



Non-coding RNAs in Glioblastoma Multiforme

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Message from the Guest Editor

Glioblastoma multiforme (GBM) is the most frequently diagnosed and aggressive brain and central nervous system (CNS) tumor. Deep study of the molecular mechanisms characterizing this tumor has led to its subtyping and to the identification of intracellular and extracellular molecular signatures that may help physicians to perform precise diagnosis, prognosis, and therapeutic interventions. Recent technological advancements in RNA sequencing have shown that the human genome is pervasively transcribed and that most of the transcriptome is made up of non-coding RNAs (ncRNAs) with a gene regulatory function (e.g., microRNAs, long non-coding RNAs, circular RNAs, etc.). ncRNAs are known to be involved in a plethora of physiological and pathological processes, including cancerogenesis. Some of them have been described as components of complex competitive endogenous RNA (ceRNA) networks and have been suggested either as drugs or therapeutic targets. The aim of this Special Issue is to summarize and expand the knowledge on the link between ncRNAs and GBM.





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