Special Issue

Next-Generation Sequencing and Whole-Genome Sequencing in Molecular Research

Message from the Guest Editor

HTS is a fast-moving technology characterized by ongoing improvements in quality, length, depth, and the number of sequences, complemented by innovative breakthroughs in biochemistry, design, and engineering. These developments have led to the introduction of more powerful instruments with increasing throughput power year by year. The numerous applications of HTS, such as Whole-Genome Sequencing (WGS), RNA-Seq, and Amplicon or Shotgun Mass Sequencing, have greatly contributed to the advancement of metagenomics, transcriptomics, proteomics, metabolomics, and phylogenomics, fostering the rapid development of novel investigative, diagnostic, and analytical methods, thus harnessing the full potential of this transformative technology.

HTS has become one of the main contributors to ‘big data’, a valuable resource for predictive modeling through the application of machine learning and artificial intelligence (AI). We cordially invite you to share your HTS-based research and review papers, emphasizing your latest discoveries and the transformative power and influence of this technology, as well as its numerous applications within varied domains of study and organizations.

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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