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. (a) Identify the row of the Part 4 table that is the same in both columns.

(b) Explain why this row is the same for replication and transcription.

9. Replication requires a primer and transcription does not. Explain how this one difference accounts for other features of replication that transcription does not have.

10. Using two rows of the Part 4 table as evidence, explain why transcription can be regulated to control gene expression but replication cannot.

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 happens only in eukaryotes.