Special Issue

Computational Methods for the Analysis of RNA Structures and Modifications

Message from the Guest Editors

From research in RNA modifications, it has become clear that RNA is a dynamic molecule that can be modified and folded into secondary and tertiary structures. Protein-coding mRNAs occupy less than a few percent of the mammalian transcriptome, leaving behind the majority of transcribed RNAs as ncRNAs. These ncRNAs include rRNAs and tRNAs, as well as other regulatory ncRNAs, such as miRNAs and lncRNAs. In particular, lncRNAs have gained momentum in recent years, due both to the acceleration in their discovery as well as their potential to explain many cellular activities and physiological phenomena, which protein-centric research has so far been unable to explain. It is now accepted in the field that lncRNAs exert their actions by binding to other macromolecules. Furthermore, since they are long RNAs, their binding to other macromolecules is closely regulated by their secondary and tertiary structures as well as their epitranscriptomic modifications. This Special Issue will highlight and discuss further developments in computational methods for analyzing RNA structures and modifications.

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Deadline for manuscript submissions

closed (1 October 2023)

BioTech

an Open Access Journal by MDPI

Impact Factor 3.1
CiteScore 4.8
Indexed in PubMed

mdpi.com/si/159917

BioTech
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