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# Non-coding RNAs in Human Health and Diseases

Guest Editor:

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Deadline for manuscript submissions:
**closed (15 January 2023)**

## Message from the Guest Editor

Noncoding RNAs (ncRNAs) are arguably the enigma of the RNA transcriptome. First, while there are more annotated noncoding genes (23,995) compared to coding genes (20,440) on the latest release of the Ensembl!Further, we are only beginning to understand the role of differential regulation or function of ncRNAs caused by genetic and epigenetic perturbations.

This Special Issue will comprise reviews and original research articles focused on the recent advances in all types of ncRNAs in human health and disease. Of special interest are hypothesis-based review articles that seek to put forward novel theories with some supportive evidence, including in silico analyses or other data. Articles can focus on ncRNAs as a whole; any of the subclasses of ncRNAs, including piRNA, miRNA, snoRNA, and lncRNA; or individual ncRNAs and should describe how genetic or genomic alterations in the ncRNAs or their interaction sites on DNA, RNA, and proteins can lead to human disease. Articles without relevance to human disease or those that do not focus on disease caused by perturbation of ncRNA expression, function, or interaction will not be accepted for this Special Issue.

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## Editor-in-Chief

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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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