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Alternative Splicing in Cancer

Guest Editor:

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Deadline for manuscript submissions:
closed (15 July 2023)

Message from the Guest Editor

Approximately 94% of genes are alternatively spliced (AS) in humans, and there are thousands of isoforms specifically associated with disease progression. A recent report demonstrates that the function of splice isoforms may be as different as being encoded by distinct genes, underlining the importance of AS in gene regulation and modulation of the cells' functional repertoire. Unsurprisingly, given its extent, numerous splice isoforms have been described to be associated with cancer, and aberrant splicing is recognized as one of the hallmarks of cancer. Besides the implications for cancer pathogenesis, de-regulated alternative splicing is recognized as one of the novel areas of cell biology where therapeutic manipulations may be designed. Indeed, using either small molecules or splicing-switching oligonucleotides, faulty splice isoforms may be switched back to their normal counterparts and therefore inhibit tumor growth.

This Special Issue welcomes the submission of research papers or reviews on any aspect linking constitutive or alternative splicing to cancer progression, pathologic mechanisms, or therapeutic aspects.

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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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