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Abstract

Alternative splicing, the process of removing introns from pre-mRNA and rearrangement of exons to give several types of mature transcripts, has been described more than 40 years ago. However, until recently, it has not been clear how extensive it is. Genome-wide studies have now conclusively shown that more than 90% of genes are alternatively spliced in humans. This makes alternative splicing one of the main drivers of proteomic diversity and, consequently, determinant of cellular function repertoire. Unsurprisingly,

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