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Molecular Landscape Genomic and Proteomic Approaches in Cancer Diagnosis

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Abstract

Understanding the molecular landscape of cancer is essential for advancing diagnostic and therapeutic strategies. Genomic and proteomic approaches have emerged as powerful tools for unraveling the complex biological mechanisms underlying cancer development and progression. This review examines the signifcance of genomic and proteomic techniques in elucidating the molecular landscape of cancer and their implications for precision diagnosis. Genomic analyses, including next-generation sequencing and whole-genome/exome sequencing, provide insights into genetic mutations, oncogenes, and tumor suppressor genes, facilitating the classifcation of tumors into distinct molecular subtypes. Proteomic profling, enabled by mass spectrometry-based technologies, ofers insights into protein expression, post-translational modifcations, and signaling pathways dysregulated in cancer. Integration of genomic and proteomic data enhances our understanding of the interplay between genetic alterations and protein dysregulation in tumorigenesis. Computational methods, such as machine learning and network analysis, aid in deciphering complex omics data and identifying biomarkers for early detection and personalized treatment. Ultimately, genomic and proteomic approaches hold promise for improving cancer diagnosis and patient outcomes by guiding targeted therapies based on the molecular characteristics of individual tumors.

expressed within cells, tissues, or bodily uids. Mass spectrometry-based techniques, such as liquid chromatography-mass spectrometry (LC-MS) and tandem mass spectrometry (MS/MS), enable the identi cation and quanti cation of thousands of proteins in complex biological samples. Proteomic pro ling o ers insights into protein expression levels, post-translational modi cations, and protein-protein interactions implicated in cancer biology [4].

One of the key advantages of proteomae2.targets for intervention. Multi-or

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