RNA Target Prediction Methods

Guest Editors:

Prof. Dr. Stefania Bortoluzzi
Department of Molecular Medicine, University of Padova, Padua, Italy

Dr. Enrico Gaffo
Department of Molecular Medicine, University of Padova, 35122 Padua, Italy

Deadline for manuscript submissions:
closed (30 June 2019)

Message from the Guest Editors

RNAs play a wide range of functions in a variety of cellular processes and in disease mechanisms, mediated by the recognition and binding of target molecules. By base-pairing with DNA or other RNAs, RNAs regulate an array of processes through direct interactions. Moreover, key to the function of many RNAs is their binding to proteins. Thousands of noncoding RNAs have been uncovered in the NGS era and the recent findings on circular RNAs further expanded the field. However, for many of these, the functions are still unknown, calling for an improved definition of RNAs' interactions. The prediction of RNA targets represents a turning point in most research projects, since it allows the prioritization of RNAs for functional experimental study. A series of computational and methodological challenges are set by the complexity of RNA biology.

This Special Issue is dedicated to all the aspects of RNA target prediction with a focus on, but not limited to, computational methods, software, and resources. We welcome submissions of reviews, research articles, short communications, and "concept papers".

Prof. Stefania Bortoluzzi
Dr. Enrico Gaffo
Guest Editors

mdpi.com/si/23514

Special Issue

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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.

Why not consider *Genes* for your next genetics paper?

Author Benefits

Open Access: free for readers, with article processing charges (APC) paid by authors or their institutions.
High Visibility: indexed within Scopus, SCIE (Web of Science), PubMed, MEDLINE, PMC, Embase, PubAg, and other databases.
Journal Rank: JCR - Q2 (*Genetics & Heredity*) / CiteScore - Q2 (*Genetics*)

Contact Us