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Genetic and Genomics of Colorectal Cancer

Guest Editor:

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Deadline for manuscript submissions:

closed (15 August 2023)

Message from the Guest Editor

It is well known that genetic factors contribute to the pathogenesis of colorectal cancer (CRC). Currently, genome-wide association studies (GWASs) have identified more than 160 genetic loci associated with the risk of CRC. However, the effects of these variants, particularly their mechanisms, remain unclear. More and more efforts are being made with a focus on deciphering the biological mechanisms behind these potential causal variants by using multi-omics data and functional experiments. CRC is a very heterogeneous disease; single-cell measurements offer a finer-grained picture of tumor cells and help to uncover the heterogeneity. The aim of this Special Issue is to collect research findings on novel risk loci of association studies, functional investigation of loci from GWASs, integrative analysis of multi-omics data, and single-cell explorations of CRC.



mdpi.com/si/122370

Special Issue



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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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