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Advances in Cancer-Related Transcriptome and Genome Analyses

Guest Editor:

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Deadline for manuscript submissions:
closed (30 March 2024)

Message from the Guest Editor

The advent of high-throughput sequencing technologies opened a new era in molecular medicine and cancer research, allowing the genome-wide study of the molecular characteristics of tumours at the nucleotide level. As a more recent technology, single-cell sequencing allows an even higher resolution for dissecting the tumour environment at the cellular scale, while long-read sequencing improves genome assembly and the detection of transcript isoforms and structural variants.

DNA-seq and RNA-seq experiments generate massive amounts of data, which require the application of advanced interdisciplinary techniques, including bioinformatics, biostatistics, and artificial intelligence, to extract meaningful information. The molecular complexity of tumours, which requires the combination of multiple levels of information, and the difficulties of cancer studies make transcriptome and genome analysis even more challenging in cancer research.

We welcome submissions on cancer-related transcriptome and genome analyses, with a focus on the analysis of novel or existing cancer omics data sets bringing new knowledge on molecular mechanisms and aberrancies driving tumour biogenesis and progression.

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Message from the Editor-in-Chief

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