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Non-Coding RNAs, from an Evolutionary Perspective

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Deadline for manuscript submissions:

closed (13 December 2018)

Message from the Guest Editors

Dear Colleagues,

Non-coding RNAs (ncRNAs), such as microRNAs and long ncRNAs (lncRNAs), pose a formidable challenge to biologists: they constitute a large fraction of eukaryotic transcriptomes and emerge as an important component of gene regulatory networks, yet, unlike protein-coding genes, their conservation in evolution is rather limited, at least at the sequence level. The evolutionary conservation of ncRNAs serves as an important indication for their functionality; however species differences in microRNAs and lncRNAs may be invaluable predictors of phylogenetic relationships and may contribute to promote plasticity and diversity in evolution.

This Special Issue will focus on evolutionary aspects of ncRNAs, from in silico to functional and mechanistic investigations. Manuscripts reporting original research, short communications and reviews will be considered

For further reading, please visit the **Special Issue website**.

Dr. Claire Rougeulle Dr. Yehu Moran *Guest Editor*











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Editor-in-Chief

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Message from the Editor-in-Chief

This field finally has a dedicated journal where its broad community can communicate and exchange its latest findings in one centralized place. This field was built stone by stone from the many scientific contributions from extremely diverse horizons, studying gene silencing in plants, position effect variegation in drosophila or quelling in fungi. This field has achieved maturity, but a lot remains to be discovered! Our aim is to publish manuscripts from all horizons that will have a high impact on the development of the field. Let's have fun and wish *Non-Coding RNA* a long and rewarding life!

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