



Synthesis and Significance of Arachidonic Acid, a Substrate for Cyclooxygenases, Lipoxygenases, and Cytochrome P450 Pathways in the Tumorigenesis of Glioblastoma Multiforme, Including a Pan-Cancer Comparative Analysis

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Simple Summary: Glioblastoma multiforme is a brain tumor with a very unfavorable prognosis, where the vast majority of patients do not survive a year after diagnosis. One line of research that may help in designing more successful therapeutic approaches is the synthesis and metabolism of arachidonic acid, which is then converted into a large number of different lipid mediators, including prostaglandins and leukotrienes (by cyclooxygenases and lipoxygenases, respectively). In this paper, we discuss the synthesis of arachidonic acid in glioblastoma multiforme tumors as well as the significance of lipid mediators synthesized from arachidonic acid, which can increase the proliferation of glioblastoma multiforme cancer cells, cause angiogenesis, inhibit the anti-tumor response of the immune system, and be responsible for resistance to treatment.

Abstract: Glioblastoma multiforme (GBM) is one of the most aggressive gliomas. New and more effective therapeutic approaches are being sought based on studies of the various mechanisms of GBM tumorigenesis, including the synthesis and metabolism of arachidonic acid (ARA), an omega-6 polyunsaturated fatty acid (PUFA). PubMed, GEPIA, and the transcriptomics analysis carried out by Seifert et al. were used in writing this paper. In this paper, we discuss in detail the biosynthesis of this acid in GBM tumors, with a special focus on certain enzymes: fatty acid desaturase (FADS)1, FADS2, and elongation of long-chain fatty acids family member 5 (ELOVL5). We also discuss ARA metabolism, particularly its release from cell membrane phospholipids by phospholipase A₂ (cPLA₂, iPLA₂, and sPLA₂) and its processing by cyclooxygenases (COX-1 and COX-2), lipoxygenases (5-LOX, 12-LOX, 15-LOX-1, and 15-LOX-2), and cytochrome P450. Next, we discuss the significance of lipid mediators synthesized from ARA in GBM cancer processes, including prostaglandins (PGE₂, PGD₂, and 15-deoxy- $\Delta^{12,14}$ -PGJ₂ (15d-PGJ₂)), thromboxane A₂ (TxA₂), oxo-eicosatetraenoic acids, leukotrienes (LTB₄, LTC₄, LTD₄, and LTE₄), lipoxins, and many others. These lipid mediators can increase the proliferation of GBM cancer cells, cause angiogenesis, inhibit the anti-tumor response of the immune system, and be responsible for resistance to treatment.

Keywords: glioblastoma multiforme; arachidonic acid; fatty acid; PUFA; prostaglandin; leukotriene; 5-HETE; cyclooxygenase-2; 5-lipoxygenase

1. Introduction

Glioblastoma multiforme (GBM) is one of the most aggressive brain tumors and has the worst prognosis, with an average survival of about one year [1–3]. In order to either improve existing therapies or develop new approaches, the mechanisms of GBM



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tumorigenesis are being intensively investigated, including those involving arachidonic acid (ARA) C20:4n-6 and the lipid mediators formed from this fatty acid.

PUFAs, in particular arachidonic acid ARA C20:4n-6, eicosapentaenoic acid (EPA) C20:5n-3, and docosahexaenoic acid (DHA) C22:6n-3, can be converted into lipid mediators, such as eicosanoids [4], and pro-resolving lipid mediators [5]. Eicosanoids are 20-carbon lipid mediators synthesized from ARA C20:4n-6, dihomo-γ-linolenic acid C20:3n-6, and EPA C20:5n-3 using cyclooxygenases (COX) and lipoxygenases (LOX), resulting in the formation of prostaglandins and leukotrienes, respectively [4]. Eicosanoids have pro-inflammatory properties, although there are also lipid mediators with anti-inflammatory properties, such as 15-deoxy- $\Delta^{12,14}$ -PGJ₂ (15d-PGJ₂) [6]. EPA and DHA can be converted into pro-resolving lipid mediators with LOX, cytochrome P450, and acetylated cyclooxygenase-2 (COX-2) [5]. This conversion produces lipoxins and resolvins, although it should be mentioned here that free PUFAs, including ARA, are the activators of peroxisome proliferator-activated receptors (PPAR) α and PPAR γ [7].

All of the aforementioned groups of ARA metabolites have either pro- or anti-cancer properties in GBM tumors, which indicates their significance in GBM tumor development. Despite their important role, some groups of these lipid mediators are little-known and rarely studied, and there is no paper in the literature that reviews the body of research in this area. The aim of this paper is to fill this gap and at the same time generate more interest in the role of ARA metabolites in GBM.

2. Methodology

This study's major objective is to characterize the significance of all ARA C20:4n-6derived lipid mediators, their receptors, and the enzymes responsible for their production in the tumorigenic pathways in GBM. The PubMed search engine (https://pubmed.ncbi. nlm.nih.gov accessed on 1 October 2022) was used for this purpose. Due to the fact that many of the lipid mediators produced from ARA C20:4n-6 have not yet been investigated in the context of GBM, two additional sources were used to conduct a bioinformatic analysis of every gene in GBM, namely, the transcriptomics analysis carried out by Seifert et al. [8] and the Gene Expression Profiling Interactive Analysis (GEPIA) web server (http://gepia. cancer-pku.cn accessed on 20 October 2022) [9].

The analyses posted on the GEPIA portal include the analysis of nearly 10,000 samples from 33 different cancers deposited in the Cancer Genome Atlas (TCGA) [10] along with the analysis of more than 8000 healthy tissue samples posted in Genotype-Tissue Expression (GTEx) [11,12]. The GEPIA served as a source of data on differences in the expression of given genes between GBM tumor and healthy brain tissue, and for linking the expression of a given gene to GBM patient prognosis.

A transcriptomics analysis was performed by Seifert et al. [8] on nearly 17,000 different genes in various grades of glioma, including GBM, from 45 patients. These results were normalized with a control: an analysis of gene expression in brain samples from 21 epilepsy patients from the REpository of Molecular BRAin Neoplasia DaTa (Rembrandt) [13], which served as a second source of data on differences in the expression of genes between GBM tumors and healthy brain tissue.

3. Arachidonic Acid Biosynthesis and Glioblastoma Multiforme

3.1. Arachidonic Acid Biosynthesis

ARA C20:4n-6 in humans is not synthesized de novo but from linoleic acid C18:2n-6 in the PUFA biosynthesis pathway (Figure 1) [14]. Linoleic acid C18:2n-6 in its activated form, linoleoyl-CoA C18:2n-6, undergoes desaturation with fatty acid desaturase 2 (FADS2)/ Δ^6 -desaturase (D6D), which is accompanied by the formation of γ -linolenoyl-CoA C18:3n-6. Subsequently, the hydrocarbon chain in this fatty acid family members 5 (ELOVL5), accompanied by the formation of dihomo- γ -linolenoyl-CoA C20:3n-6. At the same time, an alternative pathway for the synthesis of dihomo- γ -linolenoyl-CoA C20:3n-6 from linoleoyl-

CoA C18:2n-6 is also possible [15]. Linoleoyl-CoA C18:2n-6 is first elongated with ELOVL5 and then desaturated by FADS2. This means that these two enzymes can catalyze the formation of dihomo- γ -linolenoyl-CoA C20:3n-6 in reverse order. In this alternative pathway of PUFA biosynthesis, FADS2 shows activity not of Δ^6 -desaturase but of Δ^8 -desaturase. In the latter reaction, the hydrocarbon chain in dihomo- γ -linolenoyl-CoA C20:3n-6 is desaturated with fatty acid desaturase 1 (FADS1)/ Δ^5 -desaturase (D5D), which is accompanied by the production of arachidonyl-CoA C20:4n-6. In the same way as arachidonyl-CoA C20:4n-6, EPA-CoA C20:5n-3 can also be synthesized from α -linolenoyl-CoA C18:3n-3 [14]. Arachidonyl-CoA C20:4n-6 is an activated form of ARA that participates in metabolic pathways, including lipid synthesis pathways. Once synthesized, arachidonyl-CoA C20:4n-6 is used to make lipids, particularly phospholipids. Incorporated into phospholipids, ARA C20:4n-6 is stored and then released by phospholipases A₂ (PLA₂) as a free fatty acid [16]. Arachidonyl-CoA C20:4n-6 can also be further elongated via elongation of the long-chain fatty acid family members 2 (ELOVL2) and ELOVL5 in a synthesis pathway similar to the synthesis of DHA C22:6n-3 from EPA C20:5n-3 [14,17–19].



Figure 1. ARA biosynthesis. ARA C20:4n-6 in humans is not synthesized *de novo* but from linoleic acid C18:2n-6. As linoleoyl-CoA C18:2n-6, this PUFA undergoes desaturation to γ -linolenoyl-CoA C18:3n-6 with FADS2/D6D. This fatty acyl-CoA is then converted to dihomo- γ -linolenoyl-CoA C20:3n-6 with ELOVL5 and, finally, to arachidonyl-CoA C20:4n-6 with FADS1/D5D. Dihomo- γ -linolenoyl-CoA C20:3n-6 can also be formed from linoleoyl-CoA via an alternative pathway. Linoleoyl-CoA C18:2n-6 first undergoes elongation with ELOVL5 and then desaturation with FADS2. The latter enzyme in this pathway exhibits Δ^8 -desaturase activity. \uparrow —higher expression of given enzymes in GBM tumor relative to healthy tissue.

3.2. Arachidonic Acid Biosynthesis Pathway in Glioblastoma Multiforme Tumors

Expression of FADS2, an enzyme important for the viability and self-renewal of GBM cancer stem cells [20], is higher in GBM tumors than in healthy brain tissue, according to GEPIA [9] and the transcriptomics analysis performed by Seifert et al. [8]. However, our study showed that FADS2 may have lower expression in tumors than in the peritumoral area in GBM patients [21]. Discrepancies between our results and the data from GEPIA and transcriptomics analysis performed by Seifert et al. may have resulted from studying different groups of patients. FADS2 expression in GBM tumors does not differ between

men and women [21]. According to the GEPIA portal, higher FADS2 expression does not affect the prognosis for GBM patients [9]. Studies in GBM models show that FADS2 expression is higher in GBM cancer stem cells than in other GBM cancer cells [20].

The expression of FADS1, which is also important for the viability and self-renewal of GBM cancer stem cells [20], does not differ between GBM tumors and healthy brain tissue, according to GEPIA [9], Seifert et al. [8], and previous results from our research team [21]. According to the GEPIA portal, a higher FADS1 expression does not affect the prognosis for GBM patients [9]. FADS1 expression is higher in GBM cancer stem cells than in other GBM cancer cells [20].

ELOVL5 expression is higher in GBM tumors compared to healthy brain tissue, according to GEPIA [9] and Seifert et al. [8]. However, previous results from our research team did not show significant differences in the expression of ELOVL5 in GBM tumor tissue versus the peritumoral area [22]. Discrepancies between our results and the data from GEPIA and transcriptomics analysis performed by Seifert et al. may have resulted from studying different groups of patients. In addition, we observed that ELOVL5 expression was lower in GBM tumors in women relative to both the peritumoral area and GBM tumors in men [22]. Higher ELOVL5 expression does not affect the prognosis for GBM patients, according to GEPIA [9]. ELOVL5 expression can be higher in a GBM tumor as a result of hypoxia, as shown by our experiments with U87 MG line cells [22]. This is very important because hypoxia in a GBM tumor also increases the expression of COX-2 [23], an enzyme that converts ARA into prostanoids. This means that hypoxia increases the production of ARA and, at the same time, its conversion into prostanoids.

4. Phospholipase A₂ Superfamily and the Release of Arachidonic Acid from Cell Membrane Phospholipids in Glioblastoma Multiforme

4.1. Phospholipase A₂ Superfamily

The production of prostaglandins and leukotrienes requires a substrate for COX and LOX, namely, free ARA C20:4n-6, which is cleaved from cell membrane phospholipids by PLA₂. Enzymes with PLA₂ activity cleave either a fatty acid or a short acyl group from phospholipids at the *sn*-2 position [16]. All of these enzymes form the phospholipase A₂ superfamily, which can be divided into six types. Three of these types are important in the release of ARA C20:4n-6 as well as other PUFA from cell membrane phospholipids [16]:

- cytosolic phospholipase A₂ (cPLA₂),
- calcium-independent phospholipase A₂ (iPLA₂), and
- secretory phospholipase A₂ (sPLA₂).
 The remaining PLA₂ types include:
- platelet-activating factor acetyl hydrolases (PAF-AH),
- lysosomal phospholipase A₂, and
- adipose phospholipase A₂.

In humans, seven representatives of cPLA₂ are distinguished, namely, cPLA₂ α /*PLA2G4A* to cPLA₂ ζ /*PLA2G4F*. These enzymes, activated by Ca²⁺ [16], belong to the group IV (GIV) PLA₂. Significantly, cPLA₂ γ /*PLA2G4C* lacks a Ca²⁺ binding domain and is not sensitive to this second messenger [24]. cPLA₂ α is additionally activated by phosphorylation and has the highest activity towards phosphatidylcholine (PC), phosphatidylethanolamine (PE), and, to a lesser extent, towards other glycerophospholipids [16]. cPLA₂ have a specificity for cleaving PUFA from glycerophospholipids, particularly ARA C20:4n-6. cPLA₂ α shows the highest specificity for cleaving ARA C20:4n-6 [25,26], to a lesser extent, EPA C20:5n-3, and, to an even lesser extent, other PUFAs, e.g., linoleic acid C18:2n-3. cPLA2 γ also has the highest specificity for cleaving ARA C20:4n-6 and a twice-lower specificity for cleaving both linoleic acid C18:2n-3 and oleic acid C16:1n-9 [26].

In humans, there are six representatives of iPLA₂: iPLA₂ β to iPLA₂ η [16]. All of these enzymes belong to the GVI PLA₂. They are activated by ATP [27], and their activity is independent of Ca²⁺ levels and reduced by calmodulin [28]. Enzymes in this group

show different specificities for cleaving fatty acids from phospholipids at the *sn*-2 position. Depending on the enzymes, they show a higher ability to release a given fatty acid, e.g., oleic acid C16:1n-9 [27] or ARA C20:4n-6 [29].

Seventeen different groups of PLA₂ have been classified to date, which includes sPLA₂ [16]. Some sPLA₂ groups consist of only the sPLA₂ found in the venom of snakes, insects such as bees, and scorpions [16,30–32]. In humans, there are nine representatives of sPLA₂ [16]. These enzymes cleave fatty acids from phospholipids at the *sn*-2 position without showing specificity to a particular fatty acid [16,33]. Once secreted into the intercellular space, sPLA₂ not only cause the release of ARA C20:4n-6 but can also activate their receptor PLA₂R1 [34].

After fatty acids are cleaved from phospholipids by PLA₂, free fatty acids are formed, most commonly ARA C20:4n-6 and lysophosphatidylcholine (LPC) if PC was the reaction substrate (Figure 2). LPC can then be converted to lysophosphatidic acid (LPA) by the action of enzymes with lysophospholipase D (lysoPLD) activity [35,36]. An extracellular enzyme with lysoPLD activity is autotaxin (ATX)/ENPP2 [35,36]. Importantly, if the substrate for PLA₂ is phosphatidic acid (PA), then LPA is formed directly [37]. LPA is a lipid mediator that acts through its six receptors (from lysophosphatidic acid receptor 1 (LPAR₁) to LPAR₆) [38].



Figure 2. Importance of PLA₂ in metabolism of ARA and production of lipids mediators from ARA. ARA C20:4n-6 is cleaved from PC by PLA₂. This reaction also produces LPC, which can be converted in the intercellular space to LPA by ATX. LPA can be considered a lipid mediator because its biological activity is related to the activation of its specific receptors: LPAR₁-LPAR₆. Free ARA C20:4n-6, on the other hand, can be used for eicosanoid production in either the COX pathway or the LOX pathway. \uparrow —higher expression of given enzymes in GBM tumor relative to healthy tissue; \downarrow —lower expression of given enzymes in GBM tumor relative to healthy tissue.

4.2. Cytosolic Phospholipase A_2 and Calcium-Independent Phospholipase A_2 in Glioblastoma Multiforme

Expression of cPLA₂ α /*PLA2G4A* is upregulated in GBM tumors compared to healthy brain tissue [39]. This is also confirmed by bioinformatics analysis on the GEPIA portal [9] and the transcriptomics analysis by Seifert et al. [8]. At the same time, the expression of cPLA₂ β /*PLA2G4B* is lower, and the expressions of cPLA₂ γ /*PLA2G4C*, cPLA₂ δ /*PLA2G4D*, cPLA₂ ϵ /*PLA2G4E*, and cPLA₂ ζ /*PLA2G4F* are unchanged, according to GEPIA [9]. The expression of cPLA₂ γ /*PLA2G4C* is lower, and cPLA₂ ζ /*PLA2G4F* is not different in GBM tumors relative to healthy brain tissue, according to the transcriptomics analysis by Seifert et al. [8]. For six of the iPLA₂, expression in GBM tumor does not differ compared to healthy brain tissue, according to GEPIA [9]. The expression of iPLA₂ β /*PLA2G6* and iPLA₂ δ /*PNPLA6* is lower in GBM tumor than in the healthy brain, according to the transcriptomics analysis by Seifert et al. [8]. Expressions of the remaining iPLA₂ do not differ between GBM tumors and healthy brain tissue.

In the case of iPLA₂η/*PNPLA4*, higher expression in GBM tumors is associated with a worse prognosis for the patient, according to GEPIA (Table 1) [9]. For iPLA₂ ζ /*PNPLA2*, there is a trend (p = 0.087) of worse prognosis and higher expression of this gene in the GBM tumor.

Name	Expression Level in GBM Tun	Impact on Prognosis with Higher Expression in GBM Tumors	
Source	GEPIA [9]	Seifert et al. [8]	GEPIA [9]
		cPLA ₂	
cPLA ₂ α/ <i>PLA2G4A</i>	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis
cPLA ₂ β/ <i>PLA</i> 2G4B	Lower expression in the tumor	Expression does not change	No significant impact on prognosis
cPLA ₂ γ/ <i>PLA</i> 2G4C	Expression does not change	Lower expression in the tumor	No significant impact on prognosis
cPLA ₂ δ/PLA2G4D	Expression does not change	Expression does not change	No significant impact on prognosis
cPLA ₂ ε/PLA2G4E	Expression does not change	Expression does not change	No significant impact on prognosis
cPLA ₂ ζ/PLA2G4F	Expression does not change	Expression does not change	No significant impact on prognosis
		iPLA ₂	
$iPLA_2\beta/PLA2G6$	Expression does not change	Lower expression in the tumor	No significant impact on prognosis
$iPLA_2\gamma/PNPLA8$	Expression does not change	Expression does not change	No significant impact on prognosis
$iPLA_2\delta/PNPLA6$	Expression does not change	Lower expression in the tumor	No significant impact on prognosis
iPLA ₂ ε/PNPLA3	Expression does not change	Expression does not change	No significant impact on prognosis
iPLA ₂ ζ/PNPLA2	Expression does not change	Expression does not change	Worse prognosis $p = 0.087$
iPLA ₂ η/PNPLA4	Expression does not change	Expression does not change	Worse prognosis

Table 1. Description of cPLA₂ and iPLA₂.

Red background—higher expression in the tumor; blue background—lower expression in the tumor; red background—worse prognosis with higher expression of a given PLA₂.

cPLA₂ are activated in GBM cells, in particular, by sPLA₂ enzymes [40,41]. This is associated with the induction of cPLA₂ phosphorylation via MAPK kinase cascades as well as with an increase in cytoplasmic Ca²⁺ levels via phospholipase C- γ (PLC- γ) activation.

cPLA₂ α increases the proliferation of GBM cells, although the effect is not large. The most significant property of cPLA₂ α in GBM cells is causing chemoresistance to temozolomide (TMZ) and other chemotherapeutics, such as doxorubicin and 5-fluorouracil [39]. At the same time, the increased activity of cPLA₂ may also decrease the viability of GBM cells, where TMZ induces the phosphorylation of cPLA₂. This increases the activation of this enzyme [42] and thus leads to an increase in the level of free ARA 20:4n-6, whose excess reduces the viability of GBM cells. The reason for this may be in the activation of PPAR by this fatty acid [7,43,44] and the generation of reactive oxygen species (ROS) [45].

PLA₂ may also be important in the interaction of GBM cells with endothelial cells. GBM cells cause an increase in the expression and activity of cPLA₂ and iPLA₂ in endothelial cells [46,47]. An increase in cPLA₂ activity in endothelial cells can also be caused by radiation therapy [48]. A rise in the activity of cPLA₂ and iPLA₂ leads to the production of LPA [49]. GBM cancer cells may also increase COX-2 expression in endothelial cells, which increases the production of prostanoids including prostaglandin E₂ (PGE₂) [47]. LPA and

PGE₂ increase the proliferation and migration of endothelial cells [46,47,49]. This is also a mechanism of angiogenesis as a side effect of GBM radiotherapy [47,48]. At the same time, angiogenesis can be inhibited by pericytes [47].

Dying endothelial cells in a GBM tumor can secrete PGE_2 that increases the proliferation of GBM cells [50]. This is associated with the processing of iPLA₂ β by caspase 3 [16,51], which increases the activity of this iPLA₂ and, thus, leads to an increase in PGE₂ production [50].

4.3. Secretory Phospholipase A₂ in Glioblastoma Multiforme

Analyses on the GEPIA portal indicate that PLA2G5 expression is higher in GBM tumors [9]. There is also elevated expression of *PLA2G2A*, *PLA2G12A*, and *PLA2G15* but no other sPLA₂ in GBM tumors [9]. The transcriptomics analysis by Seifert et al. showed that the expressions of *PLA2G2A* and PLA2G5 are higher in GBM tumors than in healthy brain tissue [8]. This is the same as the data from the GEPIA web server. However, Seifert et al. showed that the expression of *PLA2G12A* and of the other sPLA₂ enzymes is not different in GBM tumors relative to healthy brain tissue [8]. Wu et al. also showed that *PLA2G5* expression is higher in gliomas than in healthy tissue and increases with tumor grade [52].

Higher expression of certain sPLA₂ in GBM tumors is associated with a worse prognosis. According to GEPIA, these include *PLA2G1B* and *PLA2G15* [9]. Wu et al. showed a higher number of sPLA₂ affecting prognosis. In particular, worse prognoses in patients with GBM are associated with higher expression of *PLA2G1B*, *PLA2G2E*, *PLA2G3*, and *PLA2G5* [52].

PLA2G5 is significant for tumorigenesis in low-grade gliomas and GBM. This suggests that a high expression of this sPLA₂ is associated with a worse prognosis in patients with GBM and low-grade gliomas (Table 2) [52]. Analyses on the GEPIA portal show no significant association between the expression of the aforementioned sPLA₂ and the GBM patient prognosis [9].

Name	Expression Level in GBM Tun	nor Relative to Healthy Tissue	Impact on Prognosis with Hig	her Expression in GBM Tumors
Source	GEPIA [9]	Seifert et al. [8]	GEPIA [9]	Wu et al. [52]
PLA2G1B	Expression does not change	Expression does not change	Worse prognosis $p = 0.078$	Worse prognosis
PLA2G2A	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis	No significant impact on prognosis
PLA2G2D	Expression does not change	Expression does not change	No significant impact on prognosis	No significant impact on prognosis
PLA2G2E	Expression does not change	Expression does not change	N/A	Worse prognosis
PLA2G2F	Expression does not change	Expression does not change	N/A	No significant impact on prognosis
PLA2G3	Expression does not change	Expression does not change	No significant impact on prognosis	Worse prognosis
PLA2G5	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis	Worse prognosis
PLA2G7	Expression does not change	Expression does not change	No significant impact on prognosis	No significant impact on prognosis
PLA2G10	Expression does not change	Expression does not change	N/A	No significant impact on prognosis
PLA2G12A	Higher expression in the tumor	Expression does not change	No significant impact on prognosis	No significant impact on prognosis
PLA2G12B	Expression does not change	Expression does not change	N/A	No significant impact on prognosis
PLA2G15	Higher expression in the tumor	Expression does not change	Worse prognosis	No significant impact on prognosis
PLA2G16	Expression does not change	Expression does not change	No significant impact on prognosis	No significant impact on prognosis
PLA ₂ R1/PLA2R1	Expression does not change	Expression does not change	Worse prognosis	

Table 2. Description of $sPLA_2$ and $sPLA_2$ receptors in GBM.

Red background—higher expression in the tumor; red background—worse prognosis with higher expression of a given PLA₂.

sPLA₂ are secreted outside the cells where they perform their function. They have their own receptor, PLA₂R1, from the C-type lectin superfamily and mannose receptor family [34], located in the cell membrane, through which it passes once. According to both GEPIA [9] and Seifert et al. [8], PLA₂R1 expression does not differ between GBM tumors and healthy brain tissue. An above-average expression of this receptor in a GBM tumor is associated with a worse prognosis for the patient [9], indicating that sPLA₂ may act on PLA₂R1 and be pro-tumorigenic.

sPLA₂ may act by participating in the production of LPA, a lipid mediator that has six different receptors [38]. According to GEPIA, LPAR₃ expression is downregulated in GBM tumors relative to healthy brain tissue [9], whereas LPAR₅ and LPAR₆ expression is upregulated in GBM tumors. The expression of other LPA receptors is not altered in GBM tumors. The transcriptomics analysis by Seifert et al. shows that LPAR₁ expression is lower, and LPAR₆ expression is higher in GBM tumors relative to healthy brain tissue [8]. The expression of other LPA receptors and healthy brain tissue.

sPLA₂ also have the same catalytic properties as other PLA₂. They cause the release of ARA 20:4n-6 from cell membrane phospholipids; this reaction produces free ARA 20:4n-6 and LPC. The latter is converted into LPA in the intercellular space by ATX [53], which is secreted by GBM cancer cells [54,55] and whose expression in GBM tumors is higher than in healthy brain tissue [53] and is elevated by interaction with microglial cells [55]. At the same time, GEPIA reports that ATX expression is not altered in GBM tumors [9], and Seifert et al. showed that it is lower [8] than in healthy brain tissue. The level of ATX expression in the tumor is not associated with prognosis severity for patients with GBM [9].

Another important source of ATX in the GBM tumor microenvironment is microglial cells [55], where ATX expression is upregulated by GBM cells, especially under hypoxia. Microglial cells also express the LPAR₁ receptor and can respond to LPA [55].

Increased expression of various $sPLA_2$ [52] and ATX [53] in GBM tumors also results in increased LPA production. GBM cancer cells show a loss of primary cilia, which leads to an increase in the distribution of $LPAR_1$ in the plasma membrane of these cells and to an enhancement of signal transduction by this receptor as a result of a greater association of G proteins with this receptor [56].

LPA causes GBM cells to migrate [53–55,57,58] due to the activation of LPAR₁, which results in the activation of protein kinase C (PKC) α . This is responsible for the phosphorylation of the progesterone receptor at the Ser⁴⁰⁰ residue [59,60]. GBM cancer cell migration is also facilitated by the LPA-induced decrease in oligodendrocyte adhesion [54]. It is also worth mentioning that in addition to LPAR₁, the receptor for advanced glycation end products (RAGE) may be another important receptor causing GBM cancer cell migration [61].

LPA increases the proliferation of GBM cancer cells [55]. The effect of LPA on proliferation depends on LPAR₁ receptors [55] and RAGE [61], and it occurs via the activation of two signaling pathways. The first is the Rho \rightarrow sodium-hydrogen antiporter 1 (NHE-1) pathway, which leads to an increase in intracellular pH and, thus, the proliferation of GBM cancer cells [62]. The second pathway is the activation of extracellular signal-regulated kinase (ERK) mitogen-activated protein kinase (MAPK) by the phosphatidylinositol-4,5bisphosphate 3-kinase (PI3K) \rightarrow PKC pathway [62], which can also be initiated by epidermal growth factor receptor (EGFR) transactivation. Studies on PLA₂G2A have shown that this sPLA₂ increases GBM cancer cell proliferation via EGFR transactivation [63–65]. This is associated with the activation of PKC, which activates EGFR [64]. EGFR activation results in the activation of the Src \rightarrow ERK MAPK \rightarrow Akt/PKB \rightarrow mammalian target of rapamycin (mTOR) \rightarrow ribosomal protein 70 S6 kinase (p70S6K) pathway [63,65]. Its consequence is an increase in the proliferation of GBM cancer cells.

sPLA₂ can also increase GBM cancer cell proliferation indirectly through the activation of cPLA₂ inside a GBM cell [40]. This process is independent of LPA.

LPA inhibits FasL-induced apoptosis [66] due to the LPA-induced activation of thyroid hormone receptor-interacting protein 6 (TRIP6). TPIP6 binds directly to Fas receptor (FasR)/CD95, which inhibits the induction of apoptosis by this receptor [66].

LPA causes radioresistance of GBM cancer cells [48,58]. These effects are a result of the LPA-induced activation of LPAR₁ [53,55] and LPAR₃ [48].

Phosphorylation of the progesterone receptor by LPA increases vascular endothelial growth factor (VEGF) expression in GBM cancer cells [60], the most important growth factor in angiogenesis. LPA is also important in radiotherapy-induced angiogenesis in GBM tumors [58]. An increase in tumor vascularization during exposure to ionizing radiation can be inhibited by ATX inhibitors, which could have some clinical application in future therapies against GBM [58].

The aforementioned actions of LPA were carried out on various models of specific GBM cell lines. Significantly, the action of LPA may be more pronounced in GBM cancer stem cells than non-cancer stem cells, as the former show much higher expression of LPAR₁ and LPAR₃ [67].

LPAR₁ is important in the development of GBM. Higher expression of this receptor in GBM tumors is associated with a worse prognosis [55]. At the same time, an analysis on the GEPIA portal did not link LPAR₁ and LPAR₃ expression to prognosis severity for GBM patients [9]. In addition, it did not show that the expression of the other LPA receptors had an effect on the prognosis for GBM patients.

4.4. Pan-Cancer Analysis of Phospholipase A_2 Genes and Comparison of GBM Expression against Other Cancers

We also performed a pan-cancer analysis of the expression of the PLA₂ genes with the GEPIA portal [9].

In GBM, but not in lower grade gliomas, there is higher expression of $cPLA_2\alpha/PLA_2G4A$ compared to healthy brain tissue [8,9]. Among the analyzed 31 tumor types, only four more had higher expression of this PLA₂, and eight other types showed a decrease. For this reason, higher expression of this enzyme in GBM tumors can be considered characteristic for this cancer.

In GBM, the expression of cPLA₂ β /*PLA2G4B* is decreased relative to healthy brain tissue [9], similar to lower grade glioma and 19 other types of cancer. This indicates that the decreased expression of this PLA₂ in tumor is a hallmark of cancer.

Seifert et al. also indicates that $cPLA_2\gamma/PLA2G4C$ expression may be downregulated in GBM tumors relative to healthy brain tissue [8]. According to a pan-cancer analysis based on the GEPIA, $cPLA_2\gamma/PLA2G4C$ expression is downregulated in nine types of tumors but not in GBM or lower grade gliomas, whereas it is upregulated in seven types of tumors [9]. Changes in $cPLA_2\gamma/PLA2G4C$ expression in GBM tumors could be a hallmark of cancer.

Seifert et al. also showed a decrease in the expression of iPLA₂ β /*PLA2G6* and iPLA₂ δ /*PNPLA6* in GBM tumors relative to healthy brain tissue [8]. According to GEPIA, iPLA₂ β /*PLA2G6* expression is downregulated in 15 tumor types (Table 3) [9], whereas iPLA₂ δ /*PNPLA6* expression is only downregulated in three types. For this reason, it can be thought that decreased iPLA₂ β /*PLA2G6* expression may be a hallmark of cancer. In contrast, reduced expression of iPLA₂ δ /*PNPLA6* is characteristic of GBM.

Available sources [8,9] show that *PLA2G2A*, *PLA2G5*, *PLA2G12A*, and *PLA2G15* undergo increased expression in GBM relative to healthy brain tissue. Changes in sPLA₂'s expression in GBM are characteristic of this cancer. All listed sPLA₂ undergo increased expression only in certain types of cancer (apart from GBM): *PLA2G2A* (in 2); *PLA2G5* (in 1); *PLA2G12A* (in 4); *PLA2G15* (in 3).

Name of Cancer	cPLA ₂ α/PLA2G4A	cPLA ₂ β/PLA2G4B	cPLA ₂ γ/PLA2G4C	cPLA ₂ 8/PLA2G4D	cPLA2 ɛ/PLA2G4E	cPLA2 <i>UPLA2G4F</i>	iPLA2β/PLA2G6	$iPLA_2\gamma/PNPLA8$	iPLA ₂ 8/PNPLA6	iPLA ₂ ɛ/PNPLA3	iPLA2 <i>č/PNPLA</i> 2	iPLA211/PNPLA4
Adrenocortical carcinoma (ACC)	\downarrow	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=
Bladder urothelial carcinoma (BLCA)	\downarrow	=	\downarrow	=	=	=	=	=	=	=	=	=
Breast invasive carcinoma (BRCA)	\downarrow	\downarrow	=	=	=	=	\downarrow	=	=	=	\downarrow	=
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)	=	Ļ	Ļ	=	=	1	↓	=	=	=	=	=
Cholangiocarcinoma (CHOL)	=	=	1	=	=	\uparrow	\uparrow	=	\uparrow	\downarrow	\uparrow	=
Colon adenocarcinoma (COAD)	\downarrow	\downarrow	\downarrow	=	=	\uparrow	\downarrow	=	=	=	=	1
Lymphoid neoplasm diffuse large B-cell lymphoma (DLBC)	=	=	1	=	=	=	=	=	=	=	\downarrow	1
Esophageal carcinoma (ESCA)	=	\downarrow	=	=	=	\downarrow	=	=	=	=	=	=
Glioblastoma multiforme (GBM)	\uparrow	\downarrow	=	=	=	=	=	=	=	=	=	=
Head and neck squamous cell carcinoma (HNSC)	=	↓	=	=	=	=	=	=	=	=	=	=
Kidney chromophobe (KICH)	=	\downarrow	=	=	=	\uparrow	=	=	=	=	=	=
Kidney renal clear cell carcinoma (KIRC)	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=	=
Kidney renal papillary cell carcinoma (KIRP)	=	=	=	=	=	\downarrow	=	=	=	=	=	=
Acute myeloid leukemia (LAML)	\uparrow	1	1	=	=	=	\uparrow	=	\uparrow	=	\uparrow	\downarrow
Brain lower grade glioma (LGG)	=	\downarrow	=	=	=	=	=	\uparrow	=	=	=	=
Liver hepatocellular carcinoma (LIHC)	=	\downarrow	1	=	=	=	=	=	=	=	=	=
Lung adenocarcinoma (LUAD)	\uparrow	\downarrow	\downarrow	=	=	\downarrow	\downarrow	=	\downarrow	=	\downarrow	=
Lung squamous cell carcinoma (LUSC)	=	↓	\downarrow	=	=	\downarrow	\downarrow	=	\downarrow	=	\downarrow	\uparrow
Ovarian serous cystadenocarcinoma (OV)	=	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=
Pancreatic adenocarcinoma (PAAD)	\uparrow	=	\uparrow	=	=	=	=	\uparrow	\uparrow	=	=	=
Pheochromocytoma and paraganglioma (PCPG)	\downarrow	=	=	=	=	=	=	=	=	=	\downarrow	=
Prostate adenocarcinoma (PRAD)	=	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=
Rectum adenocarcinoma (READ)	\downarrow	\downarrow	\downarrow	=	=	\uparrow	\downarrow	=	=	=	=	\uparrow
Sarcoma (SARC)	=	=	=	=	=	\downarrow	=	=	=	=	=	=
Skin cutaneous melanoma (SKCM)	=	\downarrow	1	\downarrow	\downarrow	\downarrow	\downarrow	=	=	\downarrow	\downarrow	=
Stomach adenocarcinoma (STAD)	1	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=
Testicular germ cell tumors (TGCT)	=	\downarrow	\downarrow	=	=	1	\downarrow	=	\downarrow	=	\downarrow	\uparrow
Thyroid carcinoma (THCA)	=	\downarrow	=	=	=	\downarrow	\downarrow	=	=	=	\downarrow	=
Thymoma (THYM)	=	=	\uparrow	=	=	1	\uparrow	1	=	=	=	\uparrow
Uterine corpus endometrial carcinoma (UCEC)	=	\downarrow	\downarrow	=	=	=	\downarrow	=	=	=	=	=
Uterine carcinosarcoma (UCS)	\downarrow	\downarrow	\downarrow	=	=	=	\downarrow	=	=	=	\downarrow	=

Table 3. Pan-cancer analysis of gene expression of cPLA₂ and iPLA₂.

Red background, \uparrow —expression higher in tumors than in healthy tissue; blue background, \downarrow —expression lower in tumors than in healthy tissue; gray background, =—expression does not differ between tumors and healthy tissue.

PLA2G2A expression is downregulated in 18 out of 31 types of cancer, indicating that it is generally downregulated in cancer (Table 4). In contrast, increased expression of *PLA2G2A* may occur in GBM [8,9], which may be characteristic of GBM. On the other hand, in 17 out of 31 cancers, there is a higher expression of *PLA2G7* in the tumor than in healthy tissue. Its expression in a GBM tumor is not different from its expression in healthy brain tissue [8,9].

Name of Cancer	PLA2G1B	PLA2G2A	PLA2G2D	PLA2G2E	PLA2G2F	PLA2G3	PLA2G5	PLA2G7	PLA2G10	PLA2G12A	PLA2G12B	PLA2G15	PLA2G16	PLA2R1
Adrenocortical carcinoma (ACC)	\uparrow	\downarrow	=	=	=	=	=	=	=	=	=	=	=	=
Bladder urothelial carcinoma (BLCA)	=	↓	=	=	1	=	\downarrow	\uparrow	=	=	=	=	=	=
Breast invasive carcinoma (BRCA)	=	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=	\downarrow	\downarrow
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)	Ļ	Ļ	=	=	=	=	=	1	=	=	=	=	=	Ļ
Cholangiocarcinoma (CHOL)	=	\downarrow	=	=	=	=	=	=	=	=	\downarrow	=	=	=
Colon adenocarcinoma (COAD)	=	=	=	=	=	=	\downarrow	1	1	=	\uparrow	=	=	=
Lymphoid neoplasm diffuse large B-cell lymphoma (DLBC)	=	=	1	=	=	=	=	1	=	1	=	\uparrow	\uparrow	=
Esophageal carcinoma (ESCA)	\downarrow	\downarrow	=	=	=	\downarrow	\downarrow	1	1	=	=	=	\uparrow	=
Glioblastoma multiforme (GBM)	=	1	=	=	=	=	1	=	=	1	=	1	=	=
Head and neck squamous cell carcinoma (HNSC)	=	\downarrow	=	=	=	=	=	\uparrow	=	=	=	=	\downarrow	=
Kidney chromophobe (KICH)	=	=	=	=	=	=	=	=	=	=	=	=	=	\downarrow
Kidney renal clear cell carcinoma (KIRC)	=	=	=	=	=	=	=	1	=	=	=	=	\uparrow	\downarrow
Kidney renal papillary cell carcinoma (KIRP)	=	=	1	=	=	=	=	1	=	=	\downarrow	=	\uparrow	\downarrow
Acute myeloid leukemia (LAML)	=	=	=	=	=	\downarrow	=	=	=	\downarrow	=	=	=	=
Brain lower grade glioma (LGG)	=	=	=	=	=	=	=	=	=	=	=	=	=	=
Liver hepatocellular carcinoma (LIHC)	=	\downarrow	=	=	=	=	=	=	=	=	=	=	=	=
Lung adenocarcinoma (LUAD)	\downarrow	↓	1	=	=	\downarrow	\downarrow	=	=	=	=	=	=	=
Lung squamous cell carcinoma (LUSC)	\downarrow	\downarrow	1	=	=	=	\downarrow	=	\downarrow	=	=	=	\downarrow	=
Ovarian serous cystadenocarcinoma (OV)	\downarrow	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=	\downarrow	\downarrow
Pancreatic adenocarcinoma (PAAD)	\downarrow	\downarrow	=	=	=	=	1	1	1	=	=	1	\uparrow	1
Pheochromocytoma and paraganglioma (PCPG)	\downarrow	\downarrow	=	=	=	=	=	=	=	=	=	=	=	=
Prostate adenocarcinoma (PRAD)	=	1	=	=	=	=	=	1	=	1	=	=	=	=
Rectum adenocarcinoma (READ)	=	=	=	=	=	=	\downarrow	1	1	=	\uparrow	=	=	=
Sarcoma (SARC)	=	=	=	=	=	=	=	=	=	=	\downarrow	=	=	\downarrow
Skin cutaneous melanoma (SKCM)	=	\downarrow	1	=	\downarrow	\downarrow	=	1	=	=	=	=	\uparrow	\downarrow
Stomach adenocarcinoma (STAD)	\downarrow	\uparrow	=	=	=	=	=	1	1	=	=	=	=	=
Testicular germ cell tumors (TGCT)	\downarrow	\downarrow	\uparrow	=	=	=	\downarrow	1	\downarrow	=	=	=	\downarrow	=
Thyroid carcinoma (THCA)	=	\downarrow	=	=	=	=	=	=	=	=	1	=	\uparrow	\downarrow
Thymoma (THYM)	=	=	=	=	=	=	=	1	=	\uparrow	=	\uparrow	\uparrow	\uparrow
Uterine corpus endometrial carcinoma (UCEC)	\downarrow	\downarrow	=	=	=	=	\downarrow	\uparrow	\uparrow	1	=	=	=	\downarrow
Uterine carcinosarcoma (UCS)	\downarrow	\downarrow	=	=	=	=	\downarrow	\uparrow	=	=	=	=	=	\downarrow

Table 4. Pan-cancer analysis of gene expression of sPLA₂ and sPLA₂ receptors.

Red background, \uparrow —expression higher in tumor than in healthy tissue; blue background, \downarrow —expression lower in tumor than in healthy tissue; gray background, =—expression does not differ between tumor and healthy tissue.

4.5. Lysophospholipid Acyltransferases in Glioblastoma Multiforme

When discussing the importance of PLA₂ in tumorigenesis in GBM, it is also important to mention enzymes that catalyze the opposite reaction to the enzymes in question. An example of this is lysophosphatidylcholine acyltransferases (LPCAT), which catalyze the opposite reaction towards PC [68]. LPCAT causes the formation of PC from LPC and fatty acyl-CoA. For this reason, LPCAT decreases the level of LPA, a lipid mediator important in cancer processes in GBM. According to the GEPIA portal, GBM tumors have higher expressions of LPCAT1, LPCAT2, and LPCAT3, but lower expression of LPCAT4/LPEAT2 relative to healthy brain tissue [9]. In addition, according to Seifert et al., the expression of LPCAT1 and LPCAT3 is higher in GBM tumors than in healthy brain tissue [8]. In contrast, LPCAT4 expression is lower in GBM tumors. This confirms the results obtained from the GEPIA database. An increase in the expression of the aforementioned enzymes may contribute to a decrease in LPA level but also contribute to the intense remodeling of phospholipids in the cell membranes of GBM cells. At the same time, according to the GEPIA database, the expression of the mentioned enzymes does not affect the prognosis severity of GBM patients [9].

4.6. Acyl-CoA Thioesterases and Arachidonic Acid C20:4n-6 in Glioblastoma Multiforme

The most important pathway for the formation of free ARA C20:4n-6 is through PLA₂ activity. However, free ARA C20:4n-6 can be formed from hydrolysis of arachidonyl-CoA by acyl-CoA thioesterases (ACOT) [69], a group of nine enzymes that cause hydrolysis of fatty acyl-CoA to free fatty acid and CoA [69,70]. An example of an enzyme from this group is ACOT7, which shows activity towards arachidonyl-CoA and saturated fatty acyl-CoA [69–71]. According to GEPIA and Seifert et al., there is a reduction in ACOT7 expression in GBM tumors relative to healthy brain tissue [8,9], where higher expression of this enzyme is associated with a worse prognosis for a GBM patient [9], suggesting the involvement of ACOT7 in tumorigenesis in GBM.

According to GEPIA and Seifert et al., there is also elevated expression of ACOT9 in GBM tumors [8,9], an enzyme showing the highest activity to myristoyl-CoA [69,70,72] and low activity to longer acyl-CoA. Importantly, the expression level of ACOT9 is not associated with the prognosis for a patient with GBM [9]. According to GEPIA, the expression of other ACOT does not differ between GBM tumors and healthy brain tissue [9]. In addition, Seifert et al. indicate that the expression of ACOT4 and ACOT8 in GBM tumors is lower than in healthy brain tissue [8].

5. Cyclooxygenase Pathway and Prostanoids in Glioblastoma Multiforme

5.1. Cyclooxygenase Pathway

Free PUFA, including ARA C20:4n-6, can be converted into prostanoids. This synthesis proceeds in two steps: the first reaction is catalyzed by COX: cyclooxygenase-1 (COX-1) and COX-2, whereas the second reaction is catalyzed by a prostanoid-specific synthase. The substrates for the production of prostanoids are dihomo- γ -linolenic acid C20:3n-6, ARA C20:4n-6, and EPA C20:5n-3, which are converted into 1-series [73], 2-series [73,74], and 3-series [75] prostaglandins or thromboxanes, respectively.

The most important prostanoids for tumorigenic processes in GBM are the 2-series prostanoids produced from ARA C20:4n-6. ARA C20:4n-6 is converted to prostaglandin G_2 (PGG₂) and then to prostaglandin H_2 (PGH₂) by COX [76–78], although during this reaction, the peroxygenated ARA C20:4n-6 can decompose with the generation of free radicals [79]. Cyclooxygenases also produce 9-hydroxyoctadecadienoic acid (9-HODE) from linoleic acid 18:2n-6 [80]. This compound is a ligand for PPAR γ [81], transient receptor potential vanilloid 1 (TRPV1) [82], and G2A/GPR132 [83]; the latter is also a receptor for many lipid mediators produced in the LOX pathway.

COX-1 (another name is prostaglandin-endoperoxide synthase 1 (PTGS1)) is a constitutive enzyme with a constant level of expression [84]. A second enzyme with the same activity is COX-2 (another name is prostaglandin-endoperoxide synthase 2 (PTGS2)) [85], an inducible enzyme that is regulated at the transcriptional level and is characterized by rapid degradation of the COX-2 protein [86]. The half-life of the COX-2 protein is only 5 h.

Sometimes, cyclooxygenase-3 (COX-3), a variant of COX-1 that retains intron 1 in its mRNA, is also mentioned in the context of conversion to prostanoids [87]. Although there is expression of the COX-3 protein, which is longer than COX-1, this enzyme has the same activity as the other cyclooxygenases. In mice and dogs, COX-3 is more sensitive to the inhibitors acetaminophen and phenacetin. Humans also have a variant of COX-1, but it is as sensitive to these inhibitors as standard COX-1 [88].

 PGH_2 is unstable and undergoes spontaneous nonenzymatic conversion, mainly with PGE_2 and, in smaller amounts, with prostaglandin D_2 (PGD_2) [78]. In the synthesis of PGE_2 , we can distinguish three synthases: membrane-bound prostaglandin E synthase-1 (mPGES-

1)/*PTGES* [89–91], membrane-bound prostaglandin E synthase-2 (mPGES-2)/*PTGES2* [92], and cytosolic prostaglandin E synthase (cPGES)/*PTGES3* [93]. These synthases are dependent on glutathione, which serves to reduce the endoperoxide bridge in PGH₂ with the formation of a single hydroxyl group. In addition, cPGES forms a complex with heat shock protein 90 (Hsp90), which is important in the activity of this PGE₂ synthase [94]. mPGES-1 and mPGES-2 bind with either COX-1 or COX-2 [92,95,96], whereas cPGES binds only with COX-1 [93,97]. mPGES-1 is an inducible enzyme whose expression under the influence of inflammatory reactions increases following the expression of COX-2 [96]. mPGES-2 [96] and cPGES [93] are constitutive enzymes, meaning that their expression is not altered by inflammatory reactions.

In plasma, PGE₂ undergoes enzymatic dehydration to PGA₂ [98], which can isomerize to PGC₂ via enzymes with PGA isomerase activity, and can then be isomerized to PGB₂ via enzymes with PGC isomerase activity [98,99]. Importantly, detailed studies of the enzymes involved in these reactions are lacking.

PGH₂ can also be enzymatically converted to other prostanoids by the appropriate synthase [97]. PGD₂ is formed from this prostaglandin with the participation of hematopoietictype prostaglandin D₂ synthase (H-PGDS)/*HPGDS* and lipocalin-type prostaglandin D₂ synthase (L-PGDS)/*PTGDS* [78]. It is also possible that pro-inflammatory prostaglandins are spontaneously converted into other prostaglandins with anti-inflammatory properties as a mechanism for regulating inflammatory responses [100].

PGD₂ undergoes transformations to form the following prostaglandins: 15-deoxy- $\Delta^{12,14}$ -PGD₂ (15d-PGD₂), PGJ₂, Δ^{12} -PGJ₂, and 15d-PGJ₂ [101,102]. PGD₂ undergoes spontaneous non-enzymatic conversion to PGJ₂ via dehydration or with Δ^{15} -PGD₂ [101,102]. PGJ₂ can be spontaneously transformed directly into 15d-PGJ₂ [102]. PGJ₂ can be transformed with the participation of albumin into Δ^{12} -PGJ₂ [101–104].

As PGA₂, PGJ₂, 15d-PGJ₂, and Δ^{12} -PGJ₂ have the same ring structure as cyclopentenone, they are classified as cyclopentenone prostaglandins [105]. Cyclopentenone prostaglandins have reactive electrophilic carbon atoms, which are responsible for the properties of this group of prostaglandins. These prostaglandins are inhibitors of nuclear factor κ B (NF- κ B) [6] and activators of PPAR α and PPAR γ [7,43]; thus, they have anti-inflammatory and anti-tumor properties.

It is possible that PGH₂ can be converted to other prostanoids, such as TxA_2 produced by thromboxane A synthase 1 (TBXAS1) [106,107]. TxA_2 is unstable, as it undergoes nonenzymatic conversion to TxB_2 with a TxA_2 half-life of less than 40 s [108]; for this reason, TxA_2 acts only locally at the site of synthesis.

TBXAS1 is responsible for the production of TxA_2 and can also catalyze the conversion reaction of PGH₂ into 12S-hydroxyheptadeca-5Z,8E,10E-trienoic acid (12-HHT) and malondialdehyde [106,109]. 12-HHT, produced by TBXAS1 in similar amounts to TxA_2 , is a ligand for leukotriene B₄ receptor 2 (LTB₄R2) [110–112].

PGH₂ can be converted into PGI₂ with PGIS (Figure 3) [113] or into PGF_{2 α} with aldoketoreductase (AKR)1B1 and AKR1C3 [114,115]. PGF_{2 α} can also be synthesized from PGE₂ by AKR1C1 and AKR1C2 [114]. After synthesis, prostanoids are secreted outside the cell by multidrug resistance-associated protein 4 (MRP4)/ATP binding cassette subfamily C member 4 (ABCC4) [116].

Prostaglandins are first taken into the cell via prostaglandin transporter (PGT)/solute carrier organic anion transporter family member 2A1 (SLCO2A1), and they are inactivated and degraded [117,118]. Organic anions transporting polypeptide 3 (OATP3) and OATP4 are also involved in PGE₂ uptake [119]. Then, prostaglandins are reduced by 15-hydroxyprostaglandin dehydrogenase (15-PGDH)/*HPGD* [118]. This reaction produces 15-keto-PGE₂ from PGE₂, a PPAR γ ligand [120]. In a subsequent catabolic reaction, 15-keto-PGE₂ is reduced by 12-hydroxyeicosanoid dehydrogenase (12-HEDH)/prostaglandin reductase 1 (PTGR1) [121] and prostaglandin reductase 2 (PTGR2) [120] through 15-oxoprostaglandin- Δ^{13} -reductase (13-PGR) activity. This produces 13,14-dihydro-15-keto-PGE₂ from 15-keto-PGE₂.



Figure 3. COX pathway. After release by PLA₂, ARA C20:4n-6 is converted into prostanoids with COX. It is transformed into PGH₂ with either COX-1 or COX-2. Then, this prostaglandin is transformed into other prostaglandins (PGE₂, PGD₂, PGI₂, and PGF₂ α) or TxA₂ by the respective synthases. These lipid mediators undergo further transformations. TxA₂ is unstable and undergoes a spontaneous transformation into TxB₂. Similarly, PGD₂ undergoes spontaneous transformation to PGJ₂—this prostaglandin can then be transformed into 15-deoxy- $\Delta^{12,14}$ -PGJ₂ (15d-PGJ₂) or Δ^{12} -PGJ₂. PGE₂ can be transformed into PGA₂, and then into PGC₂ and PGB₂. Prostanoids also undergo degradation. The figure shows an example of PGE₂ can also undergo degradation by β -oxidation with 15-PGDH and reduction with PTGR1/2. PGE₂ can also undergo degradation by β -oxidation and ω -oxidation, followed by the action of 15-PGDH and PTGR1/2. The resulting degradation product is PGE₂, which is removed from the body. \uparrow —higher expression of given enzymes in GBM tumor relative to healthy tissue; \downarrow —lower expression of given enzymes in GBM tumor relative to healthy tissue.

Importantly, 13,14-dihydro-15-keto-PGE₂ is unstable. It converts to 13,14-dihydro-15-keto-PGA₂, and in this form, it combines with proteins, such as with albumin in plasma [122]. 13,14-dihydro-15-keto-PGA₂ can also be converted to 11-deoxy-13,14-dihydro-15-keto-11,16-cyclo-PGE₂ and occur in the blood in this form [122,123].

PGE₂ can also be inactivated and degraded by β -oxidation [124,125]. It is first converted to PGE₂-CoA [125], and then it is oxidized in peroxisomes and mitochondria, accompanied by the production of either dinor-PGE₂ or tetranor-PGE₁ [124].

PGE₂ also undergoes ω -oxidation [126]. As a consequence of β -oxidation and ω -oxidation and also the action of 15-PGDH and PTGR1/2, 7α -hydroxy-5,11-diketotetranorprosta-1,16-dioic acid is formed from PGE₂, and then is excreted in the urine [127,128].

Acetylated COX-2 exhibits different catalytic properties than native COX-2. Although non-steroidal anti-inflammatory drugs (NSAID) prevent COX-2 catalytic activity, some NSAIDs cause acetylation of the COX-2 catalytic center. An example of such an NSAID is aspirin (acetylsalicylic acid), which causes changes in the catalytic properties of the enzyme. Acetylated COX-2 converts ARA C20:4n-6 into 15*R*-hydroxyeicosatetraenoic acid (15*R*-HETE) [129–132], whereas acetylated COX-1 has no catalytic activity [133].

Acetylated COX-2 also converts 5*S*-hydroxyeicosatetraenoic acid (5*S*-HETE) (the product of 5-lipoxygenase (5-LOX) activity) into 5*S*,15*R*-dihydroxyeicosatetraenoic acid (5*S*,15*R*diHETE) [130,131]. Native COX-2 converts 5*S*-HETE into 5*S*,11*R*-diHETE, 5*S*,15*R*-diHETE, and 5*S*,15*S*-diHETE [130,131]. Then, 5-LOX converts 15*R*-HETE into 15-epi- lipoxin A₄ (15-epi-LXA₄) which has anti-inflammatory properties [134]. Another name for 15-epi-LXA₄ is aspirin-triggered lipoxin (ATL). Acetylated COX-2 can also convert DHA C22:6n-3 and EPA C20:5n-3 into anti-inflammatory lipid mediators [5]. This means that aspirin has anti-inflammatory effects not only by inhibiting COX activity but also by causing the synthesis of lipid mediators with anti-inflammatory properties.

In addition to ARA C20:4n-6, dihomo- γ -linolenic acid C20:3n-6 and EPA C20:5n-3 are also converted with cyclooxygenases into 1-series prostaglandins [73] and 3-series prostaglandins [75], respectively. EPA C20:5n-3 reduces PGE₂ production by COX-1 and, to a lesser extent, by COX-2 [135]. PGE₃ binds to the same PGE₂ receptors with less intracellular signal transduction efficiency [75]. PGE₃ displaces PGE₂ from the shared receptor, resulting in a decrease in the receptor's activity. This means that PGE₃ has anti-cancer properties.

 PGE_1 can also inhibit the proliferation of various cancer cells [136,137], although peroxidation of dihomo-γ-linolenic acid C20:3n-6 with COX-2 can result in the formation of PGH_1 and the breakdown of the processed intermediate into free radicals [79]. COX-2 causes C-15 oxygenation of ARA C20:4n-6 and dihomo-γ-linolenic acid C20:3n-6. COX-2 can also catalyze C-8 oxygenation of dihomo-γ-linolenic acid C20:3n-6 [79,138], which often leads to the breakdown of the intermediate product and the formation of 8-hydroxyoctanoic acid (8-OH); this compound inhibits proliferation and is responsible for the antiproliferative properties of dihomo- γ -linolenic acid C20:3n-6 in cells with COX-2 expression [79,138], which is important for the inhibition of FADS1/D5D activity [139]. In the PUFA synthesis pathway, γ-linolenic acid C18:3n-6 in the acyl-CoA form is first elongated with Elov15 to dihomo- γ -linolenic acid C20:3n-6 [14] and is then desaturated to ARA C20:4n-6 with FADS1/D5D. The reduction of FADS1/D5D activity results in the accumulation of dihomo- γ -linolenic acid C20:3n-6 in the cell. If such a cell has a high COX-2 expression, this fatty acid will either be converted into PGE_1 , or it will be broken during the reaction catalyzed by COX-2. This results in the formation of 8-OH-octanoic acid which inhibits tumor cell proliferation with a developed drug targeting FADS1/D5D activity [139].

5.2. Cyclooxygenase Pathway and Glioblastoma Multiforme

After ARA C20:4n-6 is released from cell membrane phospholipids, it is processed with COX and LOX. In the healthy brain, ARA C20:4n-6 is processed mainly with LOX, whereas in GBM tumors, it is processed mainly with COX, as shown by experiments on C6 cells [140].

COX-1 expression [141] and COX-2 expression [141,142] are elevated in GBM tumors compared to healthy brain tissue, whereas according to GEPIA and Seifert et al., just COX-1 expression is elevated [8,9]. The expression of all three PGE₂ synthases, i.e., mPGES-1, mPGES-2, and cPGES, is also elevated in GBM [143], although according to GEPIA, only cPGES expression is higher compared to its expression in the healthy brain [9]. In contrast, Seifert et al. showed no change in PGE_2 synthase expression in GBM tumors [8]. cPGES is enzymatically bound with just COX-1 [93,97]. Therefore, it is possible that COX-1-cPGES may play an important role in the production of PGE_2 in GBM tumors. According to the GEPIA portal, there are also changes in the expressions of other prostaglandin synthases. In a GBM tumor, there is increased expression of H-PGDS but decreased expression of L-PGDS [9], both synthases involved in PGD_2 synthesis. In contrast, Seifert et al. showed that the expression of H-PGDS and L-PGDS in a GBM tumor is lower than their expressions in a healthy brain [8]. According to GEPIA in a GBM tumor, there is also increased expression of AKR1B1, decreased expression of AKR1C1 and AKR1C2, and no change in AKR1C3 expression [9]. Similarly, Seifert et al. showed that in a GBM tumor, there is higher expression of AKR1B1 and decreased expression of AKR1C1, but there is no difference in the expressions of AKR1C2 or AKR1C3 between the GBM tumor and healthy brain tissue [8]. AKR1B1 is involved in the synthesis of $PGF_{2\alpha}$ [115], whereas AKR1C1 and AKR1C2 are involved in the conversion of PGE₂ into PGF_{2 α} [114]. Expression of the TxA₂ synthesizing synthase TBXAS1 [8,9,144] is also elevated in GBM tumors, which may explain the increased expression and production of TxA_2 and the higher TxA_2/PGI_2 ratio in GBM tumors than in healthy brain tissue [145,146].

As for receptors for prostaglandins, according to the GEPIA portal, there is an elevated expression of $PTGER_4/EP_4$ and $TBXA_2R/TP$ in the tumor relative to healthy brain tissue [9], these two being receptors for PGE_2 and TxA_2 , respectively. In contrast, Seifert et al. showed that the expression of prostanoid receptors in GBM tumors did not differ relative to the healthy brain [8].

According to the GEPIA portal, the expression of MRP4/ABCC4 [9], a transporter responsible for the secretion of prostaglandins from the cell, is also increased in GBM tumors. The transcriptomics analysis by Seifert et al. did not confirm this [8]. GEPIA and Seifert et al. show no change in the expressions of PGT/SLCO2A1, 15-PGDH, 12-HEDH/PTGR1, and PTGR2 [8,9]—the first is a transporter that takes prostaglandins into the cell, and the second, third, and fourth are prostaglandin-degrading enzymes.

COX-2 is important in GBM tumor function. Its expression in GBM tumors is upregulated by hypoxia [23] and EGFR activation [147,148] as well as the action of epidermal growth factor receptor variant III (EGFRvIII) [147] and hepatocyte growth factor (HGF) [149]. COX-2 expression and biosynthesis of the most important product of this enzyme, PGE₂, is present in GBM cancer cells. However, PGE₂ in GBM tumors may not come mainly from GBM cancer cells but rather from tumor-associated macrophages (TAM) [150].

Under the influence of increased COX expression, there is increased production of PGE₂, which is involved in tumorigenesis. PGE₂ increases the expression of many factors relevant to tumorigenesis in GBM tumors—in particular, S100 calcium-binding protein A9 (S100A9) [151], interleukin 6 (IL-6) [152], and CXC motif chemokine ligand 8 (CXCL8)/interleukin 8 (IL-8) [153]. PGE₂ also elevates proliferation [154–156] and causes migration of GBM cancer cells [156]. The effects on proliferation and migration are dependent on the receptors EP₂ and EP₄ [155,156], and perhaps also EP₃. Activation of EP₃ results in the activation of transient receptor potential melastatin 7 (TRPM7), which increases the proliferation and migration of GBM cells [157].

COX-2 is also important for GBM cancer stem cells. COX-2 expression, and with it, the production of PGE₂, is higher in GBM cancer stem cells than in differentiated GBM cells [158,159]. This lipid mediator activates the Wnt pathway in GBM cancer stem cells, leading to the self-renewal and proliferation of these cells.

PGE₂ induces angiogenesis in GBM tumors. Therefore, COX-2 expression is positively correlated with microvessel density in GBM tumors [160]. Notably, PGE₂ causes vasculo-

genic mimicry of GBM cells, which promotes angiogenesis [161]. In GBM cells, PGE₂ also increases the expression of CXCL8/IL-8 [153], which has pro-angiogenic properties [162].

PGE₂ causes cancer immune evasion. Through EP₄, PGE₂ increases the expression of tryptophan-2,3-dioxygenase (TDO) [163], an enzyme that converts tryptophan into a signaling molecule that reduces immune cell activity.

PGE₂ also affects tumor-associated cells which are important in cancer immune evasion. PGE₂ increases the recruitment of myeloid-derived suppressor cells (MDSC) to the tumor niche in GBM [164] and interferes with the cytotoxic function of various immune cells, as shown by experiments in other cancer models. When acting chronically, PGE₂ impairs the cytotoxic function of natural killer (NK) cells [165,166], dendritic cells [167], and T cells [168]. PGE₂ also causes M2 polarization of macrophages [169], immunosuppressive cells that promote tumor growth.

PGE₂ also causes radiation resistance [170,171] and TMZ resistance in GBM [172]. COX-2 expression and PGE₂ production in GBM cancer cells are upregulated by TMZ [173] and ionizing radiation [170], which is related to caspase 3 activation in damaged cells and subsequent NF- κ B activation [174]. Then, NF- κ B increases COX-2 expression and, thus, the production of PGE₂ that trans-activates EGFR and activates the β-catenin pathway, which has a pro-survival effect and leads to resistance to further therapy [170]. Through EP₁ and EP₃, PGE₂ increases the intensity of β-oxidation and tricarboxylic acid cycle activity in mitochondria [172], leading to TMZ resistance. In response to ionizing radiation, healthy brain tissue also induces increased production of PGE₂ and pro-inflammatory cytokines [175], which increases GBM cell migration as well as causes tumor recurrence [176].

PGD₂ is also produced in GBM tumors [177]. At physiological concentrations, this prostaglandin increases the proliferation and migration of GBM cells, but, at concentrations of several micromoles, it decreases the viability and inhibits the proliferation of the GBM cells studied [177–179]. This effect may be due to 15d-PGJ₂, which has anti-cancer properties [180]. PGD₂ is non-enzymatically converted to 15d-PGJ₂ [100]. High concentrations of PGD₂ result in an accumulation of 15d-PGJ₂ to a level that causes a measurable reduction in the viability of GBM cancer cells. Cyclopentenone prostaglandins, particularly PGJ₂, Δ^{12} -PGJ₂, and 15d-PGJ₂, have anti-tumor properties, as demonstrated in in vitro studies on GBM cells. These prostaglandins inhibit tumor cell proliferation through PPAR γ activation [181,182].

TxA₂ may also play an important role in tumorigenic processes in GBM. In GBM cells, TxA₂ increases the expression of IL-6, which participates in tumorigenesis [183]. TBXAS1 inhibitors induce apoptosis and inhibit the migration and proliferation of GBM cancer cells [144,184,185], indicating an autocrine effect of TxA₂. In addition, in an in vivo model, TBXAS1 inhibitors inhibited angiogenesis and GBM tumor growth [185]. The described inhibitors increased the sensitivity of GBM cells to alkylation chemotherapy [185] and radiotherapy [186].

Given the role of COX-2 in tumorigenesis in GBM, high COX-2 expression in GBM tumors is associated with poorer patient prognoses [160,187,188], although the GEPIA data showed no correlation between COX-1 and COX-2 expression and patient prognosis severity [9]. In addition, the expression of other prostanoid metabolism enzymes worsens the prognosis for GBM patients, in particular, high expression of mPGES-1, the synthase responsible for the production of PGE₂ [121]. This is confirmed with the GEPIA data [9], although the expression levels of other PGE₂ synthases are not associated with prognosis severity [9,121]. Of the other prostaglandin synthases, high expression of AKR1B1, a PGF₂ producing synthase [115], in GBM tumors is associated with poorer patient prognoses [9].

According to the GEPIA portal, expression of MRP4/ABCC4, a transporter that secretes prostaglandins from the cell, does not affect the prognosis for GBM patients [9]. Higher expression of certain prostaglandin receptors worsens the prognosis for patients with GBM. In particular, a worse prognosis is associated with higher expression of PTGER₁/EP₁ and PTGIR/IP [9], which are receptors for PGE₂ and PGI₂, respectively.

Higher expression of G2A/GPR132 is also associated with a worse prognosis (p = 0.052) in GBM patients [9]. G2A/GPR132 is a receptor for 9-HODE [83], a product of the activity of COX that process linoleic acid 18:2n-6 [80]. The role of this receptor in GBM has not been thoroughly investigated, although studies on fibroblasts have shown that G2A/GPR132 is an oncogene [189].

Prognosis severity is also affected by the expression level of enzymes involved in prostaglandin inactivation. High expression of 15-PGDH in GBM tumors is associated with a better prognosis [121]. The opposite is true for the expression of 12-HEDH/PTGR1, the enzyme that catalyzes the second prostaglandin inactivation reaction [121]. PGT/SLCO2A1 expression levels are not associated with prognosis severity. On the other hand, according to the GEPIA portal, the expressions of PGT/SLCO2A1, 15-PGDH, PTGR1, and PTGR2 do not affect the prognosis for patients with GBM [9].

Prostaglandin levels in GBM tumors may also be associated with a worse prognosis, particularly higher levels of PGE_2 and $PGF_{2\alpha}$ [121]. PGD_2 levels in GBM tumors do not affect prognosis severity [121]. At the same time, these lipid mediators are often unstable, transforming into other lipid mediators with lesser or different properties within a short time after synthesis. For this reason, they may act locally in the immediate vicinity of the site of their synthesis.

Relating enzyme expression and levels of the discussed prostaglandins to prognosis makes it possible to estimate the significant impact of a particular pathway on cancer processes. In GBM tumors, higher expressions of production enzymes and levels of PGE₂ (COX-2, mPGES-1) and PGF_{2α} (COX-2, AKR1B1) are responsible for worse prognoses [9,121]. On the other hand, higher expression of the prostaglandin-inactivating enzyme, 15-PGDH, is associated with better prognoses (Table 5) [121]. For this reason, NSAIDs are being investigated as either potential drugs [190,191] or agents with chemopreventive properties against GBM. Various meta-analyses inconclusively discuss the chemopreventive properties of NSAIDs, such as aspirin. Depending on the meta-analyses cited, regular use of NSAIDs, including aspirin, may either reduce the risk [192,193] or have no effect [194] on the risk of developing glioma or GBM. Nevertheless, the COX pathway produces prostaglandins that exhibit pro-cancer and anti-cancer properties. A better option may be to develop drugs that specifically target only particular prostaglandins relevant to tumorigenic processes in GBM, namely PGE₂ and PGF_{2α} [9,121]. It may be possible to develop drugs that are specific inhibitors of mPGES-1.

Name	Biochemical Significance	Expression L	evel in GBM Tumo Healthy Tissue	Impact on Progn Expression in	osis with Higher GBM Tumors	
Source		GEPIA [9]	Seifert et al. [8]	Other Data Source	GEPIA [9]	Other Data Source
COX-1	PGH ₂ synthesis from ARA	Higher expression in the tumor	Higher expression in the tumor	Higher expression in the tumor [141]	No significant impact on prognosis	No significant impact on prognosis [121]
COX-2	PGH ₂ synthesis from ARA	Expression does not change	Expression does not change	Higher expression in the tumor [141,142]	No significant impact on prognosis	Worse prognosis [160,187,188]
mPGES-1	PGE ₂ synthesis from PGH ₂	Expression does not change	Expression does not change	Higher expression in the tumor [143]	Worse prognosis	Worse prognosis [121]
mPGES-2	PGE ₂ synthesis from PGH ₂	Expression does not change	Expression does not change	Higher expression in the tumor [143]	No significant impact on prognosis	No significant impact on prognosis [121]

Table 5. Description of individual enzymes involved in the synthesis, transport, and degradation of prostaglandins.

Name	Biochemical Significance	Expression L	evel in GBM Tumo Healthy Tissue	Impact on Progn Expression in	osis with Higher GBM Tumors	
Source		GEPIA [9]	Seifert et al. [8]	Other Data Source	GEPIA [9]	Other Data Source
cPGES	PGE ₂ synthesis from PGH ₂	Higher expression in the tumor	Expression does not change	Higher expression in the tumor [143]	No significant impact on prognosis	
H-PGDS	Synthesis of PGD ₂ from PGH ₂	Higher expression in the tumor	Lower expression in the tumor		No significant impact on prognosis	
L-PGDS	Synthesis of PGD ₂ from PGH ₂	Lower expression in the tumor	Lower expression in the tumor		No significant impact on prognosis	
TBXAS1	TxA ₂ synthesis from PGH ₂	Higher expression in the tumor	Higher expression in the tumor	Higher expression in the tumor [144]	No significant impact on prognosis	
AKR1B1	$PGF_{2\alpha}$ synthesis from PGH_2	Higher expression in the tumor	Higher expression in the tumor		Worse prognosis	
AKR1C1	$PGF_{2\alpha}$ synthesis from PGE_2	Lower expression in the tumor	Lower expression in the tumor		No significant impact on prognosis	
AKR1C2	$PGF_{2\alpha}$ synthesis from PGE_2	Lower expression in the tumor	Expression does not change		No significant impact on prognosis	
AKR1C3	$PGF_{2\alpha}$ synthesis from PGH_2	Expression does not change	Expression does not change		No significant impact on prognosis	
PGIS	PGIF ₂ synthesis from PGH ₂	Expression does not change	Expression does not change		No significant impact on prognosis	
MRP4	Secretion of prostaglandins from the cell	Higher expression in the tumor	Expression does not change		No significant impact on prognosis	
PGT/SLCO2A1	Uptake of prostaglandins into the cell	Expression does not change	Expression does not change		No significant impact on prognosis	
15-PGDH	First degradation reaction/ formation of PPARγ ligand from PGE ₂	Expression does not change	Expression does not change		No significant impact on prognosis	Better prognosis [121]
PTGR1	Second degrada- tion/inactivation reaction of PPARγ ligand made from PGE ₂	Expression does not change	Expression does not change		No significant impact on prognosis	Worse prognosis [121]
PTGR2	Second degrada- tion/inactivation reaction of PPARγ ligand made from PGE ₂	Expression does not change	Expression does not change		No significant impact on prognosis	No significant impact on prognosis

Table 5. Cont.

Red background—higher expression in the tumor; blue background—lower expression in the tumor; red background—worse prognosis with higher expression; blue background—better prognosis with higher expression.

5.3. Pan-Cancer Analysis of Genes Related to the COX Pathway and GBM

Changes in the expression of various genes in GBM tumors relative to healthy tissue may be the result of tumor-specific neoplastic processes or specific mechanisms found only in GBM. For this reason, we performed a pan-cancer analysis of the expression of the genes involved in the COX pathway based on the data available in the GEPIA web server [9]. It showed that increased or decreased expression of a given gene relative to healthy tissue does not occur in all types of cancer. At the same time, in some cases, a certain trend of changes in the expressions of the genes studied can be observed. An example of this is *TBXAS1*, whose expression is increased in nine types of cancer but decreased in another four types of cancer. Similarly, the expression of mPGES-1/PTGES is increased in eight types of cancers but decreased in three types of cancers. Some genes tend to undergo decreased expression in tumors. An example of this is 15-PGDH/HPGD, whose expression is reduced in 18 types of cancer but increased in two types of cancer relative to healthy tissue. Another example is the expression of PGIS/PTGIS, decreased in 17 types of cancer but elevated only in pancreatic adenocarcinoma.

According to GEPIA, there is an increase in COX-1/PTGS1 expression in GBM tumors, which is the same as in lower grade glioma. In seven types of tumors, this gene is overexpressed, but in seven more types, its expression is reduced. This indicates that the increased expression of COX-1/PTGS1 in gliomas (GBM and lower grade gliomas) is specific to these diseases. Some studies also show increased expression of PGE₂ synthases (mPGES-1/PTGES, mPGES-2/PTGES2 and cPGES/PTGES3) [9,143], although GEPIA confirms it is only for cPGES/PTGES3 [9]. According to GEPIA, in lower grade glioma, there are no changes in the expression of PGE₂ synthases relative to healthy brain tissue. According to GEPIA, expression of cPGES/PTGES3 is increased in 11 types of tumors but is decreased in one type. For this reason, the increase in cPGES/PTGES3 expression in GBM can be considered cancer-specific, just like mPGES-1/PTGES, which has increased expression in eight types of cancer and decreased in three. According to GEPIA, only four types of cancers have increased expression of mPGES-2/PTGES2, which shows that this enzyme may not be cancer-specific.

According to GEPIA in GBM, there is also increased expression of H-PGDS/HPGDS but decreased expression of L-PGDS/PTGDS [9]. At the same time, Seifert et al. showed that the expression of both PGD₂ synthases is decreased in GBM tumors [8]. H-PGDS/HPGDS expression is also upregulated in lower grade glioma. H-PGDS/HPGDS expression is downregulated in five tumor types and upregulated in an equal number of tumor types. Changes in H-PGDS/HPGDS expression can be specific to gliomas. L-PGDS/PTGDS expression is lower in GBM compared to healthy brain tissue [8,9]. L-PGDS/PTGDS expression is decreased in almost all types of tumors and, thus, can be deemed specific to cancer.

In GBM, as in lower grade glioma, there is increased expression of *TBXAS1* [8,9,144]. The expression of this enzyme is elevated in nine types of tumors, which means it may be cancer-specific.

In GBM tumors, there is also upregulation of *AKR1B1* expression but downregulation of *AKR1C1* and *AKR1C2* expressions relative to healthy brain tissue [8,9]. Lower grade gliomas show no changes in the expressions of these enzymes. The expression of *AKR1B1* increases in nine types of tumors. *AKR1C1* and *AKR1C2*, on the other hand, have decreased expressions in 14 types of tumors, which indicates that these changes may be cancer-specific.

PGIS/*PTGIS* expression is downregulated in 17 types of tumors. At the same time, in GBM tumors, PGIS/*PTGIS* expression does not differ from healthy brain tissue [8,9].

In GBM and lower grade glioma, there is an increase in MRP4/*ABCC4* expression [9]. This transporter also has increased expression in another four types of tumors but decreased expression in two types of tumors. Changes in MRP4/*ABCC4* expression may be specific to gliomas.

Finally, 15-PGDH/*HPGD* expression is often downregulated in tumors (Table 6). This was shown by a pan-cancer analysis in which 18 out of 31 cancers had decreased expression of this enzyme. At the same time, in gliomas (GBM and lower grade glioma), there were no changes in 15-PGDH/*HPGD* expression relative to healthy brain tissue.

Table 6. Pan-cancer analysis of expression of genes involved in COX pathway.

Name of Cancer	COX-1/PTGS1	COX-2/PTGS2	mPGES-1/PTGES	mPGES-2/PTGES2	cPGES/PTGES3	H-PGDS/HPGDS	L-PGDS/PTGDS	TBXAS1	AKR1B1	AKR1C1	AKR1C2	AKR1C3	PGIS/PTGIS	MRP4/ABCC4	PGT/SLCO2A1	15-PGDH/HPGD	PTGR1	PTGR2
Adrenocortical carcinoma (ACC)	=	=	=	=	1	=	\downarrow	\downarrow	\downarrow	=	\downarrow	=	↓	=	\downarrow	\uparrow	\downarrow	=
Bladder urothelial carcinoma (BLCA)	\downarrow	\downarrow	=	=	=	\downarrow	\downarrow	=	=	\downarrow	=	=	↓	\downarrow	\downarrow	\downarrow	=	=
Breast invasive carcinoma (BRCA)	=	\downarrow	=	=	=	=	\downarrow	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=	=	\downarrow	=	=
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)	=	=	=	=	=	=	\downarrow	=	=	=	=	=	\downarrow	=	\downarrow	\downarrow	=	=
Cholangiocarcinoma (CHOL)	\uparrow	=	1	\uparrow	\uparrow	=	=	=	\uparrow	=	=	\uparrow	=	\uparrow	\uparrow	\downarrow	\downarrow	=
Colon adenocarcinoma (COAD)	\downarrow	=	=	=	\uparrow	\downarrow	\downarrow	\uparrow	\downarrow	\downarrow	\downarrow	=	\downarrow	=	\downarrow	\downarrow	=	=
Lymphoid neoplasm diffuse large B-cell lymphoma (DLBC)	=	\downarrow	1	\uparrow	\uparrow	=	\uparrow	\downarrow	\uparrow	=	=	=	=	=	\uparrow	\downarrow	\uparrow	1
Esophageal carcinoma (ESCA)	\downarrow	\uparrow	=	=	=	=	\downarrow	=	=	\downarrow	\downarrow	1	\downarrow	1	=	\downarrow	\downarrow	=
Glioblastoma multiforme (GBM)	\uparrow	=	=	=	\uparrow	\uparrow	\downarrow	\uparrow	\uparrow	\downarrow	\downarrow	=	=	1	=	=	=	=
Head and neck squamous cell carcinoma (HNSC)	=	=	=	=	=	=	\downarrow	=	\uparrow	=	=	=	=	=	=	\downarrow	=	=
Kidney chromophobe (KICH)	=	=	=	=	=	=	\downarrow	=	=	=	\downarrow	\downarrow	\downarrow	=	\downarrow	=	\downarrow	=
Kidney renal clear cell carcinoma (KIRC)	\uparrow	=	\downarrow	=	=	=	\downarrow	\uparrow	=	=	=	=	=	=	=	\downarrow	\downarrow	=
Kidney renal papillary cell carcinoma (KIRP)	=	\downarrow	=	=	=	=	\downarrow	=	\uparrow	\uparrow	1	=	\downarrow	=	\downarrow	\downarrow	=	=
Acute myeloid leukemia (LAML)	=	1	=	\downarrow	\downarrow	1	\downarrow	1	\uparrow	\downarrow	\downarrow	1	=	\downarrow	=	=	1	\downarrow
Brain lower grade glioma (LGG)	1	=	=	=	=	1	=	1	=	=	=	1	=	1	=	=	=	1
Liver hepatocellular carcinoma (LIHC)	=	=	=	=	1	=	=	=	=	\uparrow	1	1	\downarrow	=	=	\downarrow	=	=
Lung adenocarcinoma (LUAD)	=	=	1	=	=	=	\downarrow	=	=	=	=	=	\downarrow	=	\downarrow	\downarrow	=	=
Lung squamous cell carcinoma (LUSC)	=	=	1	=	=	\downarrow	\downarrow	\downarrow	=	\uparrow	1	1	\downarrow	=	\downarrow	\downarrow	=	=
Ovarian serous cystadenocarcinoma (OV)	\uparrow	=	=	=	=	=	\uparrow	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=	=	\uparrow	=	=
Pancreatic adenocarcinoma (PAAD)	\uparrow	\uparrow	1	\uparrow	\uparrow	\uparrow	\uparrow	\uparrow	1	\uparrow	\uparrow	1	\uparrow	\uparrow	\uparrow	\uparrow	\uparrow	=
Pheochromocytoma and paraganglioma (PCPG)	=	=	1	=	=	=	\downarrow	=	\downarrow	=	=	=	=	=	=	=	\downarrow	=

Table 6. Cont.																		
Name of Cancer	COX-1/PTGS1	COX-2/PTGS2	mPGES-1/PTGES	mPGES-2/PTGES2	cPGES/PTGES3	H-PGDS/HPGDS	L-PGDS/PTGDS	TBXAS1	AKR1B1	AKR1C1	AKR1C2	AKR1C3	PGIS/PTGIS	MRP4/ABCC4	PGT/SLC02A1	15-PGDH/HPGD	PTGR1	PTGR2
Prostate adenocarcinoma (PRAD)	=	\downarrow	=	=	=	=	\downarrow	=	\downarrow	\downarrow	\downarrow	=	\downarrow	1	\downarrow	=	=	=
Rectum adenocarcinoma (READ)	\downarrow	\downarrow	\uparrow	=	1	=	\downarrow	1	\downarrow	\downarrow	\downarrow	1	\downarrow	=	\downarrow	\downarrow	=	=
Sarcoma (SARC)	\downarrow	=	=	=	=	=	=	=	=	=	=	=	=	=	=	\downarrow	=	=
Skin cutaneous melanoma (SKCM)	\downarrow	=	\downarrow	=	=	\downarrow	=	\uparrow	\uparrow	\downarrow	\downarrow	\downarrow	=	=	\downarrow	\downarrow	=	=
Stomach adenocarcinoma (STAD)	=	=	=	=	\uparrow	=	=	=	=	\downarrow	\downarrow	=	=	=	=	=	=	=
Testicular germ cell tumors (TGCT)	=	=	\downarrow	=	\uparrow	=	\downarrow	\uparrow	=	\downarrow	\downarrow	\downarrow	=	=	=	=	\uparrow	\downarrow
Thyroid carcinoma (THCA)	=	=	=	=	=	=	\downarrow	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=	\downarrow	=	=	=
Thymoma (THYM)	\downarrow	\downarrow	=	\uparrow	\uparrow	\uparrow	\uparrow	\downarrow	\uparrow	=	\uparrow	\uparrow	=	=	\uparrow	=	1	1
Uterine corpus endometrial carcinoma (UCEC)	\uparrow	=	=	=	=	\downarrow	\downarrow	=	=	\downarrow	=	=	\downarrow	=	\downarrow	\downarrow	=	=
Uterine carcinosarcoma (UCS)	=	=	1	=	=	=	\downarrow	=	=	=	=	=	\downarrow	=	\downarrow	\downarrow	=	=

Red background, \uparrow —expression higher in tumor than in healthy tissue; blue background, \downarrow —expression lower in tumor than in healthy tissue; gray background, =—expression does not differ between tumor and healthy tissue.

6. Lipoxygenases and Arachidonic Acid in Glioblastoma Multiforme

6.1. Lipoxygenases Pathway

In addition to the COX pathway, PUFA can be transformed with LOX. These enzymes exhibit dioxygenase activity, catalyzing the insertion of a hydroperoxyl group into a PUFA, most commonly ARA 20:4n-6. Hydroperoxyeicosatetraenoic acids (HpETE) are then formed from ARA 20:4n-6, which are further processed in the lipoxygenase pathway. The names of LOX enzymes are related to their sites of formation and the configuration of the hydroperoxyl group in ARA 20:4n-6. In humans, there are six LOX:

- epidermal lipoxygenase 3/arachidonate lipoxygenase 3 (eLOX3/ALOXE3),
- 5-lipoxygenase/arachidonate 5-lipoxygenase (5-LOX/ALOX5),
- 12S-lipoxygenase/arachidonate 12-lipoxygenase, 12S type (12S-LOX/ALOX12),
- 12R-lipoxygenase/arachidonate 12-lipoxygenase, 12R type (12R-LOX/ALOX12B),
- 15-lipoxygenase-1/arachidonate 15-lipoxygenase (15-LOX-1/ALOX15), also known as 12/15-LOX, and
- 15-lipoxygenase-2/arachidonate 15-lipoxygenase type B (15-LOX-2/ALOX15B).

The *ALOX5* gene is found on chromosome 10. The other LOX form a gene cluster on 17p13.1 [195,196]. There is also a mouse 8-LOX [197], whose sequence is 78% identical to that of human 15-LOX-2/*ALOX15B* [197,198]. It is likely that mouse 8-LOX and human 15-LOX-2/*ALOX15B* are derived from a common ancestor, which was indirectly confirmed by mutagenesis experiments on these two enzymes. Changing only two amino acids in either mouse 8-LOX or human 15-LOX-2/*ALOX15B* alters the catalytic properties of these two enzymes in 15-LOX and 8-LOX, respectively [197].

6.1.1. Epidermal Lipoxygenase 3

The *ALOXE3* gene forms a gene cluster on 17p13.1 together with other LOX [196]. The highest expression of the *ALOXE3* gene is found in the skin [196,199]; very low expression of this gene is found in the brain, placenta, pancreas, ovary, and testis.

eLOX3/ALOXE3 shows no significant activity against ARA 20:4n-6 or linoleic acid C18:2n-6 [200], which is related to the low availability of molecular oxygen in the active center of this enzyme [201]. For this reason, the processing of ARA 20:4n-6 by eLOX3/ALOXE3 is very inefficient, but eLOX3/ALOXE3 can exhibit dioxygenase activity to ARA 20:4n-6.

eLOX3/ALOXE3 has hydroperoxide isomerase activity [200]. eLOX3/ALOXE3 converts HpETE into hydroxy-epoxyeicosatrienoic acid, which is the main product of eLOX3/ ALOXE3 activity. eLOX3/ALOXE3 also converts HpETE into oxo-eicosatetraenoic acid (oxo-ETE)/ketoeicosatetraenoic acid (KETE) [200,202]. 15S-HpETE is converted by eLOX3/ALOXE3 into either 13R-hydroxy-14S,15S-epoxyeicosa-5Z,8Z,11Z-trienoic acid or 15-oxo-ETE [200].

eLOX3/*ALOXE3* also converts 12*S*-HpETE into hepoxilin A₃ (HxA₃), HxB₃ [200,203], or 12-oxo-ETE [204,205]. On the other hand, 12*R*-HpETE is converted by eLOX3/*ALOXE3* into either 11,12-bis-epi-HxA₃ or 12-oxo-ETE [200].

In addition, eLOX3/*ALOXE3* shows activity to 5-HpETE and other HpETEs [202]. Because HETE and oxo-ETE [206] as well as hepoxilins [207] exhibit biological activity, eLOX3/*ALOXE3* affects biological and pathological processes, particularly in the skin, where expression of this enzyme is highest. For this reason, mutations in the *ALOXE3* gene lead to ichthyosis [208–210].

6.1.2. 5-Lipoxygenase

The best-studied LOX is 5-LOX/*ALOX5*. The highest expression of 5-LOX/*ALOX5* is found in the bone marrow, appendix, lung, urinary bladder, spleen, and lymph node [199]. This enzyme converts ARA 20:4n-6 to 5*S*-hydroperoxyeicosatetraenoic acid (5-HpETE) and then to leukotriene A₄ (LTA₄) [211]. Importantly, 5-lipoxygenase-activating protein (FLAP)/*ALOX5AP* is required for the activity of 5-LOX/*ALOX5*. FLAP/*ALOX5AP* is a substrate carrier [212,213]. 5-HpETE is an activator of PPAR α [214]; for this reason, if it is not converted to other lipid mediators, then it will activate this nuclear receptor.

Subsequently, LTA₄ is converted to other lipid mediators, in particular to other leukotrienes. LTA₄ can also undergo spontaneous conversion to 5,6-diHETE, 5,12-diHETE, and 5-oxo-ETE [215]. In turn, 5-HpETE is converted to 5-hydroxyeicosatetraenoic acid (5-HETE) with glutathione peroxidase [216]. The identified receptor for 5-HETE is G2A/GPR132 [83]; this receptor is also activated by other lipid mediators, such as various HETE and 9-HODE.

5-oxo-ETE can also be formed from 5-HETE with the participation of an enzyme with 5-hydroxyeicosanoid dehydrogenase (5-HEDH) activity [217–219]. 5-oxo-ETE is an important lipid mediator with a receptor oxoeicosanoid receptor 1 (OXER1)/GPR99 [220–222].

LTA₄ is a precursor for the production of other leukotrienes and lipoxins; it is converted to lipoxins in a reaction catalyzed by 12-LOX or 15-LOX [223]. LTA₄ can also be converted to LTB₄ by LTA₄ hydrolase (LTA₄H) [224,225]. LTA₄H also has aminopeptidase activity unrelated to the production of leukotrienes [225]; this activity is important in moderating the immune response [226]. LTB₄ has its own membrane receptors: LTB₄R1/BLT1 [227] and LTB₄R2/BLT2 [228]. Inside the cell, LTA₄ and LTB₄ activate PPAR α , by which these leukotrienes can exert anti-inflammatory effects [7,214].

Glutathione can be attached to LTA₄ by LTC₄ synthase (LTC₄S) (Figure 4) [229,230]. LTC₄ is then formed. LTC₄S combines with 5-LOX and FLAP to increase the efficiency of LTC₄ production with ARA 20:4n-6 [231]. Subsequently, amino acids from the conjugated glutathione in LTC₄ can be removed. As a consequence of this, LTC₄ is converted into other leukotrienes, namely LTD₄, LTE₄, and LTF₄. All of these leukotrienes, together with LTC₄, form a group called cysteinyl leukotrienes. LTD₄ is then formed from LTC₄ with the involvement of γ -glutamyltransferase 1 (GGT1) and γ -glutamyltransferase 5 (GGT5) [232]. Subsequently, LTD₄ can be converted to LTE₄ with the participation of dipeptidase 1 (DPEP1) and dipeptidase 2 (DPEP2) [233,234]. LTC₄ can also be converted to LTF₄ with the participation of carboxypeptidase A [235]. Amino acids can be attached back to cysteine in cysteinyl leukotriene, as exemplified by the conversion of LTE₄ to LTF₄ with the participation of an enzyme with γ -glutamyltranspeptidase activity [236]. LTF₄, however, has a much weaker effect than LTE₄, and the latter reaction can be considered an inactivation of LTE₄.

Once synthesized, leukotrienes are secreted from the cell. LTC₄ is secreted from cells by multidrug resistance-associated proteins (MRP) [237]. In particular, MRP1/ABCC1 [238,239], MRP2/ABCC2 [240,241], MRP3/ABCC3 [242], MRP4/ABCC4 [243], MRP6/ABCC6 [244], MRP7/ABCC10 [245], and MRP8/ABCC11 [246] are responsible for this process. In contrast, OATP1/SLCO1C1 and OATP4 are responsible for the uptake of LTC₄, particularly into liver cells where leukotrienes are degraded [119,247]. In contrast, LTB₄ transport is still poorly studied; it is known that efflux of LTB₄ occurs via MRP4/ABCC4 [243].

Once leukotrienes are secreted outside the cells, they can activate their membrane receptors. LTB₄ has two receptors: LTB₄R1/BLT1 [227] and LTB₄R2/BLT2 [228], the former of which has a 20 times better dissociation constant (Kd) than LTB₄R2 in binding LTB₄ [228]. With that said, LTB₄R2 can be activated by other ARA-derived lipid mediators. These include 12*S*-HETE, 12*R*-HETE, 15-HETE, 15-HPETE [248], and 12-HHT [110–112]. 12-HHT is formed together with malondialdehyde in a reaction catalyzed by TBXAS1, whose substrate is PGH₂ [106,109]. In addition, 12-HHT can be formed independently of TBXAS1 but in smaller amounts [109].

The receptors for cysteinyl-leukotrienes are CysLTR₁ [249] and CysLTR₂ [250,251]. Both receptors show a 38% similarity in amino acid sequence [250]. CysLTR₁ shows a high affinity for LTD₄ and low affinity for LTC₄ and LTE₄, and it shows no affinity at all for LTB₄ [249]. CysLTR₂ has the best affinity for LTC₄ and LTD₄ and a very low affinity for LTE₄, and it shows no affinity at all for LTB₄ [250,251]. A receptor specific for LTE₄ is 2oxoglutarate receptor 1 (OXGR1)/GPR99 [252], which is also the receptor for 2-oxoglutarate. This receptor has a lower affinity for LTC₄ and LTD₄. Another identified receptor for cysteinyl-leukotrienes specifically for LTC₄ and LTD₄ is G protein-coupled receptor 17 (GPR17) [253], which is also activated by uridine diphosphate (UDP), UDP-glucose, and UDP-galactose [253]. Further studies have not confirmed that GPR17 is a receptor for UDP,



 LTC_4 , and LTD_4 [254,255]. This receptor can, independently of its ligand, downregulate CysLTR₁ [256], which means it can reduce the action of cysteinyl leukotrienes.

Figure 4. 5-LOX pathway. ARA C20:4n-6 is converted to 5-HpETE with 5-LOX. This enzyme also catalyzes the next step in leukotriene biosynthesis. It converts 5-HpETE into LTA₄, which can then be converted into LTB₄ with LTA₄H, into LTC₄ with LTC₄S, or into 5-oxo-ETE. 5-HpETE can also be converted to 5-oxo-ETE. LTC₄ can be converted to other cysteinyl leukotrienes. LTC₄ can be converted to LTF₄ with the involvement of carboxypeptidase A or to LTD₄ with the involvement of GGT1 and GGT5. Subsequently, LTD₄ can be converted into LTE₄ with the participation of DPEP1 and DPEP2, and then converted into LTF₄ with γ -glutamyltranspeptidase. \uparrow —higher expression of given enzymes in GBM tumor relative to healthy tissue.

Leukotrienes can be inactivated and excreted. LTB₄ is oxidized to 12-oxo-LTB₄ with 12-hydroxyeicosanoid dehydrogenase (12-HEDH)/PTGR1 [257–259]. This enzyme is also involved in prostaglandin degradation [121]. Subsequently, 12-oxo-LTB₄ is reduced with the formation of 12-oxo-10,11-dihydro-LTB₄ with an enzyme with Δ^{10} -reductase activity [260]. 12-oxo-10,11-dihydro-LTB₄ can then be converted to 10,11-dihydro-LTB₄ and 10,11-dihydro-12-epi-LTB₄, which undergo ω -oxidation, β -oxidation, or elongation [257]; compounds formed after ω -oxidation and β -oxidation are excreted in the feces [261] and urine [262]

as ω -carboxymetabolites of LTB₄. HETE are similarly degraded, such as 12-HETE with the formation of 10,11-dihydro-12-HETE and 10,11-dihydro-12-oxo-ETE [263]. Cysteinyl-leukotrienes are first converted to LTE₄ [264]; this leukotriene then undergoes ω -oxidation with the formation of ω -carboxy-tetranor-dihydro-LTE4, which is eliminated in the feces and urine.

6.1.3. 12S-Lipoxygenase

ALOX12 gene expression is found in the esophagus and skin [199]. 12S-LOX/ALOX12 can participate in the conversion of LTA₄ into lipoxins [223], but the best-described activity of 12S-LOX/ALOX12 is to catalyze the insertion of a hydroperoxyl group into ARA 20:4n-6 at position 12—12S-HpETE is then formed [265]—the compound which can also be formed with 15-LOX-1/ALOX15 [266].

12S-LOX can convert dihomo-γ-linolenic acid to 12S-hydroxy-8Z,10E,14Z-eicosatrienoic acid (12S-HETrE) [267,268]. In contrast, linoleic acid C18:2n-6 is not a substrate for 12S-LOX/*ALOX12* [267]. 12S-HpETE can be converted to 12S-HETE, whose receptors are G protein-coupled receptor 31 (GPR31) [269] and G2A/GPR132 [83].

12S-HETE also activates PPAR γ [270], as 12S-HPETE [200] and 12S-HETE can be converted to 12-oxo-ETE [260], a PPAR γ ligand and activator [204]. 12-oxo-ETE can be converted back to 12S-HETE with an enzyme with 12-oxo-ETE reductase activity [271].

12S-HpETE can be converted to HxA₃ (8-hydroxy-11,12-epoxyeicosatrienoic acid) or HxB₃ (10-hydroxy-11,12-epoxyeicosatrienoic acid) with enzymes with hepoxilin synthase activity, for example, heme, as shown by experiments on hemoglobin and hemin [272,273]. Hepoxilin synthase activity is also demonstrated by eLOX3/ALOXE3, 12S-LOX/ALOX12, and 15-LOX-1/ALOX15, as shown by experiments on human, rat, and mouse models [200,203,274,275].

Then, HxA₃ may bind glutathione via glutathione S-transferase at position 11 [276,277]. HxA₃ then gives rise to 11-glutathionyl-HxA₃, or otherwise HxA₃-C. HxB₃ is not subject to such modification [278]. HxA₃-C can be produced in the brain and may be a neuro-modulator [279]. Like cysteinyl-leukotrienes, HxA₃-C can be converted to other cysteinyl-hepoxilins [279]. HxA₃-C is converted to HxA₃-D by γ -glutamyltranspeptidase. HxA₃ and HxB₃ can also be converted into trioxilin A₃ (TrXA₃) (8,11,12-trihydroxyepoxyeicosatrienoic acid) with soluble epoxide hydrolase (sEH) (current name: epoxide hydrolase 2 (EPHX2)) [276,280]. HxA₃ and TrXA₃ are also antagonists of the TP receptor [283], the receptor for TxA₂.

6.1.4. 12R-Lipoxygenase

In addition to 12S-LOX/*ALOX12*, there is a second enzyme with 12-LOX activity [195], namely 12R-LOX/*ALOX12B* [284]. This enzyme shows activity towards ARA C20:4n-6 but not linoleic acid C18:2n-6 [284]. 12R-LOX/*ALOX12B* transforms ARA C20:4n-6 into 12*R*-HpETE, a stereoisomer of the product of 12S-LOX/*ALOX12'* senzyme activity. 12*R*-HpETE is converted to 11,12-bis-epi-HxA₃ with eLOX3/*ALOXE3* [200]. 12*R*-HpETE is a stereoisomer of 12*S*-HpETE. Similar to this compound, 12*R*-HpETE can also be converted to 12*R*-HETE [206], which is then converted to 12-oxo-ETE with an enzyme with 12-hydroxyeicosanoid dehydrogenase activity [206,260], including eLOX3/*ALOXE3* [200].

The *ALOX12B* gene is only 38% similar to the *ALOX12* gene. The highest expression of this enzyme is found in the skin, and it is much lower in the prostate and adrenal gland [196,199,284]. 12R-LOX is important in skin function; mutations in the *ALOX12B* gene lead to ichthyosis [208,210,285], as do mutations in the *ALOXE3* gene. 12R-LOX/*ALOX12B* and eLOX3/*ALOXE3* participate in a common pathway in lipid mediator production. 12R-LOX produces 12*R*-HpETE, which is converted to 11,12-bis-epi-HxA₃ with eLOX3 (Figure 5) [200]. Under the influence of eLOX3/*ALOXE3*, 12-oxo-ETE is also formed from 12*R*-HpETE in small amounts [200].



Figure 5. 12-LOX pathway. ARA C20:4n-6 is converted to 12*S*-HpETE and 12*R*-HpETE with 12S-LOX and 12R-LOX, respectively. Either 12-oxo-ETE or the corresponding 12-HETE can be formed from these compounds. 12*S*-HpETE can also be converted to HxA₃ or HxB₃ with hemin and lipoxygenases: eLOX3, 12S-LOX, or 15-LOX-1. 12*R*-HpETE can undergo a similar conversion to 11,12-bis-epi-HxA₃. HxA₃ may undergo further transformations. HxA₃ can be conjugated to glutathione. HxA₃-C is then formed, from which amino acids can be detached—HxA₃-D is then formed in a reaction similar to the transformation of cysteinyl-leukotrienes. HxA₃ can also be converted to TrXA₃. Arrows next to enzymes: higher or lower expression of given enzymes in GBM tumor relative to healthy tissue. \downarrow —lower expression of given enzymes in GBM tumor relative to healthy tissue.

6.1.5. 15-Lipoxygenases

Like the previously described LOX, 15-LOX catalyzes the formation of 15*S*-hydroperoxyeicosatetraenoic acids (15-HpETE) from ARA 20:4n-6 [286]. In humans, two 15-LOX isoforms are distinguished: 15-LOX-1/*ALOX15* [287] and 15-LOX-2/*ALOX15B* [288]. The highest expression of 15-LOX-1/*ALOX15* is found in the lung, and the lower expressions are in the skin, intestine, heart, lymph node, and testis [199]. The highest expression of 15-LOX-2/*ALOX15B* is found in the prostate and skin. Expression of this enzyme is also observed in the lung, esophagus, and cornea [196,199,288].

The enzymatic properties of the two isoforms differ. 15-LOX-1/*ALOX15* catalyzes the formation of 15-HpETE, but it also converts part of the substrate, ARA 20:4n-6, into

12-HpETE [266]—for this reason, the enzyme owns its historical name: 12/15-LOX. 15-LOX-2/*ALOX15B* has no such activity [266,288].

15-LOX-1/*ALOX15* shows much higher activity with linoleic acid C18:2n-6 than 15-LOX-2/*ALOX15B* (Figure 6) [266]. These enzymes convert linoleic acid C18:2n-6 into 13S-hydroperoxyoctadecadienoic acid (13-HpODE), which converts to 13S-hydroxyoctadecadienoic acid (13-HODE). The identified receptor for 13-HpODE is G2A/GPR132 [83]. 13-HODE also activates the TRPV1 receptor [82]. 13-HODE undergoes the same transformations as HETE and can be oxidized to 13-oxo-ODE. 13-oxo-ODE [289] and 13-HODE [290] are PPAR γ ligands.



Figure 6. 15-LOX pathway. (**A**). Linoleic acid C18:2n-6 can be converted by 15-LOX-1 and 15-LOX-2 into 13-HpODE. This compound can then be converted into 13-HODE and 13-oxo-ODE. (**B**) 15-LOX-1 and 15-LOX-2 can convert ARA C20:4n-6 into 15-HpETE. 15-LOX-1 can also convert this fatty acid into 12-HpETE. 15-HpETE can then be converted into EXA₄ and into cysteinyl-eoxins EXC₄, EXD₄, and EXE₄. 15-HpETE can also be converted into hepoxilins 14,15-HxA₃ 11*S*, and 14,15-HxB₃ 13*R*. 14,15-HxA₃ 11*S* can be converted to cysteinyl hepoxilins, such as 14,15-HxA₃-C 11*S*.

15-HpETE is transformed into many lipid mediators. It can be transformed into 15-HETE, which is an activator of PPAR γ [270] and G2A/GPR132 [83]. 15-HpETE can be converted to 13*R*-hydroxy-14*S*,15*S*-epoxyeicosa-5*Z*,8*Z*,11*Z*-trienoic acid (14,15-HxB₃ 13*R*), 11*S*-hydroxy-14*S*,15*S*-epoxy-5*Z*,8*Z*,12*E*-eicosatrienoic acid (14,15-HxA₃ 11*S*), and 15-oxo-ETE [200,291]. 14,15-HxA₃ 11*S*, analogous to HxA₃, can be conjugated with glutathione. This produces 14,15-HxA₃-C 11*S* and cysteinyl-14,15-HxA₃ 11*S*, having conjugated glutathione without further amino acids, which is analogous to that of cysteinyl-leukotriene [291].

15-HpETE can also be converted to eoxins [292], which are isomers of leukotrienes.

15-HpETE can also be converted to lipoxins with 5-LOX [223], resulting in the formation of 5S, 15S-dihydroperoxyeicosatetraenoic acid (5, 15-diHpETE), and then converted to LXA₄ or LXB₄ [293]. 5-HpETE can also be converted with 15-LOX-1/*ALOX15* into 5, 15-diHpETE and, via the same pathway, be converted into LXA₄ or LXB₄ [293]. 15-HETE can be converted to LXA₄ with 5-LOX/*ALOX5* [294]. Lipoxins can also be formed from LTA₄, which is processed by 15-LOX-1/*ALOX15* or 12-LOX [293,295].

LXA₄ is a lipid mediator with biological activity whose receptors are lipoxin A₄ receptor (ALX)/formyl peptide receptor type 2 (FPR2) [296,297], aryl hydrocarbon receptor (AHR) [298], and estrogen receptors subtypes alpha (ER α) [299], the former of which is not a receptor for LXB₄ [296]. The ALX/FPR2 receptor is responsible for the anti-inflammatory properties of lipoxins.

There are also cysteinyl lipoxins, which, just like cysteinyl leukotrienes, are lipoxins with conjugated glutathione at carbon 6 [294]. They are synthesized from 15-HETE, from which, with the participation of 5-LOX/*ALOX5*, 15-hydroxy-5,6-epoxy-eicosatetraenoic acid is formed, a compound similar in structure to LTA₄. The epoxy group from these two compounds is converted to a hydroxyl group and conjugated glutathione [294]. However, it is not known whether cysteinyl lipoxins are essential lipid mediators or merely arise as a result of the nonspecificity of enzymes conjugating glutathione to various compounds.

6.2. Lipoxygenases in Glioblastoma Multiforme

In GBM tumors, ARA C20:4n-6 is mainly processed by COX, as shown by experiments on the C6 cell line [140]. In contrast, in the healthy brain, this PUFA is mainly processed by the LOX pathway. This shows that in GBM tumors, the LOX pathway may not be as important as the COX pathway, although it is still important in tumor mechanisms in GBM tumors.

6.2.1. 5-Lipoxygenase Pathway in Glioblastoma Multiforme

The expression of 5-LOX/*ALOX5* in a GBM tumor is higher than in non-tumor brain tissue [300–302]. This is also confirmed by data obtained from the GEPIA portal [9] and from Seifert et al. transcriptomics analysis [8].

Expression of 5-LOX/ALOX5 in the GBM tumor is found in macrophage and microglial cells as well as in other cells, such as cancer cells [301,302]. It is higher in GBM cancer stem cells than in other GBM cancer cells [303]. According to GEPIA, higher expressions of FLAP/ALOX5AP, LTC₄S, LTA₄H, GGT5, and DPEP1 but not DPEP2 [9], the enzymes that synthesize LTB₄ and LTE₄ from the product of 5-LOX/ALOX5 activity, were also found in GBM tumors [224,225,229,230,232,234]. Seifert et al. showed that there are higher expressions of FLAP/ALOX5AP, LTC₄S, DPEP1, and GGT5 in GBM tumors than in healthy brain tissue [8]. In contrast, LTC₄S, DPEP1, and DPEP2 are not affected. The higher expression of enzymes responsible for leukotriene biosynthesis increases the production [304] and levels [305] of these lipid mediators further in GBM tumors than in healthy brain tissue, particularly cysteinyl-leukotrienes.

The expression level of 5-LOX/*ALOX5* in GBM tumors does not affect prognosis [9,188], although simultaneous high expression of COX-2 and 5-LOX/*ALOX5*, two major ARA C20:4n-6 processing enzymes, is associated with a worse prognosis [188]. This shows that the two pathways in cooperation can impinge on prognosis severity.

The expression levels of most enzymes involved in leukotriene production and metabolism do not affect prognosis [9]. Only for GGT1, higher expression in GBM tumors is associated with a worse prognosis [9]. GGT5 expression showed a positive trend (p = 0.055) toward a worse prognosis. GGT1 and GGT5 are enzymes that catalyze the transformation of LTC₄ into LTD₄ [232], demonstrating that the transformation of cysteinyl leukotrienes may be important in tumorigenesis in GBM.

In addition, higher expression of 12-HEDH/PTGR1, an enzyme that degrades LTB₄, as well as prostaglandins, may be associated with worse prognoses for GBM patients [121], although GEPIA did not confirm such a link [9]. In addition, GEPIA and Seifert et al. did not show that 12-HEDH/PTGR1 expression differs between GBM tumors and healthy brain tissue [8,9]. According to GEPIA [9] and Seifert et al. [8], expression levels of receptors for leukotrienes LTB₄R1, LTB₄R2, CysLTR₁, CysLTR₂, GPR17, and OXGR1/GPR99 do not differ between GBM tumors and healthy brain tissue. In addition, the expression levels of these receptors in GBM tumors do not affect prognosis [9].

Leukotrienes as well as the entire 5-LOX pathway are important in tumorigenesis in GBM. They may also be important in the onset of GBM and in the first stages of tumorigenesis. The GA genotype of rs2291427 in the *ALOX5* gene is associated with a higher risk of GBM in men [306].

Expression of 5-LOX/*ALOX5* is higher in GBM cancer stem cells than in other GBM cancer cells [303]. The products of 5-LOX/*ALOX5* activity induce proliferation and self-renewal of GBM cancer stem cells. The effects of 5-LOX/*ALOX5* on GBM cancer stem cells are autocrine in nature.

LTB₄ also increases the proliferation of GBM cells [307]. This is associated with an increase in Ca²⁺ levels in the cytoplasm of GBM cells [307]. Studies of various cell lines show that 5-LOX/*ALOX5* expression is present in only a portion of them [308,309]. Expression of 5-LOX/*ALOX5* causes an autocrine increase in the proliferation of such a line and, thus, makes culture growth dependent on 5-LOX/*ALOX5* activity. All GBM lines express LTA₄H, LTB₄R1/BLT1, LTB₄R2/BLT2, and CysLTR₂, but only some lines express LTC₄S [309], indicating heterogeneity in the production of cysteinyl-leukotrienes and 5-HETE by GBM cancer cells.

The dependence of the proliferation of some GBM cancer cell lines on the 5-LOX pathway may be a potential therapeutic target for GBM treatment in personalized therapy. For this reason, the pan-LOX inhibitor Nordy [303,310], 5-LOX inhibitors such as caffeic acid [307], A861 [311], AA-863, and U-60,257 (pyriprost) [312], LTA₄H inhibitors such as bestatin [311], and CysLTR₁ and CysLTR₂ receptor inhibitors such as montelukast and zafirlukast [313] have anti-tumor properties against GBM and inhibit proliferation. This is associated with decreased ERK MAPK activation and induction of apoptosis as a result of decreased expression of anti-apoptotic Bcl-2 and increased expression of pro-apoptotic Bax [308].

Cysteinyl leukotrienes may have anticancer properties by increasing the bioavailability of various chemotherapeutics. In the brain, as well as in GBM tumors, there is a blood-brain barrier (BBB) that is poorly permeable to many substances, including anticancer drugs [314]. However, cysteinyl leukotrienes have BBB permeability, as shown by experiments on rat RG-2 glioma tumors [315]. BBB permeability is highest for LTE₄ [315], with cysteinyl leukotrienes not causing BBB permeability in healthy brain tissue [315,316]. For this reason, the administration of LTC₄ prior to the administration of chemotherapeutics that pass poorly through the BBB increases the bioavailability of drugs such as cisplatin [317]. However, this method does not increase the bioavailability of all chemotherapeutics, as exemplified by paclitaxel [318].

The receptor for cysteinyl leukotrienes is GPR17 [253]. According to GEPIA [9] and Seifert et al. [8], the expression level of this receptor does not differ between GBM tumors and healthy brain tissue. Higher GPR17 expression is associated with better prognosis in patients with low-grade gliomas, according to the Chinese Glioma Genome Atlas (CGGA) [319] and GEPIA [9], but the expression of this receptor is not associated with prognosis in a GBM patient [9]. GPR17 expression is also higher in low-grade gliomas than in healthy brain tissue [319]. Activation of this receptor by the ligand inhibits proliferation in the G₁ phase and induces apoptosis of GBM cell lines LN-229 and SNB-19 [319]. In addition, GPR17 ligands inhibit tumor growth, as shown by experiments using patient-derived xenograft mouse models. The action of GPR17 is associated with a decrease in the levels of cyclic adenosine monophosphate (cAMP) and Ca²⁺ in the cytoplasm, which reduces the activation of the PI3K \rightarrow Akt/PKB pathway [319,320]. An increase in GPR17 expression can cause the proliferation and migration of GBM cells [321], particularly with an increase in the expression of this receptor by long non-coding RNA (lncRNA) colorectal neoplasia differentially expressed (CRNDE) in low-grade glioma cells [321].

The receptor for 5-HETE, and also other lipid mediators, is G2A/GPR132 [83]. Higher expression of this receptor, according to GEPIA, is associated with a worse prognosis for a GBM patient (p = 0.052) [9], yet there is no significant upregulation of this receptor expression in GBM tumors [8,9].

5-oxo-ETE may also play an important role in tumorigenic mechanisms in GBM. The receptor for this lipid mediator is OXER1/GPR99 [220–222]. The expression of this receptor does not differ between GBM tumor and healthy brain tissue [8,9]. According to GEPIA, higher expression of OXER1/GPR99, the receptor for 5-oxo-ETE, is associated with a worse prognosis for a GBM patient [9]. OXER1/GPR99 is also a receptor for 2-oxoglutarate, LTC₄, and LTD₄ [252]. There is a lack of thorough research on the importance of 5-oxo-ETE in tumorigenesis in GBM tumors.

6.2.2. 12-Lipoxygenase Pathway in Glioblastoma Multiforme

In GBM tumors, expression of 12S-LOX/ALOX12 and 12R-LOX/ALOX12B is not different from healthy brain tissue [8,9], nor is it associated with prognosis severity [9], nor is the expression of the receptor for 12S-HETE, i.e., GPR31, elevated and affecting prognosis [8,9]. In contrast, the expression of eLOX3/ALOXE3 in GBM tumors is lower than in other brain tissue [9,205]. On the other hand, the transcriptomics analysis by Seifert et al. showed no differences between eLOX3/ALOXE3 expression levels in GBM tumor and healthy brain tissue [8]. Downregulation of eLOX3/ALOXE3 expression in GBM tumor is associated with increased expression of miR-18a, which downregulates eLOX3/ALOXE3 expression [205]. At the same time, eLOX3/ALOXE3 expression is also not related to the prognoses of GBM patients [9].

12-LOX is involved in tumorigenesis in GBM. Studies on various cell lines have shown that 12-LOX expression is common in GBM cancer cells [309]. For this reason, 12-LOX inhibitors inhibit proliferation and reduce the viability of GBM cells [309,322]. 12-LOX inhibitors also inhibit the migration of GBM cells because they reduce the expression of matrix metalloproteinase 2 (MMP2) in these cells [309]. However, the exact mechanism of 12-LOX action on tumorigenic processes in GBM is poorly studied. The fact that eLOX3/ALOXE3 is anticancer in nature [205] suggests that a lipid mediator not formed by eLOX3/ALOXE3 is responsible for the pro-cancer properties of 12-LOX. Perhaps it is 12-HETE, a lipid mediator with proven pro-cancer properties in other cancers [323,324]. In addition, higher expression of G2A/GPR132, a receptor for 5-HETE, 12-HETE, 15-HETE, and 9-HODE, is associated with a worse prognosis for a GBM patient (p = 0.052) [9]. The oncogenic properties of G2A/GPR132 were also demonstrated in a study on fibroblasts [189], although there is no higher expression of G2A/GPR132 in GBM tumors than in healthy brain tissue [8,9].

12-LOX may also have anti-cancer properties. It converts ARA 20:4n-6 into 12-HpETE, a lipid from the hydroperoxyl group, and for this reason, it can cause lipid peroxidation, which, when free ARA 20:4n-6 is in excess and this PUFA is over-processed, has a destructive effect on the cell [325].

eLOX3/ALOXE3 has anti-tumor properties in GBM. eLOX3/ALOXE3 converts 12-HpETE into 12-oxo-ETE. In the absence of eLOX3/ALOXE3, 12-HpETE is converted to 12-HETE [205], meaning that eLOX3/ALOXE3 decreases 12-HETE production. This lipid mediator increases GBM cell migration. When 12-HETE production is decreased, GBM cell migration is reduced.

The lipid mediators produced by eLOX3/*ALOXE3*, including 12-oxo-ETE, have antitumor effects, particularly 12-oxo-ETE, which is a ligand for PPARγ [204,205]. Activation of this nuclear receptor inhibits proliferation and induces apoptosis of GBM cancer cells [326–328].

The products of eLOX3/*ALOXE3* activity are hepoxilins and trioxilins [200,203], lipid mediators of physiological importance. However, there is a lack of studies on the importance of these lipid mediators in tumorigenesis in GBM.

Analysis on the GEPIA portal [9] and the transcriptomics analysis by Seifert et al. [8] showed no differences in the expression of EPHX2, the enzyme responsible for converting hepoxilins into trioxilins, between GBM tumors and healthy brain tissue [276,280]. At the same time, according to GEPIA, higher EPHX2 expression in GBM tumors is associated with a tendency toward a worse prognosis (p = 0.072), which may indicate that hepoxilins and trioxilins may have some role in neoplastic processes in GBM.

6.2.3. 15-Lipoxygenase Pathway in Glioblastoma Multiforme

GEPIA [9] and Seifert et al. [8] showed no differences in the expression of 15-LOX-1/ALOX15 and 15-LOX-2/ALOX15B between GBM tumors and healthy brain tissue. According to GEPIA, the expression level of these enzymes does not affect the prognosis for patients [9]. Studies on various GBM lines have shown differences in the expression of 15-LOX-1/ALOX15 and 15-LOX-2/ALOX15B in GBM cancer cells [309]. 15-LOX is important in the function of GBM cancer cells, and 15-LOX inhibitors reduce the viability and migration of GBM cancer cells [309]. On the other hand, increasing the expression and activity of 15-LOX-1/ALOX15 throughout the body may have an anti-tumor effect against GBM, as shown by gene therapy using an adenovirus transducing the ALOX15 gene [329]. This effect may depend on 13-HODE and 15-HETE.

All GBM lineages secrete 13-HODE, a product of the linoleic acid C18:2n-6 conversion with 15-LOX-1/*ALOX15* and 15-LOX-2/*ALOX15B* [266]. 13-HODE increases MMP2 expression in GBM cells, which causes migration [309]. At the same time, 13-HODE also decreases the viability of GBM cells [309], which may depend on the activation of PPAR γ via this lipid mediator [290]. This mechanism was confirmed in other cancers, including non-small cell lung cancer [330].

15-HETE can activate G2A/GPR132 [83]. Higher expression of this receptor. according to GEPIA. is associated with a worse prognosis for a GBM patient (p = 0.052) [9]. At the same time, the importance of this receptor in GBM has not been thoroughly investigated. Studies in other models have shown that G2A/GPR132 is an oncogene [189]; that is, 15-HETE through activation of G2A/GPR132 has a pro-cancer effect. At the same time, there is no significant upregulation of this receptor expression in GBM tumors [8,9].

The significance of lipoxins in GBM tumors has not been thoroughly investigated. The expression level of the LXA₄ receptor ALX/FPR2 does not differ between GBM tumors and healthy brain tissue (Table 7) [8,9]. The expression level of this receptor in GBM tumors does not affect prognosis. However, it may be important in tumorigenesis in GBM tumors. Studies on U-87 MG cells have shown that silencing ALX/FPR2 reduces the proliferation and migration of the cells tested [331]. In addition, cells with silenced ALX/FPR2 showed lower expressions of VEGF, a major pro-angiogenic factor. However, this receptor is activated not only by LXA₄ but also by other factors [332]—for this reason, the importance of LXA₄ in tumorigenic processes in GBM cannot be determined.

Name	Biochemical Significance	Expression Level In GBM Tumors Relative To Healthy Tissue		Impact on Prognosis with Higher Expression in GBM Tumors
Source		GEPIA [9]	Seifert et al. [8]	GEPIA [9]
eLOX3/ALOXE3	Production of hepoxilins/hydroxy-epoxyeicosatrienoic acid and oxo-ETE from HpETE	Lower expression in the tumor	Expression does not change	No significant impact on prognosis
5-LOX/ALOX5	5-HpETE production from ARA; the first enzyme in leukotrienes and the 5-oxo-ETE synthesis pathway; synthesis of lipoxins from 15-HpETE and 15-HETE	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis
FLAP/ALOX5AP	Substrate carrier for 5-LOX	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis
12S-LOX/ALOX12	12S-HpETE production from ARA; the first enzyme in the hepoxilin production pathway; production of lipoxins from LTA ₄	Expression does not change	Expression does not change	No significant impact on prognosis
12R-LOX/ALOX12B	12R-HpETE production from ARA	Expression does not change	Expression does not change	No significant impact on prognosis
15-LOX-1/ALOX15	15-HpETE production from ARA; 12-HpETE production from ARA; production of lipoxins, eoxins, 15-oxo-ETE and 15-HETE; production of 13-HpODE from linoleic acid C18:2n-6	Expression does not change	Expression does not change	No significant impact on prognosis
15-LOX-2/ALOX15B	15-HPETE production from ARA; production of 15-HPETE, lipoxins, eoxins, 15-oxo-ETE and 15-HETE	Expression does not change	Expression does not change	No significant impact on prognosis
LTA ₄ H	LTB ₄ production from LTA ₄	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis
LTC ₄ S	LTC ₄ production from LTA ₄	Higher expression in the tumor	Expression does not change	No significant impact on prognosis
GGT1	LTD ₄ production from LTC ₄	Expression does not change	Expression does not change	Worse prognosis
GGT5	LTD ₄ production from LTC ₄	Higher expression in the tumor	Higher expression in the tumor	Worse prognosis (<i>p</i> = 0.055)
DPEP1	LTE ₄ production from LTD ₄	Higher expression in the tumor	Expression does not change	No significant impact on prognosis
DPEP2	LTE ₄ production from LTD ₄	Expression does not change	Expression does not change	No significant impact on prognosis
EPHX2	Conversion of hepoxilins into trioxilin	Expression does not change	Expression does not change	Worse prognosis ($p = 0.072$)
	R	eceptors		
LTB ₄ R1	LTB ₄ receptor	Expression does not change	Expression does not change	No significant impact on prognosis
LTB ₄ R2	LTB ₄ receptor	Expression does not change	Expression does not change	No significant impact on prognosis
CYSLTR ₁	Cysteinyl-leukotrienes receptor	Expression does not change	Expression does not change	No significant impact on prognosis
CYSLTR ₂	Cysteinyl-leukotrienes receptor	Expression does not change	Expression does not change	No significant impact on prognosis
OXER1	5-oxo-ETE receptor	Expression does not change	Expression does not change	Worse prognosis
ALX/FPR2	LXA ₄ receptor	Expression does not change	Expression does not change	No significant impact on prognosis
GPR17	Cysteinyl-leukotrienes receptor	Expression does not change	Expression does not change	No significant impact on prognosis
GPR31	12S-HETE receptor	Expression does not change	Expression does not change	No significant impact on prognosis
OXGR1/GPR99	LTE ₄ receptor	Expression does not change	Expression does not change	No significant impact on prognosis
G2A/GPR132	5-HETE, 12-HETE, 15-HETE, 9-HODE receptor	Expression does not change	Expression does not change	Worse prognosis ($p = 0.052$)

Table 7. Description of the various enzymes involved in the synthesis, action, and degradation of lipoxygenases along with their involvement in tumorigenesis in GBM.

Red background—higher expression in the tumor; blue background—lower expression in the tumor; red background—worse prognosis with higher expression.

The expression levels of various LOX are not associated with prognoses for GBM patients [9]. This indicates that the LOX pathway is not as relevant to cancer processes as other pathways. For this reason, drugs targeting LOX may show poor efficacy in GBM therapy. At the same time, the analyses performed in this study show that higher expression of OXER1 (the receptor for 5-oxo-ETE) and higher expression of G2A/GPR132 (the receptor for various HETE) are associated with poor prognosis [9]. This indicates a therapeutic

target for future drugs developed for the treatment of GBM. In addition, higher expression of GGT1 in GBM tumors is associated with worse prognosis, and higher expression of GGT5 and EPHX2 is associated with a trend of worse prognosis for GBM patients. This indicates a future direction for research into tumor mechanisms in GBM.

6.3. Pan-Cancer Analysis of Genes Related to LOX Pathway and GBM

Similar to the COX pathway, we performed a pan-cancer analysis of the expression of the genes involved in the LOX pathway using the data from the GEPIA web server [9].

The expression of eLOX3/LOXE3 is reduced in GBM tumors. At the same time, there is no change in the expression of this enzyme relative to healthy brain tissue in lower grade gliomas. It is also reduced in two more types of tumors. For this reason, a decrease in eLOX3/LOXE3 expression may be considered specific to GBM.

In GBM tumors, there is elevated expression of 5-LOX/ALOX5 and FLAP/ALOX5AP relative to healthy brain tissue, which is similar to lower grade gliomas [9]. Expression of these proteins is elevated in 9 and 11 tumor types, respectively. In a similar number of tumor types, there is a reduction in the expressions of 5-LOX/ALOX5 and FLAP/ALOX5AP. This indicates that the elevated expressions of 5-LOX/ALOX5 and FLAP/ALOX5AP may be glioma-specific.

The expression of other LOX is not altered in GBM and lower grade gliomas, which is similar to most other types of cancer. In GBM tumors, there are elevated expressions of LTA₄H/*LTA4H* and LTC₄S/*LTC4S* relative to healthy tissue [9]. In lower grade gliomas, there is higher expression of only LTC₄S/*LTC4S* [9]. According to Seifert et al., in II and III grade gliomas, there are higher expressions of LTA₄H/*LTA4H* but not LTC₄S/*LTC4S* relative to healthy brain tissue [8]. LTA₄H/*LTA4H* expression is elevated in 4 out of 31 analyzed tumor types. LTC₄S/*LTC4S* is upregulated in six tumor types but downregulated in eleven types [9]. Therefore, the elevated expression of LTA₄H/*LTA4H* and LTC₄S/*LTC4S* can be considered as specific to GBM and glioma, respectively.

GGT5 expression is upregulated in GBM and lower grade gliomas [8,9]. It is downregulated in eleven tumor types and upregulated in seven. Therefore, the elevation of *GGT5* expression can be considered characteristic for gliomas.

DPEP1 expression is elevated in GBM tumors but not in lower grade gliomas (Table 8) [9]. It is decreased in six types of tumors but increased in four types, including GBM. For this reason, it can be thought that changes in *DPEP1* expression are characteristic of GBM. *EPHX2* expression is often decreased in tumors. In a pan-cancer analysis, 17 types of tumors had a reduced expression of this enzyme relative to healthy tissue. At the same time, in GBM tumors, *EPHX2* expression does not differ relative to healthy brain tissue [8,9].

Table 8. Pan-cancer analysis of expression of genes involved in the LOX pathway.

Name of Cancer	eLOX3/AL <i>OXE</i> 3	5-LOX/ALOX5	FLAP/ALOX5AP	12S-LOX/ALOX12	12R-LOX/ALOX12B	15-LOX-1/ALOX15	15-LOX-2/ALOX15B	LTA ₄ H/LTA4H	LTC ₄ S/LTC4S	GGT1	GGT5	DPEP1	DPEP2	EPHX2
Adrenocortical carcinoma (ACC)	=	\downarrow	\downarrow	=	=	=	\downarrow	=	=	=	\downarrow	=	=	\downarrow
Bladder urothelial carcinoma (BLCA)	=	=	\downarrow	=	=	=	=	=	\downarrow	=	\downarrow	=	=	\downarrow
Breast invasive carcinoma (BRCA)	=	=	=	=	=	=	\downarrow	=	=	=	=	=	=	=
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)	=	=	=	=	=	=	=	=	\downarrow	=	\downarrow	=	=	\downarrow
Cholangiocarcinoma (CHOL)	=	\uparrow	\uparrow	=	=	=	=	\uparrow	\uparrow	=	=	=	=	\downarrow
Colon adenocarcinoma (COAD)	=	=	=	=	=	=	=	=	\downarrow	\uparrow	=	\uparrow	\downarrow	=
Lymphoid neoplasm diffuse large B-cell lymphoma (DLBC)	=	\downarrow	\downarrow	\downarrow	=	=	\uparrow	=	=	=	\uparrow	=	\downarrow	=
Esophageal carcinoma (ESCA)	=	=	=	\downarrow	=	=	\downarrow	=	=	=	=	=	=	\downarrow
Glioblastoma multiforme (GBM)	\downarrow	1	\uparrow	=	=	=	=	1	1	=	\uparrow	\uparrow	=	=
Head and neck squamous cell carcinoma (HNSC)	1	=	=	\downarrow	=	=	=	=	=	=	\uparrow	=	=	\downarrow
Kidney chromophobe (KICH)	=	=	=	=	=	=	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=	=
Kidney renal clear cell carcinoma (KIRC)	=	1	1	=	=	=	=	=	=	\uparrow	=	\downarrow	1	\downarrow
Kidney renal papillary cell carcinoma (KIRP)	=	\uparrow	1	=	=	=	\uparrow	=	=	1	\downarrow	\downarrow	1	=
Acute myeloid leukemia (LAML)	=	\uparrow	\uparrow	=	=	=	=	1	\uparrow	=	1	=	\uparrow	\downarrow
Brain lower grade glioma (LGG)	=	1	\uparrow	=	=	=	=	=	\uparrow	=	1	=	=	=
Liver hepatocellular carcinoma (LIHC)	=	=	=	=	=	=	=	=	=	=	\downarrow	=	=	\downarrow
Lung adenocarcinoma (LUAD)	=	\downarrow	\downarrow	=	=	=	\downarrow	=	\downarrow	=	=	=	\downarrow	=
Lung squamous cell carcinoma (LUSC)	=	\downarrow	\downarrow	=	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=	=	\downarrow	=
Ovarian serous cystadenocarcinoma (OV)	=	\uparrow	1	=	=	=	=	=	=	=	\downarrow	=	=	\downarrow
Pancreatic adenocarcinoma (PAAD)	=	1	1	=	=	=	\uparrow	\uparrow	\uparrow	\uparrow	\uparrow	\downarrow	1	\downarrow
Pheochromocytoma and paraganglioma (PCPG)	=	=	\downarrow	=	=	=	=	=	=	=	\downarrow	=	=	\downarrow
Prostate adenocarcinoma (PRAD)	=	=	=	=	=	=	=	=	=	\uparrow	=	=	=	=
Rectum adenocarcinoma (READ)	=	=	=	=	=	=	=	=	\downarrow	\uparrow	=	\uparrow	=	=

Table 8. Cont.														
Name of Cancer	eLOX3/ALOXE3	5-LOX/ALOX5	FLAP/ALOX5AP	12S-LOX/AL <i>OX</i> 12	12R-LOX/ALOX12B	15-LOX-1/ALOX15	15-LOX-2/ALOX15B	LTA ₄ H/LTA4H	LTC ₄ S/LTC4S	6671	GGT5	DPEP1	DPEP2	EPHX2
Sarcoma (SARC)	=	=	=	=	=	=	=	=	=	\downarrow	=	\downarrow	=	\downarrow
Skin cutaneous melanoma (SKCM)	\downarrow	\downarrow	=	\downarrow	\downarrow	=	\downarrow	=	\downarrow	=	\downarrow	=	=	\downarrow
Stomach adenocarcinoma (STAD)	=	=	1	=	=	=	=	=	=	=	=	=	=	=
Testicular germ cell tumors (TGCT)	\downarrow	=	\uparrow	=	=	\downarrow	=	=	\downarrow	=	=	\downarrow	=	\downarrow
Thyroid carcinoma (THCA)	=	\uparrow	\uparrow	=	=	=	\uparrow	=	=	=	=	=	=	=
Thymoma (THYM)	=	\downarrow	\downarrow	=	=	=	=	=	\uparrow	=	\uparrow	\uparrow	\downarrow	\uparrow
Uterine corpus endometrial carcinoma (UCEC)	=	\downarrow	=	=	=	=	=	=	\downarrow	\uparrow	\downarrow	=	=	\downarrow
Uterine carcinosarcoma (UCS)	=	\downarrow	\downarrow	=	=	=	=	=	\downarrow	=	\downarrow	=	=	\downarrow

Red background, \uparrow —expression higher in tumor than in healthy tissue; blue background, \downarrow —expression lower in tumor than in healthy tissue; gray background, =—expression does not differ between tumor and healthy tissue.

7. Cytochrome P450 Pathway in Glioblastoma Multiforme Tumors

7.1. Cytochrome P450 Pathway

In addition to the processing of ARA C20:4n-6 by COX and LOX, this fatty acid can also be converted into lipid mediators with cytochrome P450. It results in the formation of epoxyeicosatrienoic acids (EET) and HETE [333].

ARA C20:4n-6 can undergo either hydroxylation or epoxidation. The ω -hydroxylation reaction converts ARA C20:4n-6 into 20-hydroxyeicosatetraenoic acid (20-HETE). The enzymes responsible for this reaction are CYP1A2 [334], CYP1B1 [335], CYP2U1 [336], CYP4A11 [337,338], CYP4F2 [337,339], CYP4F3A, and CYP4F3B [339].

ARA C20:4n-6 can also be converted to 19-hydroxyeicosatetraenoic acid (19-HETE) in the (ω -1)-hydroxylation reaction. The cytochromes P450 responsible for this are CYP1B1 [335], CYP2C19 [340], CYP2E1 [334], and CYP2U1 [336].

ARA C20:4n-6 can also undergo hydroxylation at other positions with the formation of various HETE [335,340–344]. The cytochromes P450 carrying out this reaction include CYP1A2 [343], CYP1B1 [335], CYP2C9 [334,340], and CYP3A4 [343]. The HETE receptor, with an OH residue at positions 5 to 15, is G2A/GPR132 [83]. In contrast, receptors for 20-HETE include G-protein receptor 75 (GPR75) [345], transient receptor potential vanilloid 1 (TRPV1) channel [346], free fatty acid receptor 1 (FFAR1)/GPR40 [347], and PPAR α [348]. HETE can then undergo ω -hydroxylation with CYP4F [333], resulting, for example, in the formation of 10,20-dihydroxyeicosatrienoic acid (10,20-DHET) from 10-HETE, which may be a mechanism for regulating the activity of these lipid mediators.

In the cytochrome P450 pathway, ARA C20:4n-6 can also undergo epoxidation with the formation of epoxyeicosatrienoic acids (EET). Because ARA C20:4n-6 has four double bonds, this reaction produces 5,6-EET, 8,9-EET, 11,12-EET, or 14,15-EET, albeit a given cytochrome P450 can produce mainly only some EET [340]. The enzymes responsible for this reaction are CYP1A2 [334], CYP1B1 [335], CYP2C8 [349,350], CYP2C9 [350], CYP2C19 [340], CYP2J2 [351], and CYP4X1 [352].

The receptor for EET is GPR40 [353]. 14,15-EET can activate receptors for prostaglandins, including PGE₂ (PTGER₂, PTGER₃, and PTGER₄), PGD₂ (PTGDR), and PGF₂ α (PTGFR) [354,355]. EET can also activate PPAR α (in particular, 11,12-EET [348] and PPAR γ [356,357]).

Another important property of EET is that it enters the cell membrane and intracellular membranes. This is as a result of the incorporation of EET into glycerophospholipids at the *sn*-2 position [357–359]. EET can also be metabolized by EPHX1 and EPHX2 [357,360]. This is the same enzyme that catalyzes the conversion of hepoxilins (a hydroxy-epoxy derivative of ARA) to trioxilins [276,280]. EET are then converted to dihydroxyeicosatrienoic acid (DHET). In this form, particularly 14,15-DHET, they can activate PPARα [348,361].

EET can also undergo ω -hydroxylation with CYP4F [333]. For example, 8,9-EETs give rise to 20-hydroxy-8(9)-epoxyeicosatrienoic acid (20,8(9)-HEET) (Figure 7) [333,362]. EET can also be converted into either shorter or longer lipid mediators via β -oxidation and elongation, respectively [357]. Another possible reaction is the conversion of 5,6-EET, 8,9-EET, and 11,12-EET with COX [357,363,364], resulting in the formation of lipid mediators with proangiogenic properties. 5,6-epoxy-PGH₂ is formed from 5,6-EET, [364]. In contrast, 11-hydroxy-8,9-EET (8,9,11-EHET) and 15-hydroxy-8,9-EET (8,9,15-EHET) are formed from 8,9-EET [364–366].

HETE and EET are the direct products of cytochrome P450 activity. However, cytochromes p450 are not only involved in the production of these ARA-derived lipid mediators. In addition, CYP4F and CYP4A cause ω -hydroxylation of the already discussed eicosanoids formed in COX and LOX pathways. CYP4A and CYP4F8 are responsible for the ω -hydroxylation and (ω -1)-hydroxylation of prostaglandins, respectively [126,333], and CYP4F is responsible for the transformation of LTB₄ and lipoxins [333]. The aforementioned reactions often result in the inactivation of these lipid mediators.



It should be mentioned that the aforementioned cytochromes P450 are not only involved in the metabolism of ARA C20:4n-6. They can also metabolize other fatty acids [336], such as linoleic acid [367], and many drugs, including anticancer drugs [349,368].

Figure 7. Cytochrome P450 pathway. ARA 20:4n-6 can be converted in the cytochrome P450 pathway, resulting in the formation of various ETT and HETE. ETT can undergo further transformations where they are incorporated into glycerophospholipids in the *sn*-2 position; in this form, they build the cell membrane and intracellular membranes. In addition, the epoxide bond in ETT can be transformed by EPHX1 and EPHX2 into two hydroxyl groups, resulting in the formation of various DHET. ETT can also undergo ω -hydroxylation, which results in the formation of various HEET. ETT can be converted with COX. 5,6-EET then produces 5,6-epoxy-PGH₂, whereas 8,9-EET produces either 8,9,11-EHET or 8,9,15-EHET. \uparrow —higher expression of given enzymes in GBM tumor relative to healthy tissue; \downarrow —lower expression of given enzymes in GBM tumor relative to healthy tissue.

7.2. Cytochrome P450 Pathway in Glioblastoma Multiforme Tumors

ARA C20:4n-6 is converted to 20-HETE [369], which increases the proliferation of GBM cells [370]. 20-HETE may also be an important pro-angiogenic factor in GBM tumors by acting on endothelial cells [369] and enhancing vascular mimicry of GBM cells [371]. Importantly, 20-HETE may not be produced by GBM cells [372] but by TAM and endothelial

progenitor cells (EPCs) [373]. CYP2U1 [336,374], whose expression in GBM tumors is elevated relative to healthy brain tissue [8,9], may be responsible for 20-HETE production in GBM tumors. Nevertheless, there is very little research focused on 20-HETE production in GBM tumors.

In the rat glioma RG2 cell line, there is production of various lipid mediators, including 15-HETE, 12-HETE, 8-HETE, 5-HETE, 14,15-diHETE, 14,15-EET, 11,12-diHETE, and 11,12-EET [375]. In part, this may be due to the effect of elevated levels of glutamate in the intercellular space, which is characteristic for GBM tumors [376]. This amino acid increases the expression of CYP1B1 and CYP2U1 in GBM cells [374], leading to increased production of lipid mediators with these cytochrome P450 enzymes.

According to the GEPIA [9] and to Seifert et al. [8], the expression of most of the discussed cytochromes P450 do not differ between GBM tumors and healthy brain tissue. Both sources only show higher expression of *CYP2U1* and lower expression of *CYP4X1* in GBM tumors compared to healthy brain tissue. *CYP2U1* is the cytochrome P450 producing 20-HETE and 19-HETE [336], which shows a possible source of these two lipid mediators in GBM tumors.

GEPIA, in contrast to Seifert et al. shows reduced expression of *CYP2C8* in GBM tumors (Table 9). According to the GEPIA [9], the expression of this cytochrome P450 was not linked to the prognosis of GBM patients. Expression of the receptor for 20-HETE, i.e., *GPR75*, does not differ in GBM tumors compared to healthy brain tissue. The expression level of *GPR75* is not associated with prognosis.

 Table 9. Significance of cytochromes P450 and GPR75 receptors in ARA metabolism and tumorigenic processes in GBM.

Name	Expression Level in GBM Tun	nor Relative to Healthy Tissue	Impact on Prognosis with Higher Expression in GBM Tumors
Source	GEPIA [9]	Seifert et al. [8]	GEPIA [9]
CYP1A2	Expression does not change	Expression does not change	N/A
CYP1B1	Expression does not change	Expression does not change	No significant impact on prognosis
CYP2C8	Lower expression in the tumor	Expression does not change	No significant impact on prognosis
CYP2C9	Expression does not change	Expression does not change	N/A
CYP2C19	Expression does not change	Expression does not change	N/A
CYP2J2	Expression does not change	Expression does not change	No significant impact on prognosis
CYP2U1	Higher expression in the tumor	Higher expression in the tumor	No significant impact on prognosis
СҮРЗА4	Expression does not change	Expression does not change	Worse prognosis $p = 0.07$
CYP4A11	Expression does not change	Expression does not change	No significant impact on prognosis
CYP4F2	Expression does not change	Expression does not change	No significant impact on prognosis
CYP4F3	Expression does not change	N/A	No significant impact on prognosis
CYP4X1	Lower expression in the tumor	Lower expression in the tumor	No significant impact on prognosis
GPR75	Expression does not change	Expression does not change	No significant impact on prognosis

Red background—higher expression in the tumor; blue background—lower expression in the tumor; red background—worse prognosis with higher expression.

The expression of EPHX1 and EPHX2, enzymes involved in the conversion of EET to DHET, does not differ between GBM tumor and healthy brain tissue [8,9]. In addition, the expression levels of these enzymes are not associated with the prognosis of a GBM patient.

7.3. Pan-Cancer Analysis of Cytochrome P450 Genes and Comparison of GBM Expression against Other Cancers

Changes in the expression of various genes in GBM tumors relative to healthy tissue could be the result of tumor-specific neoplastic processes or specific mechanisms found

only in GBM. For this reason, a pan-cancer analysis of the expression of the cytochromes P450 genes described above was performed using the GEPIA portal [9].

CYP2C8 expression was lower in GBM tumors relative to healthy brain tissue [9], similar to lower grade gliomas (Table 10). Downregulation of *CYP2C8* expression occurs in a variety of tumors. Out of 31 analyzed cancers, seven show decreased expression of this enzyme, which shows that reduced expression of *CYP2C8* is common in cancers. In 11 types of cancers out of 31, there is an increase in *CYP2J2* expression. However, in GBM and lower grade gliomas, there is no change in the expression of this cytochrome P450. GEPIA also shows that in 8 out of 31 cancers, including GBM tumors, there is higher expression may be associated with cancerous processes. In GBM and lower grade gliomas, there is lower expression of *CYP2U1* compared to healthy brain tissue [8,9]. In the other seven types of tumors, there is also a decrease in the expression of this cytochrome p450, which suggests that decreased *CYP4X1* expression in tumor may be a common feature of cancer.

Table 10. Pan-cancer analysis of the expression of the cytochromes P450 and GPR75 receptor genes in question.

Name of Cancer	CYP1A2	CYP1B1	CYP2C8	CYP2C9	CYP2C19	CYP2J2	CYP2UI	CYP3A4	CYP4A11	CYP4F2	CYP4F3	CYP4X1	GPR75
Adrenocortical carcinoma (ACC)	=	\downarrow	\downarrow	=	=	=	=	=	=	=	=	=	=
Bladder urothelial carcinoma (BLCA)	=	\downarrow	=	=	=	=	\downarrow	=	=	=	=	=	=
Breast invasive carcinoma (BRCA)	=	=	=	=	=	=	=	=	=	=	=	=	=
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)	=	↓	=	=	=	1	\downarrow	=	=	=	\uparrow	=	=
Cholangiocarcinoma (CHOL)	\downarrow	1	\downarrow	\downarrow	\downarrow	\downarrow	=	\downarrow	\downarrow	\downarrow	\downarrow	=	=
Colon adenocarcinoma (COAD)	=	\downarrow	=	=	=	1	=	=	=	1	\uparrow	=	=
Lymphoid neoplasm diffuse large B-cell lymphoma (DLBC)	=	=	=	=	=	=	\uparrow	=	=	=	\downarrow	=	=
Esophageal carcinoma (ESCA)	=	=	=	\downarrow	=	\downarrow	=	=	=	=	\downarrow	\downarrow	=
Glioblastoma multiforme (GBM)	=	=	\downarrow	=	=	=	\uparrow	=	=	=	=	\downarrow	=
Head and neck squamous cell carcinoma (HNSC)	=	=	=	=	=	\downarrow	=	=	=	=	=	\downarrow	=
Kidney chromophobe (KICH)	=	\downarrow	=	=	=	=	=	=	\downarrow	\downarrow	\downarrow	\downarrow	=
Kidney renal clear cell carcinoma (KIRC)	=	\downarrow	=	=	=	1	=	=	\downarrow	\downarrow	\downarrow	=	=
Kidney renal papillary cell carcinoma (KIRP)	=	\downarrow	=	=	=	=	=	=	\downarrow	\downarrow	\downarrow	↓	=
Acute myeloid leukemia (LAML)	=	1	=	=	=	=	\uparrow	=	=	=	=	=	↑
Brain lower grade glioma (LGG)	=	=	↓	=	=	=	1	=	=	=	=	\downarrow	Î ↑
Liver hepatocellular carcinoma (LIHC)	\downarrow	=	\downarrow	\downarrow	\downarrow	=	=	Ļ	\downarrow	=	=	=	=
Lung adenocarcinoma (LUAD)	=	=	=	=	=	1	=	=	=	=	=	=	=
Lung squamous cell carcinoma (LUSC)	=	=	=	=	=	=	=	=	=	=	=	=	=
Ovarian serous cystadenocarcinoma (OV)	=	=	=	=	=	1	=	=	=	=	=	1	=
Pancreatic adenocarcinoma (PAAD)	=	1	=	1	=	1	1	\downarrow	=	=	1	=	=
Pheochromocytoma and paraganglioma (PCPG)	=	=	=	=	=	=	1	\downarrow	=	=	=	=	=
Prostate adenocarcinoma (PRAD)	=	=	=	=	=	1	=	=	=	=	=	=	=
Rectum adenocarcinoma (READ)	=	\downarrow	=	=	=	1	=	=	=	1	1	=	=
Sarcoma (SARC)	=	=	=	=	=	=	=	=	\downarrow	4	\downarrow	=	=
Skin cutaneous melanoma (SKCM)	=	=	=	=	=	\downarrow	1	\downarrow	=	=	\downarrow	\downarrow	=
Stomach adenocarcinoma (STAD)	=	=	\downarrow	\downarrow	=	1	=	=	=	=	\uparrow	\downarrow	=
Testicular germ cell tumors (TGCT)	=	=	\downarrow	=	=	\downarrow	=	=	=	\downarrow	=	=	=
Thyroid carcinoma (THCA)	=	1	=	=	=	=	=	=	=	=	=	\downarrow	=
Thymoma (THYM)	=	1	=	=	=	=	\uparrow	=	=	=	\downarrow	=	=
Uterine corpus endometrial carcinoma (UCEC)	=	\downarrow	=	=	=	1	↓	=	=	=	=	=	=
Uterine carcinosarcoma (UCS)	=	\downarrow	=	=	=	\uparrow	\downarrow	=	=	=	=	=	=

Red background, \uparrow —expression higher in tumor than in healthy tissue; blue background, \downarrow —expression lower in tumor than in healthy tissue; gray background, =—expression does not differ between tumor and healthy tissue.

8. Conclusions

The importance of the most important ARA C20:4n-6-derived lipid mediators in cancer mechanisms in GBM is very well understood. These compounds, particularly PGE_2 and leukotrienes, cause the proliferation and migration of GBM cancer cells, are important in the function of GBM cancer stem cells, cause angiogenesis, and by acting on cells of the immune system, inhibit the body's anti-tumor response. However, the importance in

GBM cancer processes of lesser-known ARA C20:4n-6-derived lipid mediators has not yet been investigated. We are talking, for example, about EET, lipoxins, hepoxilins, and some prostanoids, including $PGF_{2\alpha}$ and TxA_2 . Investigating the function of these compounds will provide a better understanding of GBM tumor function. It may also contribute to the development of new therapeutic approaches.

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