

Special Issue

RNA Target Prediction Methods

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".

Guest Editors

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Deadline for manuscript submissions

closed (30 June 2019)

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Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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?

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