

The Role of Endogenous Circular RNAs in Glioblastoma Treatment Resistance: A Literature Review

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Abstract

Introduction: Glioblastomas are a high-grade primary brain cancer of astrocytes, a glial cell. The average survival upon diagnosis is 15 months. Researchers have been continuously attempting to develop new drugs and therapies that would exhibit greater efficiency against this cancer. However, tumor resistance is often observed in glioblastomas. Circular RNA is a relatively novel finding of non-coding RNA that is highly stable compared to linear RNA. Recent studies have found a variation in circular RNA expression levels in resistant versus non-resistant cancer cell lines. Thus, researchers have been exploring this endogenous entity to understand the role it may play in chemo- and radioresistant glioblastomas.

Methods: A comprehensive look into the most recent findings on this topic was done using Google Scholar and PubMed search engines. Key words used include "circRNA," "glioblastoma," and "chemo- and radio-resistance". This review mainly stems from primary research published between 2017 and 2024.

Results: Only a few specific circular RNAs have been found to be implicated in chemoresistance. Research has focused on understanding resistance to temozolomide. However, variation in certain circular RNA expression has also been noted in cisplatin and histone deacetylase inhibitor therapies for glioblastoma treatment. These circular RNAs inhibit the cytotoxic effects of chemotherapeutics primarily through microRNA sponging. Additionally, similar results were found in radioresistant glioblastoma tumors, whereby specific circular RNAs block apoptosis by altering various protein mechanisms through microRNA sponging and inhibiting translocation.

Discussion: Developing methods that inhibit this tumor's ability to resist otherwise effective therapies may be an ideal method of treatment. Many studies have attempted to modify cellular pathways to facilitate apoptosis of cancer cells. However, due to complex interactions and possible off-target effects, these methods are inefficient. Circular RNAs may serve as improved therapeutic targets due to their tissue specificity and increased stability.

Conclusion: The newly identified circular RNAs involved in glioblastoma therapy resistance may be used to increase cancer cell susceptibility to treatments. Knock-out and overexpression analysis indicate these molecules to be sufficient in altering resistance abilities of these cells. Highly specific targeting techniques may therefore be a viable solution for chemo- and radioresistance.

Keywords: circular RNA; circRNA; glioblastoma; chemoresistance; radioresistance

Introduction

Gliomas are one of the most common types of central nervous system tumors in adults that arises from the dysregulation of glial cells. Glioblastomas (GB) are grade IV gliomas that originate in astrocytes, a glial cell involved in neurotransmission, blood flow regulation, and immunity of the brain [1, 2]. Arising from such an important cell, it is understandable that this is the most aggressive and the most fatal primary tumor of the central nervous system [1, 3]. The median overall survival upon diagnosis is less than 15 months [1]. Current treatment of this disease includes immediate surgical resection of the tumor followed by radiotherapy and chemotherapy [3]. Temozolomide (TMZ) is the most common drug used in the treatment of GB [3].

Though this therapy has not been successful in curing patients, research does show a significant decrease in disease progression compared to an untreated tumor, lengthening the lifespan by a noticeable amount [3, 4]. However, despite recent advancements in cancer research, GB survival rate remains very low compared to other forms of tumors. The main reason for this discrepancy is due to the ability of this disease to be both chemo- and radioresistant [4]. Thus, lasting remission is nearly impossible to achieve with the current techniques.

Circular RNA (circRNA) is a relatively recent cellular discovery. It belongs to the family of non-coding, single stranded RNA, though it has been found to encode some genes, and is quite stable compared to other members of

this family due to the lack of exposure of the 3' and 5' ends [5]. The biogenesis of these molecules is still debated and its function is not fully known (Figure 1). However, circRNAs have been found to play a rather critical role in microRNA (miRNA) sponging and gene expression regulation [7, 8]. These RNAs are found in seemingly all cells of the body and appear to have some tissue-specificity [5]. Notably, many studies have found that certain circRNAs may act as oncogenes or tumor suppressor genes,

with their expression altered during tumor formation [9]. Due to the high prevalence of circRNAs, and the evolutionary conservation of these molecules, it is assumed that they play an essential role in the proper functioning of our cells [5, 7]. Interestingly, researchers have found that circRNAs are quite prominent in neuronal tissues, making up around 20% of the coding region in neuronal cells. Thus, their dysregulation is presumably a causative factor in neurological disease [10].

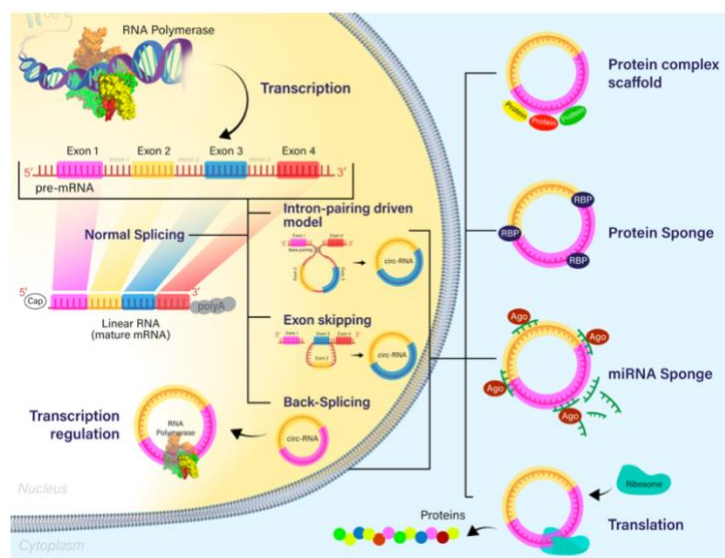


Figure 1. Biogenesis and function of circular RNA. These non-coding RNAs can be generated in multiple ways including through back splicing and exon skipping. Their main functions include miRNA sponging, altering translocation, modifying protein activity and acting as a protein scaffold. Through these various roles circular RNAs are able to alter normal cellular function and increase resistance to treatment induced apoptosis. Adapted from Tirpe et al. (2023) with permission from Dr. Tirpe from the International journal of Molecular Science published by MDPI [6].

In recent years, scientists discovered that various circRNAs are up- or downregulated in GB patients compared to healthy controls. In fact, quite a few circRNAs have been identified to play a crucial role in tumor formation, cell proliferation and even found some to be linked to radio- and chemoresistance [11]. Hence, the manipulation of circRNA expression may be effective in increasing the efficiency of current therapeutic techniques for treating GB. This review aims to summarize the most recent findings on circRNA and how changes in expression levels can decrease this tumor's resistance to radiotherapy and chemotherapy.

Methods

Search Strategy

Relevant articles published between 2017 to 2024 were obtained through a computerized search through PubMed and Google Scholar. Key terms searched included "Glioblastoma", "Circular RNA" and "therapeutic interventions." Literature was selected based on relevance following abstract screening.

Selection Criteria

The selection criteria for the included articles were as follows:

- The full report was published in English.
- Only full reports were selected.
- Primary and review articles were selected, though greater emphasis was placed on primary articles.

Results

Circular RNAs Involved in Chemoresistance

Resistance to Temozolomide

Temozolomide therapy (TMZ) is the primary treatment strategy that is first prescribed to glioblastoma patients after surgical resection [3]. TMZ readily penetrates the blood-brain-barrier and kills tumor cells by inducing site-specific DNA methylation which generates DNA damage and triggers apoptosis in the cell. The enhanced cell death causes a reduction in tumor mass [12-14]. Though this is the first line of treatment, around 50% of GB patients have TMZ-resistant tumors and therefore do not respond appropriately to this drug [14]. Many studies have

identified specific chemoresistance in GB cell lines and potential pathways involved [15-20]. Only recently have researchers found circRNAs that may partake in the manipulation of these pathways.

Zhao et al. (2019) explored microarray expression profiles of circRNAs, as well as other non-coding RNAs, in these resistant cell lines and were able to identify 53 circRNAs that were differentially expressed in TMZ resistant GB tissue. Specifically, the transcription sites of these molecules were primarily related to metabolic and translation pathways. A significant portion of these circRNAs were found to be upregulated in general in GB tumors [21]. They identified circ0043949 to be of particular importance in the TMZ-resistance of GB cells. Findings of Li et al. (2022) also indicate an essential role of circ0043949 [22]. Many studies have previously shown that circRNAs participate in cell proliferation and tumorigenesis, acting as oncogenes in many cancers including GB [23-30].

The mechanisms by which these non-coding RNAs may influence a cancer's ability to withstand apoptosis has garnered great attention. Han et al. (2021) identified

circ-HIPK3, a specific circRNA that appeared to be upregulated in TMZ-resistant gliomas. In contrast, they found miRNA-421 to be significantly downregulated in these tumor cells. This strongly suggested that circ-HIPK3 acts to block the expression of miRNA-421, resulting in increased resistance to TMZ. Though they were unable to identify the exact mechanism by which this resistance occurred, they confirmed this correlation via a knock-out experiment of circ-HIPK3 in xenograft mice [31].

Quite a few similar studies have been conducted identifying important circRNAs involved in glioma chemoresistance to TMZ [32-34]. Though many circRNAs have been shown to correlate to this acquired resistance, not many studies have found targetable pathways that could be useful for therapeutic intervention. Only three notable articles were published in the last few years concerning important pathways involving circRNAs and glioblastoma TMZ-resistance. These results are shown in [Table 1](#) [22, 35, 36]. All three of the identified circRNA were found to be directly linked to the regulation of proteins implicated in cell death and cellular division.

Table 1. CircRNAs Involved in Resistance to TMZ Treatment of Glioblastomas

Source	CircRNA Identified	Methods of Study	Mechanism of Action
Wei et al. (2020) doi:10.1093/neuonc/noaa214 [35]	CircASAP1	Knockdown and overexpression analysis in vivo	Knock down of circASAP1 reduced TMZ resistance. Found circRNA led to increased levels of NRAS through sponging of miRNA-502. NRAS activation leads to increased cell proliferation and inhibition of apoptotic pathways.
Yuan et al. (2022) doi: 10.1111/cns.13821 [36]	Circ0072309	Analyzing TMZ resistance via western blotting, immunoprecipitation and rescue experiments.	Found that increasing levels of circ007239 led to increased TMZ sensitivity. Inhibits the activity of miRNA-100 which inhibits the activity of wild-type p53. p53 is involved in the regulation of cellular division, proliferation, and apoptosis
Li et al. (2022) doi:10.1007/s11011-022-01069-3 [22]	Circ0043949	Real time qPCR, flow cytometry, bioinformatics and dual luciferase reporter assay in vivo.	High levels of circ0043949 found in TMZ resistant GB cancer cells. This circRNA was found to mediate levels of integrin α 1 by inhibiting miRNA-876. Integrin α 1 is an oncogene that blocks apoptosis, inhibits cell proliferation and induces cell migration.

Resistance to Cisplatin

Due to the high percentage of GB patients being resistant to TMZ therapy, physicians may indicate the use of various other therapeutic agents that could be used in the treatment of this cancer [37, 38]. Cisplatin is one of many platinum-based drugs used in cancer chemotherapy. Like

TMZ, cisplatin interacts with the DNA and damages it leading to a list of downstream events including inducing apoptosis, inhibiting cell division, and preventing transcription [39, 40]. While this drug is quite efficient, it has many side effects and there are some GB tumors that have developed resistance to this drug [39].

Findings presented by Luo et al. (2021) show that circPTN plays a significant role in cisplatin resistance in many GB cells. This is a circRNA that is often highly expressed in GB tumors in general with an even greater expression found in the cytoplasm of cisplatin-resistant GB cells. Through a knockout analysis of circPTN, they found increased sensitivity of these tumors to cisplatin therapy indicating an important role in resistance. Upon further investigation, they found circPTN to be involved in the

downregulation of miRNA-542, which directly targets and inhibits PIK3, a kinase that is often upregulated in cancer and increases the expression of AKT [41-43]. AKT is a well-established molecule that induces cell proliferation and inhibits apoptosis (Figure 2) [45]. The increased expression of PIK3, due to the decrease in miRNA-542 levels via sponging by circPTN, can therefore counteract the effects of cisplatin treatment by blocking the death of GB cancer cells.

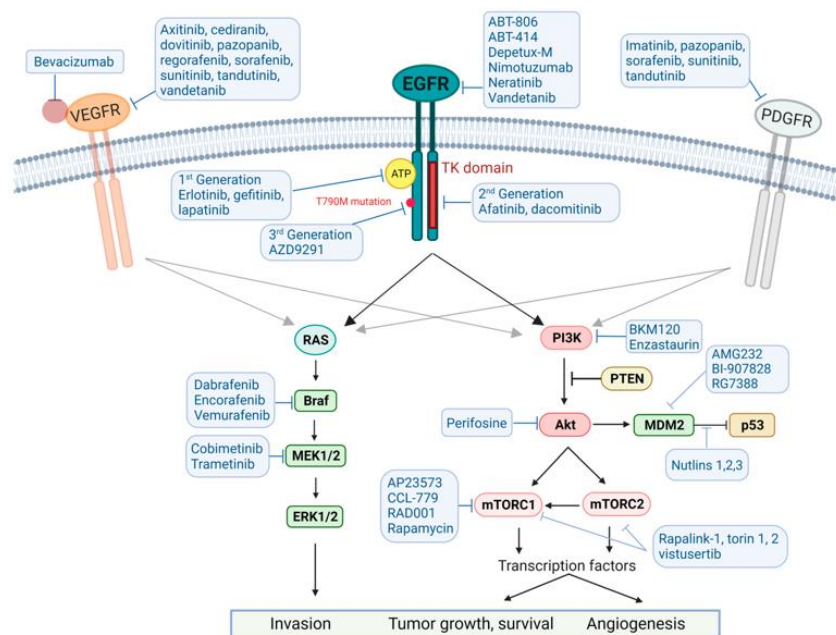


Figure 2. The important pathways implicated in cancer. The Ras and the PI3K pathways are two of the most common mechanisms of action that can be altered in cancer. Each of the proteins downstream of the growth factor receptors can act as either an oncogene or tumor suppressor gene. Subtle changes in expression levels of these proteins can increase cell survival and proliferation and thus contributes to the progression of cancer. Adapted from Obrador et al. (2024) with permission from Dr. Obrador from the International Journal of Molecular Science published by MDPI [44].

Resistance to Histone Deacetylase Inhibitors

Another prominent drug family used in the chemotherapy treatment of GB are the histone-deacetylase inhibitors (HDACis). They mainly compromise short chain fatty acids such as suberoylanilide hydroxamic acid (SAHA) [46]. Unlike other therapeutic agents used in the treatment of GB, this drug does not directly modify the DNA sequence of cancerous cells. Instead, it works through an epigenetic mechanism whereby transcriptional events are altered [47, 48]. In a study by Meng et al. (2023), circ-0000741 was found to be involved in the resistance of GB cells to SAHA treatment. This circRNA decreased the expression of miRNA-379, allowing for the increased expression of tripartite motif-containing 14 protein (TRIM14) [49]. TRIM14 is an oncogene that promotes cell proliferation [50]. Thus, inhibiting the activity of circ-0000741 could increase the efficiency of SAHA treatment by reducing the cancer cells ability to resist cell death.

CircRNAs Involved in Radiotherapy Resistance

Radiation therapy is a standard treatment for most forms of cancer. It involves exposing cancerous tissue to high beams of radiation, causing DNA damage such as double strand breaks, leading to the release of reactive oxygen species. The cells will then respond to this injury by halting division and/or instigating cell death [51]. Following surgical resection, radiation therapy has been a predominant line of treatment for GB patients for the last 40 years [52]. With the development of drugs such as TMZ, researchers have noted improved prognosis and increased safety while using a combination of radiotherapy and chemotherapy tactics. Though recent technological advances are a foot to make radiation therapy more effective and safer, a large percentage of GB patients develop radioresistant tumors, rendering this treatment inefficient [53-55]. To this end, scientists are exploring the biological mechanisms by which this resistance is acquired

in attempt to reverse the cells ability to withstand apoptosis.

In the last five years, four notable circRNAs have been identified to play a causal role in a GB tumor's ability to be radioresistant. These papers have attempted to find the

pathways that are acted upon by these circRNAs in order to recognize potential targets for therapeutic intervention. [Table 2](#) summarizes the four main circRNAs involved in radioresistance of GB tumors [56-59].

Table 2. CircRNAs Involved in Radiation Therapy Resistance of Glioblastoma

Source	CircRNA Identified	Method of study	Mechanism of action
Zhao et al. (2019) doi:10.3892/or.2019.6972 [56]	circATP8B4	RNA-sequencing and bioinformatics	In radioresistant U251 cells, extracellular vesicles were found to contain circATP8B4, causing sponging of miRNA-766.
Wang et al. (2021) doi:10.7150/ijbs.57168 [57]	circMETRN	Exosome analysis from low-dose radiation induced therapy in xenograft mice	Low dose radiation therapy stimulated the secretion of exosomes which delivered high levels of circMETRN. These circRNAs increased the expression of γ -H2AX via a miR-4709-3p/GRB14/PDGFR α pathway. Increased γ -H2AX allows for improved DNA repair mechanisms, thus the cells could withstand radiation induced DNA damage.
Yuan et al. (2022) doi:10.1007/s12640-022-00548-w [58]	circ006055	Dual luciferase reporter assay in mice	Circ006055 binds and down regulates miRNA-197. This allows for the increased expression of API5 (apoptosis inhibitor 5). The cancerous cells can then withstand cell death from radiation induced DNA damage due to increased API5.
Xu et al. (2023) doi:10.21203/rs.3.rs-3474740 [59]	circFOXO3	Metabolic analysis of radioresistant versus radiosensitive glioblastomas	CircFOXO3 increased in radioresistant cells. Found to block the translocation of apoptosis-promoting proteins to the cytoplasm. Decreasing lipid peroxidation found to be implicated in radioresistant promoting function of circFOXO3.

Discussion

To this day, primary tumors of the central nervous system are some of the deadliest cancers due to their aggressivity and resistance to treatment. Glioblastomas constitute an especially threatening form of glial cell tumor [2]. The typical treatment strategy for GB involves immediate surgical resection followed by combination therapy using chemical agents and radiation [3]. Both chemo- and radiotherapy attempt to eliminate cancerous cells by inducing DNA damage and causing cell death and arrested cell division. Though these treatments do appear to slow the progression of the disease and increase overall survival, the 5-year survival of this cancer is still only at 10% [4]. The primary reason behind the inefficiency of these therapies is due to acquired resistance [3, 4]. Improving our current methods of treatment by preventing

chemo- and radioresistance is fundamental in improving patient outcomes.

The introduction of TMZ therapy in 2005 was the last time in which we observed a significant increase in patient survival for this cancer [13]. Seeing as glioblastomas remain a fatal prognosis even with recent advancements, new strategies are vital for enhancing TMZ therapy efficiency. Studies suggest that circRNAs can promote the proliferation of cancerous cells when dysregulated, thus acting against chemical agents that aim to inhibit the cell cycle. Though many circRNAs have been identified to have a correlational role with TMZ resistance in GB [21, 22], only three direct pathways have been found that could serve as potential targets of therapeutic intervention [22, 35, 36]. Each of these circRNAs were shown to either upregulate pro-cancer proteins or downregulate anti-cancer

proteins through the inhibition of certain miRNAs. Findings by Sang et al. (2019) demonstrate that genetically amplifying the expression of circ0025202 in a mouse model of breast cancer led to increased TMZ sensitivity and significant reduction in tumor size by allowing for the increased expression of the tumor suppressor gene, FOXO3a [60]. This was done through cloning of circ0002502 and inserting it into mice via adenovirus associated plasmids [60]. Ethically, genetic modifications such as this are not yet accepted in humans. However, this technology could potentially be of great use in future medicine. Furthermore, quite a few studies have shown successful enhancement of TMZ treatment in xenograft mice using small interfering RNAs [61-63]. Again, this is a viable gene silencing technique that may be quite useful for use in humans in years to come.

The use of platinum-based anticancer drugs such as cisplatin has also been shown to be an effective agent against GB. Though it does not cross the blood brain barrier with the same ease as TMZ, cisplatin can be a useful alternative for TMZ-resistant tumors provided the use of an appropriate delivery system [39]. As cisplatin is not the primary line of treatment for GB, little research has been done on resistance to this drug. However, like with TMZ, GB tumors often acquire resistance after repeated exposure [47]. Notably, circPTEN was found to be upregulated after many trials of cisplatin and eventually correlated with resistance to this chemotherapeutic agent through the increased expression of PIK3 and AKT [44, 45]. AKT is a protein often discussed in cancer research. It is an oncogene with the ability to both inhibit cell death and increase cell proliferation. For this reason, AKT targeted therapy has been a topic of high importance [64, 65]. Unfortunately, inhibitors of this protein are often nonspecific and cause other detrimental side effects. Two possible therapies using this approach are currently in clinical trials, but none have yet received FDA approval [66, 67]. Thus, creating a therapy that targets circRNA rather than the protein itself may prove to be a more sensible approach.

Epigenetic modifying techniques such as SAHA are relatively new as a method of chemotherapy for various cancers. Used alone, this drug has thus far proven to be inadequate in reducing tumor size. However, when combined with other anticancer agents, HDACis appear to have synergistic effects. Moreover, adding this drug into the mix has helped decrease toxicity and chemoresistance. However, like all other drugs, resistance of GB tumors to treatment does eventually occur [47, 48]. Thus, the identification of targetable pathways to inhibit onset of resistance is needed. One such pathway was found by Meng et al. (2023) whereby a circ-000074 appeared to be significantly upregulated in SAHA-resistant GB tumors, leading to the overexpression of TRIM14 [49]. Similarly, to AKT, targeted therapies for TRIM14 to inhibit cancer progression have not been successful due to lack of specificity in inhibitors [68]. Downregulating non-coding

RNA using short interfering RNAs could allow for increased sensitivity to SAHA treatment [69].

Before the arrival of anticancer drugs, radiotherapy was the main treatment for cancer following surgical resection [52]. Over the last 50 years, methods of radiation therapy have seen vast improvements in terms of efficiency and safety for patients [53, 54]. As aforementioned, the current, most successful treatment plan for GB involves a combination of both chemotherapy and radiotherapy [3]. Unfortunately, a large percentage of GB tumors develop radioresistance, reducing the already low chance of patient survival [3, 4]. Recent research in circRNAs is providing a similar explanation for this resistance as it has for chemoresistance. For this reason, many scientists are turning to non-coding RNA therapies to enhance current treatment. For GB tumors, four main mechanisms of action have been identified to explain the role of circRNAs in radioresistance. Each of these pathways involves alterations in expression of genes involved in sensing DNA damage or genes involved in initiating apoptosis due to radiation induced DNA damage [56-59]. Most of these mechanisms stem from the specific miRNA sponging ability of the identified circRNAs [56-58]. However, one study demonstrated the ability of circFOXO3 to sequester proteins in order to inhibit the apoptotic pathway [59]. This function was found in another circRNA, circApot11, in breast cancer research. In this study, it was found that circAmotl1 increases the nuclear translocation of c-myc, an oncogene, to promote tumorigenesis [70]. This is further indication that circRNA can act to interfere with radiotherapy by altering the sequestration of proteins.

Interestingly, specific circRNAs appear to be associated with specific forms of resistance in GB [5]. With this knowledge, circRNAs may be able to predict which form of therapy would be the most effective for a particular GB case. Studies mainly in lung cancer have identified specific circRNAs as effective biomarkers for prognosis. Thus, performing a circRNA microarray of a tumor prior to treatment prescription could entail a more specific and tailored therapy to decrease likelihood of resistance and drug toxicity.

Conclusions

In the articles summarized, it is apparent that circRNAs primarily function through miRNA sponging in order to cause therapy resistant tumors. Other mechanisms of action have been identified in breast, lung and gastric cancers, further outlining the important role circRNAs play in proper cellular function. The malignant nature and aggressiveness of this GB emphasize the need for highly efficient therapies, hence circRNAs may be an ideal target. Many animal studies have indicated a much improved prognosis when certain circRNAs are genetically altered in expression. Unfortunately, gene editing technology is not yet ethically safe and acceptable for use in human medicine. Thus, genetically modifying expression of these

RNAs is not a viable option. However, circRNAs may be essential therapeutic targets for pharmacological agents. Due to their increased stability and their tissue and cell-type specificity, in theory these drugs would result in less off-target action compared to proteins and other non-coding RNAs. Furthermore, the identification of altered circRNA expression in GB tumors could be vital in deciding on the most effective treatment plan for a certain tumor cell line. As specific circRNAs correlate with specific tumor resistance, assessing cancer cell composition prior to prescription of treatment may ensure increased patient survival more effective and targeted approach. In sum, our current understanding of the role of circRNA in GB demonstrates the importance of these molecules in treatment resistance. Further analysis on the topic is essential to improve GB treatment strategies and increase patient survival.

List of Abbreviations Used

circRNA: circular RNA
GB: glioblastoma
HDACi: histone-deacetylase inhibitor
miRNA: microRNA
SAHA: suberoylanilide hydroxamic acid
TMZ: temozolomide
TRIM14: tripartite motif-containing 14 protein

Conflicts of Interest

No conflicts of interest were observed in the making of the article.

Ethics Approval and/or Participant Consent

As this is a literature review, ethical approval was not necessary.

Authors' Contributions

SM: Established the design of the study and was the principle researcher on the subject. Primary contributor to collection and analysis of information, drafting and revision of the manuscript and gave final approval of the version to be published.

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