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Alternative Splicing in Human Physiology and Disease

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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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Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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