

Special Issue on
Noncoding RNAs in Health and Disease

CALL FOR PAPERS

Over the past two decades, the structural and functional complexity of eukaryotic genomes has been confirmed. Most of the attention has specifically fallen on the *RNA world*. The advent of new molecular biology techniques (e.g., high-throughput sequencing of DNA and RNA), together with the outbreak of computational biology, has allowed identifying a plethora of transcripts that are not translated into proteins: these have been named *noncoding RNAs (ncRNAs)*. Many *in silico*, *in vitro*, and *in vivo* studies have been focused on the characterization of expression profiles and molecular functions of these ncRNAs (*i.e.*, microRNAs, piwi-interacting RNAs, long noncoding RNAs, and circRNAs), both in physiological and in pathological conditions. Accordingly, the pathogenetic involvement of many ncRNAs in several neoplastic and degenerative diseases has been demonstrated, but more knowledge needs to be gathered to pinpoint their precise mechanistic and systemic role in controlling the genotype-phenotype relationship and their causal involvement in pathology. This special issue will be focused on new findings on these issues as on the different molecular strategies ncRNAs exploit to regulate gene expression; it will also include papers describing ncRNAs use as biomarkers for pathological conditions or response to a pharmacological treatment.

Potential topics include but are not limited to the following:

- ▶ Involvement of noncoding RNAs in cancer
- ▶ Involvement of noncoding RNAs in degenerative, neurodegenerative, and neuropsychiatric disorders
- ▶ Epigenetics of noncoding RNAs
- ▶ Cellular networks of noncoding RNAs
- ▶ Evolution of noncoding RNAs

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/ijg/rnahd/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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