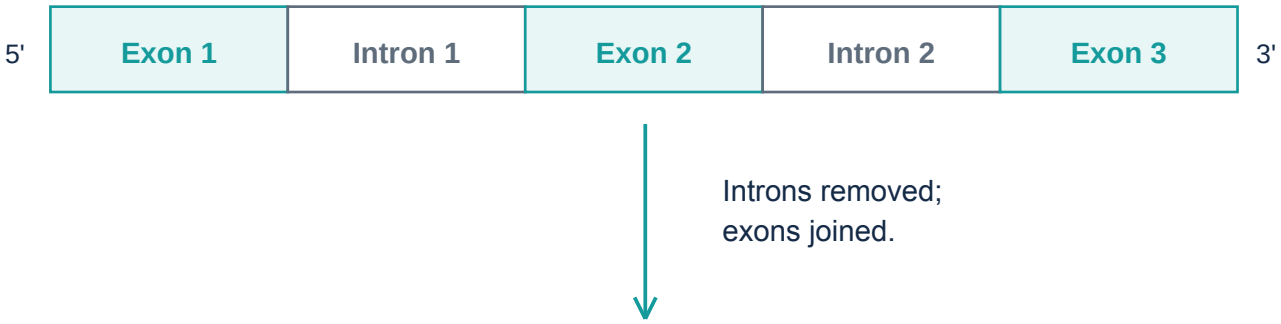
Remove introns, join exons

In eukaryotes, an intron-containing gene produces a primary RNA transcript (pre-mRNA). This RNA must be processed before it can serve as mature messenger RNA.

1. FOLLOW THE RNA THROUGH SPLICING

Primary transcript: exons AND introns



Spliced RNA: exons retained in order



Boxes represent RNA regions, not individual bases. Widths are not to scale. The shorter row shows removal of introns; end modifications are omitted.

2. PROCESS THE RNA, NOT THE DNA

Introns are transcribed into the primary RNA and then removed during splicing. Exon sequences are joined to make a continuous RNA molecule. The corresponding intron sequences remain in the DNA; the gene itself is not cut shorter.

Splicing takes place in the nucleus and can begin while transcription is still underway. After processing, mature mRNA can leave through a nuclear pore. Ribosomes then translate its coding region in the cytoplasm.

Introns in primary RNA and their removal: NHGRI, Intron.
Splicing and nuclear RNA processing: OpenStax Biology 2e, section 15.4.

Scope: Cambridge Biology 9700 syllabus, section 6.2, outcome 5, p. 25.

What stays in the mature message?

The essential distinction is retention: introns are removed from pre-mRNA; exon sequences remain in the mature mRNA. Splicing joins RNA regions, not amino acids.

INTRONS: REMOVED

Present in the primary transcript but absent from the mature mRNA after splicing. They do not provide amino acids for this polypeptide.

EXONS: RETAINED

Remain in mature mRNA. Exons contain the coding sequence, but can also include untranslated regions that do not specify amino acids.

1. WORKED LENGTH EXAMPLE: COUNT WHAT REMAINS

Region	Length (RNA nucleotides)
Exons 1, 2 and 3	120 + 180 + 90 = 390
Introns 1 and 2	200 + 110 = 310
Primary transcript	390 + 310 = 700

After splicing: 700 - 310 = 390 nucleotides

This example counts only exon and intron sequences and ignores cap/tail additions. It does not imply a 130-amino-acid protein: untranslated regions and a stop codon may be present.

2. ADDITIONAL PROCESSING - SUPPORTING CONTEXT

Typical eukaryotic mRNAs also receive a 5' cap and a 3' poly-A tail. These help protect the RNA and support its use or export. The syllabus focus here is removal of introns and joining of exons; these other modifications are not splicing.

Do not describe introns as DNA that is never transcribed, or as necessarily useless. Some intron sequences have regulatory roles. Likewise, retained in mRNA does not mean every exon nucleotide is translated.

Retained exons and untranslated sequences: NHGRI, Exon.
Capping and polyadenylation: OpenStax Biology 2e, section 15.4.

Scope: Cambridge Biology 9700 syllabus, section 6.2, outcome 5, p. 25.