



cancers



Special Issue Reprint

Application of Multi-Omics Analysis in Cancer Diagnosis, Treatment and Prognosis

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This reprint highlights recent developments in computational biology, deep learning algorithms, and cancer biology that enable the decoding of the cancer genome and tumor microenvironment ecosystem. One of its major focuses is on the integration of multi-omics data such as WGS, WES, scRNAseq, spatial transcriptomics, and proteomics, along with radiomics and digital pathology, to better understand cancer initiation, evolution, drug-tolerant persist cancer states, and full therapy resistance. Unbiased, systematic analyses using artificial intelligence, machine learning, and deep learning approaches could advance our knowledge and improve cancer treatment. In this reprint, leading experts in the field share their insights, research findings, and visions for the future of cancer informatics. Cutting-edge computational approaches and bioinformatics algorithms provide powerful toolkits to systematically identify clinically relevant biomarkers for early cancer diagnosis, prognosis, and precision cancer therapy stratification.



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