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Transcriptomics and Bioinformatics in Precision Medicine

Guest Editor:

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Deadline for manuscript submissions: closed (10 January 2023)

Message from the Guest Editor

The mRNA transcriptome effectively shows the cellular context of active functions. Due to the significant information on individual cells and the relatively easy capturing process of gene expression, transcriptomics was explored from high-throughput genomic studies using microarray. Along with the advances of next-generation sequencing technology, three factors of cost-effectiveness (data creation), diverse analyses (interpretation), and easy usage (diagnosis) serve as a foundation for the accumulation of huge amount of RNA-seg data. Accordingly, transcriptomic studies became the essence of studies. with diverse bioinformatics genomic methodologies to better understand human disease and identify novel therapeutic targets. From transcriptomic data, scientists capture the expression profiles of genes, alternative splicing, identify disease-specific study transcripts, roles in the multi-omics landscape, and etc. In this Special Issue, authors are encouraged to submit original manuscripts describing diverse transcriptomics and bioinformatics studies applied to precision medicine. Also encouraged are papers describing reviews or comparisons of relevant bioinformatics methodologies.









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Editor-in-Chief

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Message from the Editor-in-Chief

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