Special Issue

Special Protein or RNA Molecules Computational Identification 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.

Guest Editor

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Deadline for manuscript submissions

closed (31 October 2018)

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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