Special Issue

Selected Papers from the HSG-2022 Conference

Message from the Guest Editor

The advent of high-throughput sequencing platforms opened a new era in biology by allowing researchers to obtain and analyze huge data bodies. Every year, novel methods and techniques emerge which broaden our capabilities and interests, reaching far beyond the central dogma of molecular biology, i.e., DNA-seq, RNA-seq, and Ribo-seq. The transcriptomes of single cells, protein-nucleic interactions, rare somatic mutations (DNA-seq with UMI), immunoglobulin repertoires, 3D arrangements of a genome (Hi-C), microbial communities, and many other approaches already acknowledge the presence of sequences. This has illuminated several conclusions about the molecular mechanisms of these processes. The HGS-2022 conference will feature talks about genomics of prokaryotes and eukaryotes, metagenomics of microbial communities, medical genomics, transcriptomics, protein-nucleic interactions, and translations, providing a forum to report and discuss novel high-throughput sequencing methodologies and their perspective application in research and technology. Abstracts accepted for the conference can be published in a Special Issue of the journal IJMS (subject to peer review).

Guest Editor

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The *International Journal of Molecular Sciences* (*IJMS*) 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, and molecular biophysics. *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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