Special Issue

New Insights into Computational Genomics

Message from the Guest Editors

The past few years have seen the emergence of novel experimental strategies that have revolutionised our capability to study the genome, epigenome, and transcriptome of living organisms. The advent of longread sequencing, which can identify complex structural variants to study the epigenome and the transcriptome with unprecedented resolution, and the diffusion of single-cell sequencing in biomedical research settings paved the way for the detection and quantitative analysis of cellular content, allowing the profiling of the omic layers of single cells and laying the groundwork for heterogeneity-oriented studies. As experimental protocols have improved rapidly, computational workflows for processing the data have also been refined, enabling novel methods capable of handling this continuously growing data. This Special Issue invites articles that address the many aspects of the analyses of single-cell and long-read sequencing data, highlighting the key technological and computational developments that favoured their adoption in clinical applications.

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Deadline for manuscript submissions

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Biomolecules is a multidisciplinary open-access journal that reports on all aspects of research related to biogenic substances, from small molecules to complex polymers. We invite manuscripts of high scientific quality that pertain to the diverse aspects relevant to organic molecules, irrespective of the biological question or methodology. We aim for a competent, fair peer review and rapid publication. Please look at some of the exciting work that has been published in Biomolecules so far. We would be delighted to welcome you as one of our authors.

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