

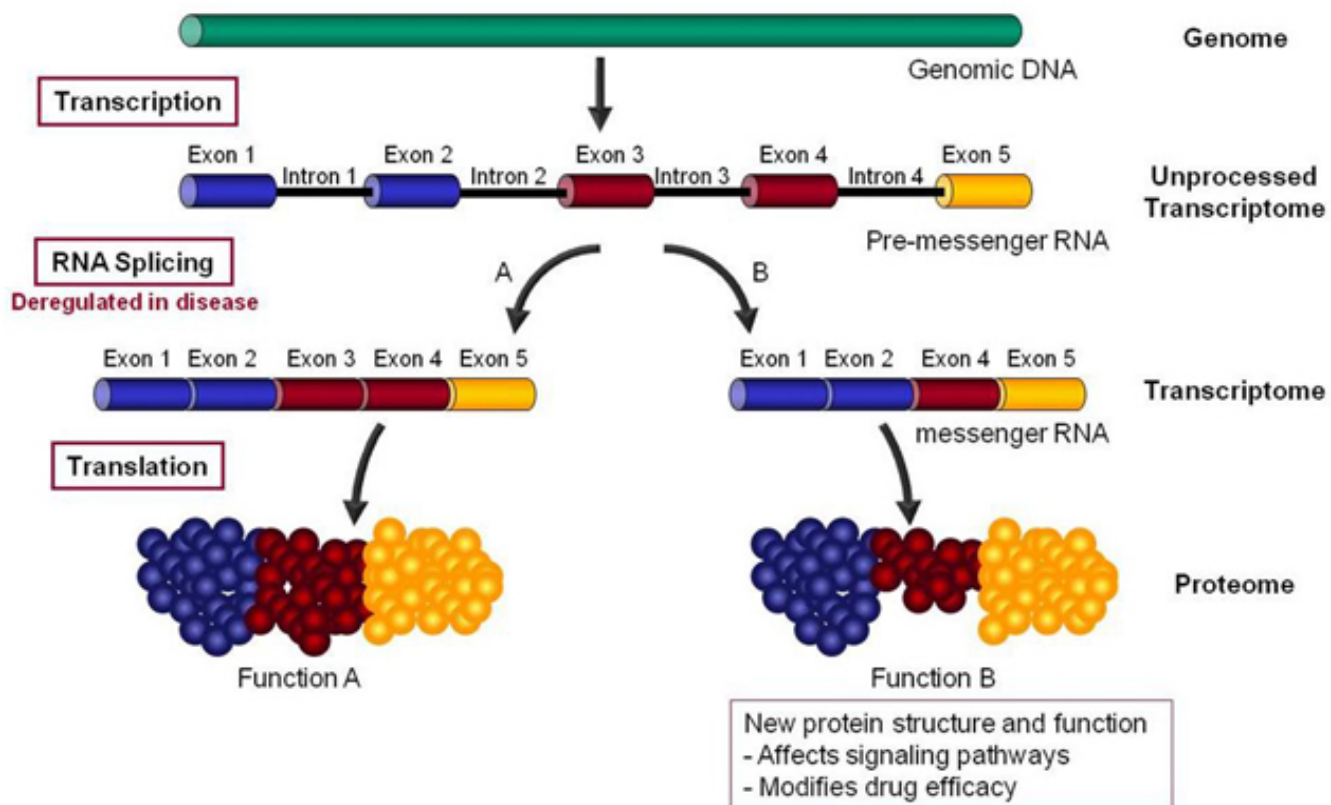
## Alternative RNA splicing

**RNA splicing is an essential and precisely regulated post-transcriptional process that occurs prior to mRNA translation.**

It is thought that at least **70%** of the approximately 30,000 genes in the human genome undergo alternative splicing and that, on average, a given gene gives rise to **4** alternatively spliced variants - encoding a total of **90-100,000** proteins which differ in their sequence and therefore, in their activities.

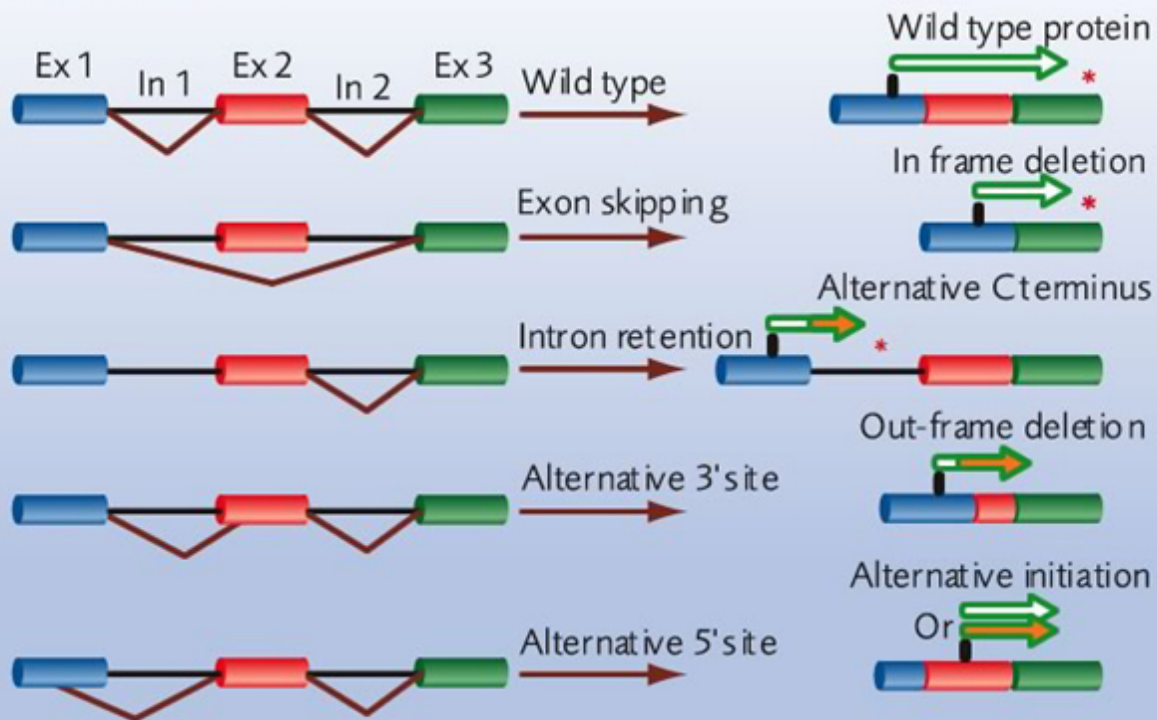
A gene is first transcribed into a pre-messenger RNA (pre-mRNA), a copy of the genomic DNA containing both introns (destined to be removed during pre-mRNA processing) and exons (destined to be retained within the mRNA in order to code the protein sequence).

During RNA splicing, exons are either retained in the mRNA or targeted for removal in different combinations to create a diverse array of mRNAs from a single pre-mRNA. This process is known as **alternative RNA splicing**.



Types of splicing alteration observed include exon skipping, intron retention and use of alternative splice donor or acceptor sites. These give rise to different protein isoforms in different tissues, developmental states, or disease conditions.

## The RS-domain dependent and RS-domain independent splice site selection.



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■ initiation codon \* Stop codon → wild type amino-acid sequence → alternative amino-acid sequence

RNA splicing is specifically deregulated in disease conditions. A precise understanding of these deregulations can reveal new targets for the discovery of more efficacious drugs or new biomarkers for the development of more accurate diagnostics.

**For more information** about alternative RNA splicing, search our [Literature References](#) and [Useful Links](#) or visit our [SpliceArray portal](#).

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