

Special Issue

Alternative Splicing in Human Physiology and Disease

Message from the Guest Editors

Alternative splicing, first proposed by Gilbert in 1978, allows multi-exon genes to produce multiple splice variants. Several of the linear transcripts encode protein isoforms with distinct amino acid sequence, structure, and function(s). Alternatively spliced transcripts are generated from a single gene through selection of cassette exons, mutually exclusive exons, retained introns, alternative 3' or 5' splice sites, and/or usage of alternative promoters or polyadenylation sites. High-throughput sequencing has revolutionized transcriptomics, revealing that the post-transcriptional maturation of primary transcripts from more than 95% of human multi-exon genes involves alternative splicing.

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Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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