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Epigenetic Regulation of Solid Tumors

Guest Editors:

Dr. Donghong Zhang

Raybiotech, Atlanta, GA 30092, USA

Dr. Yuning Hou

Cancer Animal Models Shared Resource, Winship Cancer Institute, Emory University, Atlanta, GA 30322, USA

Dr. Xina Xie

The First Affiliated Hospital of Shenzhen University, Shenzhen 518000, China

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Message from the Guest Editors

Dear Colleagues,

Tumors are aggressive diseases with a high mortality rate and a costly treatment process. As the majority of cancer cases are firstly diagnosed at an advanced stage and with metastasis, the current management of cancer faces serious challenges, despite the development of advanced therapeutics. Therefore, employing cutting-edge bioinformatics, sequence technology and molecular biology to develop novel biomarkers for the accurate screening, detection, diagnosis, and prognosis prediction of cancer is essential in order to enhance patients' survival rate.

Increasing evidence indicates that epigenetic modifications, including DNA/RNA methylation, histone modifications, and non-coding RNAs (ncRNAs), have gained substantial attention in recent years, as it is now well established that these aberrations are significant biomarkers for tumor diagnosis, prognosis, and treatment response.

For this Special Issue, we invite basic and clinical oncologists to submit their contributions, including reviews, new methods, and original research, related to the role of epigenetics in tumor diagnosis and prognosis.













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Editor-in-Chief

Prof. Dr. Felipe Fregni

1. Neuromodulation Center and Center for Clinical Research Learning, Spaulding Rehabilitation Hospital and Massachusetts General Hospital, Harvard Medical School, Boston, MA 02114, USA 2. Department of Epidemiology, Harvard T.H. Chan School of Public Health, Boston, MA 02115, USA

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