



Special Protein or RNA Molecules Computational Identification 2018

Guest Editor:

Prof. Quan Zou

School of Computer Science and
Technology, Tianjin University,
Tianjin, China

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closed (31 October 2018)

Message from the Guest Editor

Dear colleagues,

New molecules discovery is still an important and challenging task. For some special proteins include cytokines, enzymes, cell-penetrating peptides, anticancer peptides, cancerlectins, G protein-coupled receptors, etc. and some noncoding RNAs are also required to be annotated in the sequencing data, such as microRNA, snoRNA, snRNA, circle RNA, tRNA, etc, researchers often employed computer programs to list candidates, and validated the candidates using molecular experiments. The “computer program” is a key issue, which could save on wet experiments costs. High false positive software would lead to high costs in the validation process.

We have successfully organized a related Special Issue last year (see Int. J. Mol. Sci. 2018, 19, 536 as a summary). For all the new submissions, please state the relationship and differences from the papers in the 2017 Special Issue. In addition, we encourage authors to pay attention to noncoding RNA molecules. MicroRNA and other noncoding RNA detections are still open challenging for bioinformatic researchers. RNA function and RNA-disease relationship would be interesting and welcome. We also hope to receive more novel and robust methods and golden benchmark datasets in the new Special Issue.





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Prof. Dr. Maurizio Battino

Department of
Odontostomatologic and
Specialized Clinical Sciences,
Sez-Biochimica, Faculty of
Medicine, Università Politecnica
delle Marche, Via Ranieri 65,
60100 Ancona, Italy

Message from the Editor-in-Chief

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*International Journal of Molecular
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MDPI, Grosspeteranlage 5
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