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Impact of 3'UTR Variants on mRNA Stability

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Message from the Guest Editors

In this Special Issue we are interested in the mechanisms that generate 3'UTR diversity in normal and disease cells (such as alternative polyadenylation, alternative splicing, or the exonization of repetitive elements), in addition to their impact on mRNA function. Furthermore, we are also especially interested in the use of alternative 3'UTRs for the stabilization of mRNA vaccines.<false,>We are also willing to receive originals on technical developments that have facilitated the generation as well as analysis of transcriptonic information of 3'UTR variants and their impact on mRNA stability and function: <false,>Development of software to extract variant 3'UTR data from RNA.seq/single-cell RNA.seq runs;
Generation of databases of variant 3'UTRs in human diseases;
New experimental techniques for the high-throughput targeting of mRNA–miRNA as well as miRNA–lncRNA interactions;
Software for modeling mRNA–miRNA–lncRNA networks, including alternative 3'UTRs

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Message from the Editor-in-Chief

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