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Experimental Models in the Molecular and Genomic Characterization of Hepatocellular Carcinoma

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Message from the Guest Editor

Hepatocellular carcinoma (HCC) accounts for over 90% of primary liver tumors and has become the fifth most common cancer in the world. While improved treatment options have led to a reduction in mortality of distinct malignant tumors, the incidence of HCC is still almost equal to its mortality rate. Even in medically developed countries, patients with advanced hepatocellular carcinoma face overall 1-year and 5-year survival rates of less than 50% and 10%, respectively. In contrast, patients with HCC that is detected at a very early stage have a high probability of successful curative treatment and can achieve overall 5-year survival rates of up to 75%. Hepatocellular carcinoma is characterized by a wide inter- and intratumor heterogeneity, and this molecular heterogeneity contributes to the high risk of cancer recurrence following resection and potentially contributes to primary and secondary resistance to systemic targeted therapies. Therefore, in order to improve treatment and prevention, a more comprehensive genetic and mechanistic understanding of HCC is urgently needed.



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Special Issue



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