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Impact of 3'UTR Variants on mRNA Stability

Guest Editors:

Dr. Estanislao Navarro

Experimental Nephrology Lab,
Institut d'Investigació Biomèdica
de Bellvitge-IDIBELL, C/ Feixa
Llarga s/n, L'Hospitalet de
Llobregat, 08907 Barcelona,
Spain

Dr. Miguel Hueso

Department of Nephrology,
Hospital Universitari de Bellvitge,
08907 L'Hospitalet de Llobregat,
Spain

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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. We are also willing to receive originals on technical developments that have facilitated the generation as well as analysis of transcriptomic information of 3'UTR variants and their impact on mRNA stability and function: 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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Special Issue



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Editor-in-Chief

Prof. Dr. Felipe Fregni

1. Neuromodulation Center and
Center for Clinical Research
Learning, Spaulding
Rehabilitation Hospital and
Massachusetts General Hospital,
Harvard Medical School, Boston,
MA 02114, USA
2. Department of Epidemiology,
Harvard T.H. Chan School of
Public Health, Boston, MA 02115,
USA

Message from the Editor-in-Chief

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Biomedicines Editorial Office
MDPI, Grosspeteranlage 5
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