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Computational Biology in Cancer Genomics and Proteomics

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Deadline for manuscript
submissions:

closed (20 January 2023)

Message from the Guest Editors

Dear Colleagues,

Genomics and proteomics are emerging technologies which accelerate the rate and number of discoveries in cancer research. Fueled by the huge number of genomic and proteomic data, computational biology is dealing with the challenges of technically and statistically understanding these complex data, translating the information to fit cancer studies.

This Special Issue aims to provide insight into some of the cutting-edge technologies in computational biology/bioinformatics and their potential applications in the field of cancer research. Contributions may illuminate the new bioinformatics methods, explore genotype–phenotype correlations through datamining, and apply machine learning methods to characterize tumors from diverse perspectives (including but not limited to genetic pathology, diagnostic biomarkers, and single cells). To progress in the knowledge of such intricate issues, contributions by experts in the field in the form of research papers and critical reviews are required.

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mdpi.com/si/123654

Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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