

EXONS: An exon is a coding region of a gene that contains the information required to encode a protein. In eukaryotes, genes are made up of coding exons interspersed with non coding introns. These introns are then removed to make a functioning mRNA that can be translated into a protein. In the DNA of eukaryotic organisms, exons can be together in a continuous gene or separated by introns in a discontinuous gene. When gene is transcribed into pre mRNA, transcript contains both introns and exons, the pre mRNA is processed and the introns are spliced out of molecule. Mature mRNA consist of exons and short untranslated regions on either end. Exons make up the final reading frame which

consist of nucleotides arranged in triplets

Function of Exons:

Exons are pieces of coding DNA that encode protein. The presence of exons and introns allows for greater molecular evolution through exon shuffling (exon shuffling occurs when exons on sister chromosome are exchanged during recombination). Exon shuffling allows for the formation of new genes. Exons allow for multiple proteins to be translated from the same gene through alternative splicing. Alternative splicing can result in a no. of diseases including alcoholism and cancer.

Q: What is inducible system?

1.10.3 Introns

An *intron* is any nucleotide sequence that is removed when the primary transcript of the gene is processed to give the mature processed RNA product. The sequences retained in the mature RNA product are termed *exons*. A mature transcript starts and ends with exons. The exons are present in the same order in the gene and in the RNA. The term 'intron' refers to both the DNA sequence within a gene and the corresponding sequence in primary transcripts. It was first discovered in 1977, independently by Phillip Sharp and Richard Roberts. Introns are present in most genes of higher eukaryotes, although they are not universal. Many genes like interferon genes, histone genes, ribonuclease genes (many), heat shock protein genes, G protein-coupled receptor genes (many) lack introns. In addition, introns are not found in most genes of lower simple eukaryotes, such as yeast. Conversely, introns are rare in genes of prokaryotes.

The sizes of the exons and introns vary as well. Indeed, introns are very often much longer than the exons. Introns range in size from about 50 nucleotides to >100,000 nucleotides. Exons are usually short, typically on the order of 150 nucleotides and the introns are relatively long (>1 kb). The length of a gene is defined by the length of the primary transcript instead of the length of the mature RNA.

The overall length of a gene is determined largely by its introns. The number of introns found within a gene also varies enormously—from one (as in case of most coding genes of budding yeast) to as many as 363 (in the case of the *titin* gene of human). A typical mammalian coding gene has six to seven introns. Comparisons of related genes in different species show that the sequences of the corresponding exons are usually conserved but the sequences of the introns are much less similar. Introns evolve much more rapidly than exons because of the lack of selective pressure to produce a polypeptide with a useful sequence.

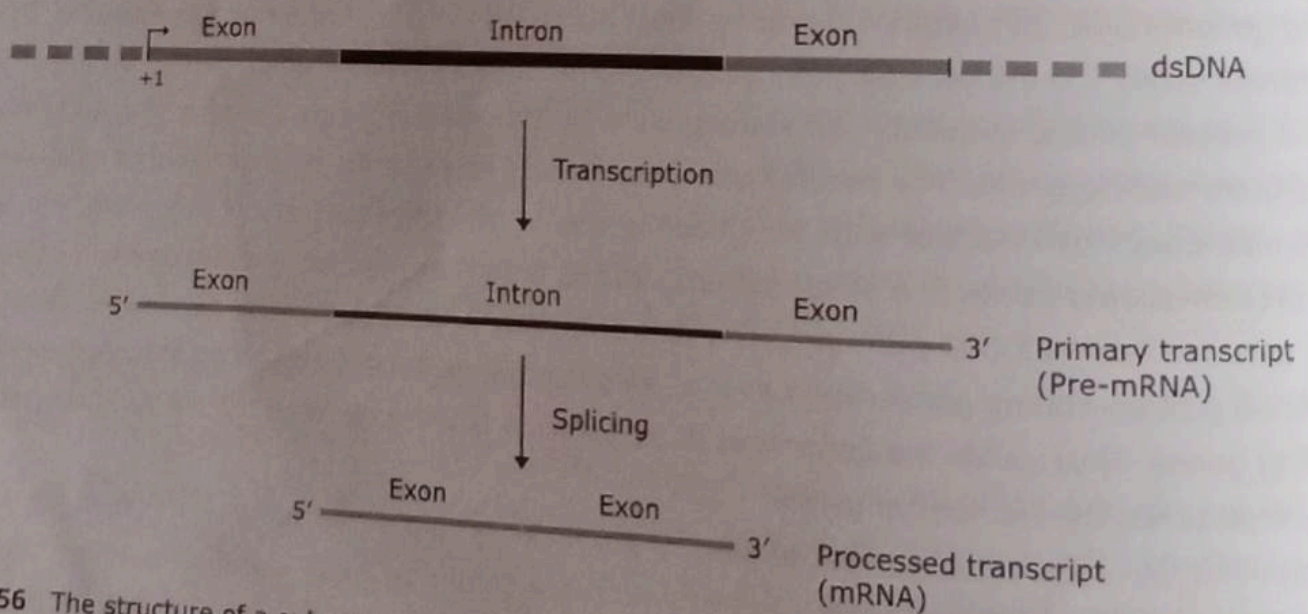


Figure 1.56 The structure of a eukaryotic *split gene* i.e. gene with intron. Most eukaryotic genes contain segments of coding sequences (exons) interrupted by noncoding sequences (introns). Both exons and introns are transcribed to yield a long primary RNA transcript. Introns are the intervening sequences that are removed when the primary RNA transcript is processed to give the mature RNA product. The mRNA has only the exons.

Table 1.11 Average sizes of exons and introns in human genes

Gene product	Size of gene (kb)	Number of exons	Average size of Intron (bp)
Insulin	1.4	3	480
β -Globin	1.6	3	490
Serum albumin	18	14	1100
CFTR (cystic fibrosis)	250	27	9100
Titin	283	363	466
Dystrophin	2400	79	30770

Several distinct types of introns have been reported in eukaryotes and prokaryotes. All classes of genes may contain introns: nuclear genes coding for proteins, rRNA and tRNA. Introns are also found in mitochondrial and chloroplast genes. Examples of some most common types of introns are mentioned in the table 1.12. Introns usually do not code for proteins. However, certain introns of group I and group II classes contain open reading frames that are translated into proteins. Expression of the protein allows the intron to be mobile.

Table 1.12 Types of most common introns

Intron type	Where found
GU-AG introns	Eukaryotic nuclear pre-mRNA
AU-AC introns	Eukaryotic nuclear pre-mRNA
Group I introns	Eukaryotic nuclear pre-rRNA, organelle RNAs, some prokaryotic RNAs
Group II introns	Organelle RNAs, some prokaryotic RNAs
Pre-tRNA introns	Eukaryotic nuclear pre-tRNA
Archaeal introns	Various RNAs

Source: Adapted from T.A. Brown, *Genomes 3*, Garland Science

Origin of introns: intron-early versus intron-late hypothesis

All eukaryotes have introns, but these elements are rare—almost non-existent—in bacteria. There are two likely explanations for this situation. First, in the so-called **introns-early hypothesis**, introns existed in all organisms but were lost from bacteria. If introns originally did exist in bacteria, why might they subsequently have been lost? The argument is that these 'gene-rich' organisms have well-organized their genomes in response to selective pressure to increase the chromosomal replication and cell division. In the alternative view, introns never existed in bacteria but, rather, arose later in evolution. This is called **introns-late hypothesis**. According to this hypothesis, introns were inserted into genes that previously had no introns, perhaps by a transposon-like mechanism.