Discovery of novel ID2 antagonists from pharmacophore-based virtual screening as potential therapeutics for glioma

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1 **Highlights**

- 2 • Two pharmacophores were built from the first-in-class pan-ID antagonists
- 3 AGX51
- 4 • A pharmacophore-based virtual screening was carried out and 16 hit
- 5 compounds were purchased for pharmacological evaluations in glioma
- 6 inhibition
- 7 • Compound AK-778-XXMU was identified to be a potent ID2 antagonist in the
- 8 low submicromolar range (KD: 159 nM)

9 **Abstract**

10 Glioma, especially the most aggressive type glioblastoma multiforme, is one of

11 the central nervous system malignant cancer with a poor prognosis. Traditional

12 treatments are mainly surgery combined with radiotherapy and chemotherapy, which is

13 still not satisfactory. Therefore, it is of great clinical significance to find new

14 therapeutic agents. Served as an inhibitor of differentiation, protein ID2 (inhibitor of

15 DNA binding 2) plays an important role in neurogenesis, neovascularization and

16 malignant development of gliomas. It has been shown that ID2 affects the malignant

17 progression of gliomas through different mechanisms. In this study, a

18 pharmacophore-based virtual screening was carried out and 16 hit compounds were

19 purchased for pharmacological evaluations on their ID2 inhibitory activities. Based on

20 the cytotoxicity of these small-molecule compounds, two compounds were shown to

21 effectively inhibit the viability of glioma cells in the low micromolar range. Among

22 them, AK-778-XXMU was chosen for further study due to its better solubility in water.

1 A SPR assay proved the high affinity between AK-778-XXMU and ID2 protein with
 2 the KD value as 129 nM. The plausible binding mode in the binding site of ID2 was
 3 studied by molecular docking. Subsequently, the cancer-suppressing potency of the
 4 compound was characterized both *in vitro* and *in vivo*. The data demonstrated that
 5 compound AK-778-XXMU is a potent ID2 antagonist which has the potential to be
 6 developed as a therapeutic agent against glioma.

7 **Keywords:** glioma, inhibitor of differentiation, pharmacophore, virtual screening

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Introduction

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Malignant glioma is the most aggressive brain tumor with a high rate of fatality and poor prognosis [1–3]. Despite the enormous efforts invested to improve the efficacy of classical combination of surgical resection supplemented by chemotherapeutic agents, the overall survival of the patients is still not promising [2]. The chemotherapeutic agents currently approved by the FDA for the treatment of malignant glioma include temozolomide (Temodar, TMZ) and bevacizumab (Avastin). Unfortunately, as the first-line drug for glioblastoma, which is the most aggressive type of glioma, the emergence of TMZ resistance has greatly limited the effectiveness of the drug. Bevacizumab is currently the only targeted drug approved by FDA for the treatment of recurrent glioblastoma [4]. It has also been reported that bevacizumab can prolong the progression-free survival of newly diagnosed glioblastoma patients, but the overall survival time cannot be prolonged [5]. Moreover, the discovery of a subtype of tumor cell with stem cell-like self-renewal properties [6], along with insufficient tumor resection due to invasion of normal brain tissue by tumor cells [7] has been shown to result in relatively ineffective treatment of glioma [8]. Therefore, it is of great urgency to develop novel potential therapeutics against novel targets that play key roles in the progression of glioma.

Inhibitors of DNA binding (ID) proteins, commonly expressed in mammals synergistically, regulate gene expression, cell lineage localization and cell differentiation in tissues [9,10]. They belong to the family of helix-loop-helix (HLH)

transcription factors. However, the absence of a basic motif which is necessary for binding to DNA distinguishes it from the basic helix-loop-helix transcription factors (bHLH), which contributes to its role of transcription factor inhibitor. Ever since the first ID gene, ID1, was identified in 1990 by Benezra *et al* [9], three more ID groups were discovered and named ID2, ID3, and ID4 [11–14]. The crucial role of the ID proteins is due to their dominant-negative effect when they form heterodimers with other DNA-binding members of the HLH family, therefore disrupting the protein-DNA interaction. Not surprisingly, strong association of ID proteins with tumor angiogenesis has been suggested [15,16]. In particular, the emerging role of ID2 in glioma has attracted much attention [17]. It was found that ID2 was expressed to varying degrees in different grades of glioma and was significantly increased in mesenchymal astrocytoma and glioblastoma compared to low-grade malignant astrocytoma, which was not detected in normal cerebral white matter [18]. Furthermore, the expression level of ID2 was significantly correlated with the survival of glioblastoma cells in a low glucose metabolic stress environment by influencing mitochondrial function [19,20]. During the development of myeloid cells, Kinase insert domain receptor (KDR, a type IV receptor tyrosine kinase), also known as vascular endothelial growth factor receptor 2 (VEGFR-2), a critical gene for VEGF signaling, has the ability to drive differentiation of hematopoietic progenitor cells (HPCs) into tumor-promoting myeloid-derived suppressor cells (MDSCs) which could be enhanced by ID2 by upregulating KDR and then stimulates the formation of an aggressive pro-angiogenic phenotype in gliomas [17,21]. It is believed that neural precursor cells (NPCs), a type of neural stem cells,

1 may also be one origin for glioma cell [22,23]. Phosphorylation of ID2 N-terminal
2 seems to affect its protein expression level in NPCs, in the case of this phosphorylated
3 mutant, ID2 appears to be protected from degradation by the ubiquitin-proteasome
4 system (UPS) to perform a range of pro-oncogenic functions [24].

5 The ID genes/proteins are critically important during embryonic development but are
6 only active in adults when cancer is present [25–27]. It was found that they are
7 expressed in virtually all cancers [25,28]. The overexpression of ID genes in tumors is
8 linked to an aggressive phenotype and poor clinical outcome. It was proposed that
9 targeting ID proteins was an effective strategy to develop anti-cancer drugs [17].

10 So far, a variety of strategies have been proposed to interfere with ID activity,
11 including the use of targeted antisense delivery, cell-permeable peptides, antagonists of
12 Id expression, and inhibitors of stability-inducing deubiquitinases, antagonists of ID
13 proteins [29–34]. Among them, the first and only small-molecule pan-ID antagonist is
14 AGX51, discovered by Benezra group [35]. It was shown that AGX51 was able to
15 inhibit Id1-E47 interaction, leading to ubiquitin-mediated degradation of IDs, cell
16 growth arrest, and reduced viability. AGX51 was also able to phenocopy the genetic
17 loss of Id expression in age-related macular degeneration (AMD) and retinopathy of
18 prematurity (ROP) models by inhibiting retinal neovascularization [35]. Due to the
19 therapeutical potential of ID antagonists, it is important to develop more such
20 compounds to target ID proteins.

21 Therefore, we launched a drug discovery project by utilizing a pharmacophore-based
22 virtual screening approach. Docking-based virtual screening was not chosen because

1 even though ID2 protein has been already solved by crystallography (PDB: 4AYA), the
2 binding site is located at the loop region. Such a region is very flexible in nature so that
3 the binding site may not have a well-defined shape [36]. In contrast,
4 pharmacophore-based virtual screening does not require the structure of the protein
5 [37–40]. The pharmacophore was extracted from AGX51 and subjected to a series of
6 small commercial databases for virtual screening.

7 In the end, a variety of potential ID2 antagonists were obtained and 16 hit
8 compounds were purchased for pharmacological evaluations for their ID2 inhibitory
9 activities. Based on the cytotoxicity of these small-molecule compounds, two
10 compounds were shown to effectively inhibit the viability of glioma cells at low
11 micromolar concentrations. Among them, AK-778-XXMU was chosen for further
12 study due to its better solubility in water. A SPR (surface plasma resonance) assay
13 proved the high affinity between AK-778-XXMU and ID2 protein with the KD value as
14 129 nM. Subsequently, the cancer-suppressing potency of the compound was
15 characterized both *in vitro* and *in vivo*. The data demonstrated that compound
16 AK-778-XXMU is a potent ID2 antagonist which has the potential to be developed as a
17 therapeutic agent against glioma.

18 Results and Discussion

19 1. Results from pharmacophore-based virtual screening

20 The commercial compound databases used for virtual screening were
21 CHEMBRIDGE, SPECS, CHEMDIV, ENAMINE, IBS, LIFECHEMICALS,
22 VITAS-M, kindly provided in their electronic form by Topscience Co., Ltd

(<https://www.tsbiochem.com/>). They contained 2,281 compounds in total that were commercially available. Two pharmacophore models (*R*-model and *S*-model) were built from the two enantiomers of AGX51 and they were subjected for virtual screening against those databases mentioned above by using LigandScout 4.0 [38,40]. The screening yielded 24 compounds from the *R*-model and 33 compounds from the *S*-model. After consultation with synthetic chemists for the feasibility of future chemical modifications of those compounds, 16 compounds were purchased. Their chemical structures are listed in **Fig. 1** with their compound names from the respective databases.

Fig. 1. Chemical structures of AGX51 and the 16 hit compounds purchased. The chiral center was labeled with an asterisk. AK-778/43420895 was highlighted in the round rectangle and renamed as AK-778-XXMU for further study.

2. Determination of the cytotoxicity of the 16 hit compounds by CCK8 assay

CCK8 assays were conducted next to measure the viability of different glioma cell lines, namely U87, HS683, and GL261, after treated with different concentrations of the 16 hit compounds *in vitro* to examine the cytotoxicity of these compounds against

glioma. As shown in **Table 1**, all compounds except three demonstrated detectable cytotoxicity ($IC_{50} < 100 \mu M$) against all three glioma cell lines, proving the validity of our pharmacophore-based virtual screening. Among them, compounds AK-778/43465022 and AK-778/43420895 had the lowest IC_{50} values to glioma cells ($IC_{50} < 30 \mu M$), indicating they could inhibit cell viability more effectively. Although compound AK-778/43465022 showed the most potent inhibition in all three glioma cell lines, it had poor water solubility (**Fig. 2A**). Therefore, compound AK-778/43420895 was chosen for further studies. Normal cell lines, human normal hepatocytes (L-02) and mouse embryo fibroblasts (3T3) were exposed to AK-778/43420895 to rule out the potential toxicity and other possible side effects. It was shown in **Fig. 2C** that AK-778/43420895 had little cytotoxicity on normal cell lines. The compound was re-named as AK-778-XXMU for the subsequent studies.

Table 1. The cytotoxicity against various glioma cell lines from CCK8 assay

Compound Names	IC_{50} (μM)		
	U87	HS683	GL261
K784-9509	56.2±3.1	55.3±2.1	48.1±0.8
E755-0111	46.5±1.3	40.8±1.5	47.9±2.7
C141-0292	77.9±3.1	84.5±1.7	90.2±1.5
E642-0121	60.3±1.0	62.3±0.4	56.7±1.6
Z32554393	>100	>100	94.6±1.6
AK-778/43465022	15.5±0.95	18.7±1.3	21.3±0.8
AO-080/42479467	88.5±0.7	91.4±1.3	90.4±3.4

Fig. 2. Characterization of compound AK-778/43420895 (AK-778-XXMU) *in vitro*. A:

AK-778/43420895 had better water solubility as compared to compound AK-778/43465022. B and C:

Compound AK-778/43320895 reduces the viability of glioma cells but not normal cells. The effect of

compound AK-778/43320895 on cell viability of Human astroblastoma (U87), mouse glioma (GL261),

human normal hepatocytes (L-02) and mouse embryo fibroblasts (3T3) after being exposed to a range of AK-778/43320895 in a concentration gradient for 24 h via CCK8 assay. The percent of cell viability is plotted in a dose-dependent manner. Data points represent percent of cell viability relative to DMSO control of triplicates and expressed as the mean $\pm$ SD.

3. Determination of the binding affinity between AK-778-XXMU and ID2 protein

Biacore is a new biometric sensing technology based on SPR with advantages of high sensitivity, real-time, fast and label-free, which has been widely used to describe interaction and measure affinity between two partners [41,42]. To identify the quantitative affinity between ID2 protein and compound AK-778-XXMU, SPR assay was performed using a Biacore 8K system (GE Healthcare). ID2 protein was immobilized on the sensor surface as the ligand which was capable of capturing the target compound AK-778-XXMU in solution. By following the kinetics of a binding process of ID2 protein and AK-778-XXMU in real time, the association/disassociation rate constants (k_a and k_d) and equilibrium disassociation constants (K_D) of interactions were obtained. To our delight, the results showed the K_D between compound AK-778-XXMU and ID2 protein was 0.129 μ M (**Fig. 3**). The submicromolar K_D demonstrated that compound AK-778-XXMU was able to bind to ID2 protein with high affinity to exert its inhibitory effects.

Fig. 3. Change in response as a function of time in SPR and the fitting curves of affinity between compound AK-778-XXMU and ID2 at various concentrations. Using 1:1 binding model, k_a was determined to be 2.48×10^4 (1/Ms), k_d was determined to be 3.19×10^{-6} (1/s), and K_D was determined to be 1.29×10^{-7} (M). R_{max} was 83.6 (RU). χ^2 was 0.23 (RU²).

4. Binding modes of AGX51 and AK-778-XXMU with ID2

Compound AK-778-XXMU was identified from the pharmacophore-based virtual screening described above. The validity of the screening was firmly established by the SPR assay that determined the potent binding of AK-778-XXMU to ID2 with high affinity in the low submicromolar range. The molecular superimposition of AGX51 and AK-778-XXMU as well as their pharmacophores were shown to be nearly perfect, as they should be (**Fig. 4A**). Molecular docking studies were performed to provide more insight into the binding modes of both compounds in the ID2 binding site (**Fig. 4B**). It was shown that both AGX51 and AK-778-XXMU were fit quite well into the hydrophobic crevice in the loop region of ID2 (PDB: 4AYA) [36]. The binding modes of both AGX51 and AK-778-XXMU with ID2 were similar to that of AGX51 with ID1 [35]. As shown in **Fig. 4C** and **Fig. 4D**, in addition to the apparent hydrophobic interactions, a hydrogen bond was observed between the benzodioxole moiety of

1 AGX51 and Gln55. The corresponding hydrogen bond was between the hydroxyl
2 group of AK-778-XXMU and Gln55. Two more hydrogen bonds for AK-778-XXMU
3 were formed between the ketone group and Lys47 as well as between the amide group
4 and Lys58. Pi-cation interactions for both compounds were observed between the two
5 phenyl groups in their structures and Lys47/Lys58. Such interactions offered possible
6 explanations at the atomic level that why AK-778-XXMU was a potent ID2 antagonist.

5. Effect of compound AK-778-XXMU on cell migration and invasion

To determine whether compound AK-778-XXMU can influence the migration and invasion of glioma cells, wound healing assay was carried out. The results are shown in **Fig. 5**. As expected, compound AK-778-XXMU could slow down glioma cells wound healing. The wound closure rates were depressed significantly as low as $(13.11 \pm 1.52)\%$ for GL261 and $(5.59 \pm 1.04)\%$ for U87 after exposed to AK-778-XXMU at the concentration of $12.5 \mu\text{M}$. By comparison, closure rates in control group were up to $(63.13 \pm 0.78)\%$ for GL261 and $(61.50 \pm 10.21)\%$ for U87 cells. To further verify the effect, the Transwell assay was carried out. As shown in **Fig. 6**, compound AK-778-XXMU could inhibit the migration and invasion of GL261 and U87 cells in a concentration-dependent manner.

1 treatment, and Y axis is the average number of migrated cells or invaded cells in three independent
2 experiments at least. Each treatment group was compared with the control group. (* $p < 0.05$; ** $p < 0.01$;
3 *** $p < 0.001$; **** $p < 0.0001$ vs. Control).

4

5 6. Compound AK-778-XXMU induces apoptosis in glioma cells

6 To explore the effect of AK-778-XXMU on induction of apoptosis in glioma cells,
7 Annexin V/PI double stained with flow cytometry was performed *in vitro*. Cells were
8 treated with 25 μM and 50 μM AK-778-XXMU for 24 h. It was shown in **Fig. 7** that
9 exposures of U87 and GL261 tumor cells to different concentrations of
10 AK-778-XXMU resulted in increased apoptosis.

11

12

13 **Fig. 7.** Compound AK-778-XXMU induces apoptosis in glioma cells. Human astroblastoma (U87)

14 and mouse glioma (GL261) were treated at different concentrations (0, 25, 50 μM) of compound

15 AK-778-XXMU for 24 h. Significantly increased apoptosis percentage of GL261 (A) and U87 (B) were

1 detected by Annexin V/PI double stained by flow cytometry. Data represents the mean $\pm$ SD of at least
2 three independent experiments. (** $p < 0.001$ vs. Control; **** $p < 0.0001$ vs. Control).

3

4 7. Effect of compound AK-778-XXMU on ID2-KDR signaling

5 Glioma has abundant neovascularization network to support its invasive growth.

6 KDR, also named VEGFR2, as an endotheliocyte-specific tyrosine kinase receptor, is

7 critical in VEGF signaling and proangiogenic response in glioma malignant

8 progression [43,44]. It has been reported that ID2 plays a critical role in KDR activation

9 [17]. Therefore, western blot was performed to determine whether ID2-KDR signaling

10 could be impaired by compound AK-778-XXMU. As expected, compared with the

11 control group (0 μ M), three proteins involved in ID2-KDR signaling (ID2, VEGFA,

12 KDR) were greatly decreased in a dose-dependent manner (**Fig. 8**), and this expression

13 pattern was validated by qRT-PCR (**Fig. 9**). Moreover, with increasing concentrations

14 of compound AK-778-XXMU, an accumulation of tumor suppressor gene *PTEN* and

15 an impaired expression of MMP2, MMP9 were found (**Fig. 8**).

16

17 **Fig. 8.** Compound AK-778-XXMU inhibits ID2-KDR signaling using Western blotting. Human

18 glioma cells U87 and HS683 were treated at different concentrations of compound AK-778-XXMU for

1 24 h. The expression of ID2, VEGFA, PTEN, MMP2, MMP9 and KDR were detected in the whole cell
 2 lysates by Western blot. β -actin was used as the internal reference protein for each sample. The data were
 3 normalized to β -actin expression. (* p <0.05; ** p <0.01; *** p <0.001; **** p <0.0001 vs. Control).
 4

5
 6 **Fig. 9.** qRT-PCR analysis of ID2 and KDR mRNA expression level. The mRNA expression levels of
 7 ID2 and KDR (VEGFR2) in U87 under the same conditions were assessed by qRT-PCR. The data were
 8 normalized to GAPDH expression. (** p <0.01; *** p <0.001; **** p <0.0001 vs. Control)
 9

10 **8. Compound AK-778-XXMU slows down tumor growth *in vivo***

11 Inspired by the potent effect of AK-778-XXMU in inhibiting glioma cell growth *in*
 12 *vitro*, next we inoculated our NCG mouse with xenograft U87 cells into the right axilla
 13 to determine the antitumor effect of compound AK-778-XXMU *in vivo*. As shown in
 14 **Fig. 10**, in contrast to control group, tumors in treatment group (AK-778-XXMU:
 15 2.5mg/kg) had significantly smaller volumes at the endpoint with 49.7% tumor
 16 inhibitory rate. Furthermore, the treatment group showed a reduction of tumor weight
 17 of 57.8% compared with control group at day 12. Notably, there was no significant

1 reduction between the two groups in body weight. Overall, these data confirmed that
2 compound AK-778-XXMU could inhibit tumor growth, possibly by impairing ID2
3 functions in glioma without obvious side-effects.

4 To provide more insight into the experimental results above that compound
5 AK-778-XXMU could inhibit the growth of the tumor in NCG mice and further
6 understand the differences of tumor growth between the two groups, we removed tumor
7 blocks from the armpit of ten mice after euthanasia of them. As a proliferating cell
8 associated nuclear antigen, Ki67 antigen was expressed in G1, S, G2 and M phases of
9 cell cycle, but not in quiescent phase G0 [45]. Its function is closely related with cell
10 proliferation, which means the higher positive ratio of Ki67, the faster tumor growth. A
11 large number of neovascularization is a typical feature of malignant tumors and often
12 an important cause of distant metastasis of tumors. A recent study demonstrated that
13 glioblastoma stem cells could differentiate into endothelial cells which advance
14 angiogenesis [46,47]. CD31 antigen, also known as platelet endothelial cell adhesion
15 molecule-1 (PECAM-1), is a classical marker of endothelial cell that is also strongly
16 related to the malignant progression of glioma [46,48]. Then immunohistochemical
17 staining was performed on the interior of the tumor. As shown in **Fig. 11A** and **11B**,
18 after treated with compound AK-778-XXMU, notable reduced positive rates of Ki67
19 and CD31 were detected inside the tumors with no destructive side effects on normal
20 tissues (**Fig. 11C**) by staining the heart, liver, lungs, and kidneys with hematoxylin &
21 eosin (HE) in treatment group, further demonstrating that compound AK-778-XXMU
22 had a potent inhibitory effect on glioma.

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3 **Fig. 10.** Inhibitory effects of compound AK-778-XXMU in U87 glioma in vivo. NCG mice bearing U87
4 tumors were injected with DMSO for control group or compound AK-778-XXMU for treatment group
5 (2.5mg/kg every other day for 5 days, n=5 for each group). A: Tumor volume growth curve after
6 compound AK-778-XXMU treatment. B: Body weight change of the mice. C and D: the excised tumor
7 and the tumor weight graph at the end of experiment. (** $p < 0.01$ vs Control).

8

Fig. 11. Immunohistological analysis. Representative immunohistochemical staining photographs of endothelial marker CD31 (A) for tumors vessels and proliferation marker Ki67 (left B) for cell proliferation in U87 tumors from NCG tumor-bearing mice at endpoint. (C) Histological analysis of different tissues from tumor-bearing NCG mice at endpoint. Different tissues (heart, liver, lung, kidney) from U87 tumor-bearing mice were fixed with 10 % (v/v) formalin and stained using Hematoxylin and Eosin (H&E). No histological and morphological heterogeneity of these viscera from tumor-bearing NCG mice in two groups were detected.

Conclusions

Given the poor prognosis of glioma patients, it has become imperative to search for new targeted therapeutic regimen to control the malignant progression of glioma and

1 improve the life quality of patients. In view of the strong correlation between ID2
2 protein and glioma, a pharmacophore-based virtual screening was conducted to obtain
3 16 small-molecule compounds, of which 13 had IC₅₀ values lower than 100 μM from
4 CCK8 assays. Further studies were focused on compound AK-778-XXMU, which is an
5 indole derivative. The affinity between AK-778-XXMU and ID2 was determined to be
6 129 nM by SPR experiment, which is in the low submicromolar range. Its binding
7 mode was studied by comparison with AGX51 in the binding site of ID2 protein,
8 providing the explanation of its potency at the atomic level. It was also shown that
9 AK-778-XXMU could inhibit cell migration and invasion of glioma cell lines, induce
10 apoptosis, and more importantly, slow down the tumor growth *in vivo*. Therefore,
11 compound AK-778-XXMU could be a promising agent for the treatment of glioma
12 with ID2 overexpression in the future.

13

14 **Material and methods**

15 **1. Cell lines and cell culture**

16 Cell lines (Human astroblastoma, U87; human glioma, HS683; mouse glioma,
17 GL261) used in this study were obtained from ATCC. All these cell lines were cultured
18 in Dulbecco's Modified Eagle's medium (DMEM High Glucose; Hyclone, USA)
19 containing 10% fetal bovine serum (FBS) (Gibco, New York, USA), 1% (v/v)
20 antibiotic solution containing penicillin and streptomycin (Sigma-Aldrich, USA) in a
21 5% CO₂ atmosphere at 37 °C.

22 **2. Molecular modeling and virtual screening**

23 Compound AGX51 was used to build the pharmacophores. The 3D model of AGX51
24 was built and fully optimized with Discovery Studio 3.5 (BIOVIA, Dassault Systèmes).

1 Since AGX51 has one chiral center, both enantiomers were used and two
2 pharmacophores were generated by LigandScout 4.0 software by Inte:Ligand GmbH
3 (<http://www.inteligand.com/ligandscout/>) [40]. They were subjected to commercial the
4 following databases: CHEMBRIDGE, SPECS, CHEMDIV, ENAMINE, IBS,
5 LIFECHEMICALS, VITAS-M (2,281 compounds in total) provided in their electronic
6 form by Shanghai-based Topscience Co., Ltd (<https://www.tsbiochem.com/>) for virtual
7 screening also in LigandScout. The pharmacophore models built from the *R* and *S*
8 configurations yielded 24 and 33 hits, respectively. In the end, 16 compounds were
9 purchased after consideration of possible future chemical modifications. Molecular
10 docking was performed using Glide from Schrödinger, Inc using the default XP
11 protocol [49,50].

12 **3. CCK8 assay**

13 CCK8 assay was used to elucidate the cytotoxicity of inhibitor on glioma cells. The
14 cells were seeded into 96-well plate at 4×10^3 cells per well with 100 μ L DMEM
15 supplemented with 10% fetal bovine serum and incubated at 37 °C. When the cells
16 were grown to 60-70% confluency, different concentrations (0, 1.56, 3.125, 6.25, 12.5,
17 25, 50 μ M) of inhibitor were added. After incubation for 24 h, 10 μ L CCK-8 was added
18 to each well. The absorbance of each well was detected at 450 nm after incubating at
19 37 °C for 4 hours. Every experiment was performed in triplicates.

20 **4. SPR**

21 In SPR assay, the surface of the Series S Sensor CM5 chip (GE, BR-1005-30) was
22 activated with 400 mM EDC and 100 mM NHS at a flow rate of 10 μ L/min for 420 s.

1 Then human ID2 protein (Cat#PROTQ02363, purchased from Boster Biological
2 Technology Co. Ltd, China.) was diluted to 50 µg/mL with fixative reagent (10 mM
3 sodium acetate, pH 4.5) and immobilized on the surface of Chip CM5 with a fixed
4 volume of approximately 6000 RU prior to the measurement of the compound
5 AK-778-XXMU interaction. For compounds, they were first diluted 20-fold with
6 dilution buffer (1 × PBS, 0.05% Tween20) to change the DMSO content to 5%, and
7 then diluted with running reagent (1 × PBS, 0.05% Tween20, 5% DMSO) at
8 concentrations of 100, 50, 25, 12.5, 6.25, 3.125, and 0 µM, respectively. The diluted
9 compounds were injected into the experimental channel and the reference channel at a
10 flow rate of 30 µL/min with a binding time of 60 s and a dissociation time of 120 s. The
11 KD value of each antibody was calculated using Biacore 8K (GE Healthcare) analysis
12 software. All SPR measurements were performed in triplicates.

13 **5. Apoptosis analysis**

14 Apoptosis of U87 and GL261 cells were detected by Annexin V-FITC/PI apoptosis
15 detection kit (Key Gen Bio TECH). Glioma cells were treated with different
16 concentrations (0, 25, 50 µM) of inhibitors for 24 h, harvested and washed twice with
17 PBS and centrifuged. All cells were then suspended in 500 µL binding buffer, and
18 stained with 5 µL Annexin V-FITC and 5 µL PI for 20 min at room temperature in the
19 dark. Samples were run on a flow cytometer within 1 h.

20 **6. Wound healing assay**

21 In the migration assay, glioma cells were planted into 6-well plate at the density of
22 5×10^5 cells per well with 2 mL high-glucose DMEM containing 10% FBS, incubated

1 at 37 °C in a 5% CO₂ incubator for 24 h. Then a straight physical “wound” within cell
2 monolayer was created. The cells were washed twice with PBS buffer gently and the
3 cells that have been scratched out were discarded. 2 mL high glucose medium (DMEM)
4 containing different concentrations of compound (0 μM, 2.5 μM, 12.5 μM) was added
5 to each well. Then continue to culture in 37 °C incubator. Monitor the process of cell
6 migration into the gap by taking photos at different time points (0 h, 12 h, 24 h).

7 **7. Migration assay**

8 In the migration assay, Transwell inserts with an 8 μM pore size were placed in
9 24-well plates with 500 μL DMEM culture medium added 10% fetal bovine serum. The
10 U87 and HS683 cells were diluted to 2×10⁵ cells/mL with DMEM high glucose
11 medium with 2% fetal bovine serum. A total of 200 μL of cell suspension was added to
12 the inserts. Meanwhile different concentrations (0, 12.5, 50 μM) of inhibitors were
13 added. Then the chambers were cultured in a 5% CO₂ incubator at 37°C for 24 h. The
14 cells were fixed with 4% paraformaldehyde, stained with crystal violet then take
15 pictures and count in five different fields with an inverted microscope (200×).

16 **8. Invasion assay**

17 In the invasion assay, 30 μL Matrigel (BD Bioscience) was added to the up chamber
18 then allowed to polymerize for at least 40 min at 37°C. The U87 and HS683 cells were
19 resuspended to 2×10⁵ cells/mL with DMEM high glucose medium with 2% fetal
20 bovine serum. A total of 200 μL of cell suspension was added to the inserts. Meanwhile
21 different concentrations (0, 12.5, 50μM) of inhibitors were added. Then the plates were
22 cultured in a 5% CO₂ incubator at 37 °C for 24 h. Gently wipe off the Matrigel (Corning,

1 Cat#356234) in the upper chamber with a cotton swab. Then the cells were fixed with
2 4% paraformaldehyde, stained with crystal violet (Beyotime) then take pictures and
3 count in five different fields with an inverted microscope Pierce (200×).

4 **9. Western blotting**

5 Glioma cells were treated with different concentrations (0, 12.5, 25, 50 μ M) of
6 compound for 24 hours before being lysed by RIPA containing protease inhibitor.
7 Lysates were incubated on ice for 20 min prior to centrifugation at 12000 rpm for 20
8 min at 4°C. After being determined concentrations using a BCA kit (Pierce), 30 μ g total
9 protein was separated by SDS-PAGE then transferred to the polyvinylidene fluoride
10 membrane. The primary antibodies used were as follows: anti-KDR (Cell Signaling
11 Technology, #2479), anti-PTEN (Cell Signaling Technology, #9188), anti-MMP-9
12 (Cell Signaling Technology, #13667), anti-MMP-2 (Cell Signaling Technology,
13 #87809), anti-VEGFA (Cell Signaling Technology, #65373), anti-ID2 (Cell Signaling
14 Technology, #3431), anti- β -actin (Cell Signaling Technology, #4970). The dilutions
15 for the antibodies were as follows: 1:1000 for KDR, 1:1000 for PTEN, 1:1000 for
16 MMP-9, 1:1000 for MMP-2, 1:1000 for VEGFA, 1:1000 for ID2, 1:1000 for β -actin,
17 1:10000 for Goat anti-Rabbit IgG.

18 **10. Real-time PCR**

19 To quantify the genes involved ID2-KDR signaling expression, human glioma cells
20 HS683 were exposed to different concentrations (0, 12.5, 25, 50 μ M) of the compound,
21 after 24 h, cells were lysed by RNAiso Plus (Takara, 9108, Japan). Before performing
22 RT-PCR, Prime Script RT reagent Kit (Takara, RR047A, Japan) were used to reverse

transcribe the extracted RNA into cDNA according to the given instructions. The results were assessed by calculating $2^{-\Delta\Delta Ct}$. The sequences of primers are as follows: GAPDH forward primer: 5'-GGAGCGAGATCCCTCCAAAAT-3', reverse primer: 5'-GGCTGTTGTCATACTTCTCATGG-3'; ID2 forward primer: 5'-AGTCCCGTGAGGTCCGTTAG-3', reverse primer: 5'-AGTCGTTTCATGTTGTATAGCAGG-3'; VEGFR2 forward primer: 5'-GTGATCGGAAATGACACTGGAG-3', reverse primer: 5'-CATGTTGGTCACTAACAGAAGCA-3'.

9

11. Subcutaneous tumorigenesis in NCG mice

To generate mouse models, ten 8-week-old NCG mice were injected i.h. with human glioma cell U87 into the right axilla according to the number of 1×10^6 cells/mouse. When the tumor volume was visible and reached 100 mm³, ten mice were randomly divided into two cohorts: control group (n=5) and treatment group (n=5). The control group (DMSO, 2.5 ml/kg), AK-778-XXMU (2.5mg/kg) compound was injected i.p. into the two groups tumor-bearing mice respectively. Control group received DMSO (1% v/v) on the 1st, 3rd and 5th day. Treatment group were injected with AK-778-XXMU compound (1% v/v, dissolved in DMSO) on the 1st, 3rd and 5th day. The body weight and tumor size of mice were measured at the same time of each administration, and the changes of body weight and activity ability of mice were dynamically monitored. On the endpoint, the 7th day of the first administration, the mice were euthanized, the tumor were excised and weighed.

12. IHC (Immunohistochemistry) assay

The expression of micro vessel density marker CD31 and cell proliferation index Ki67 in tumor samples from tumor-bearing NCG mice were tested via IHC. IHC staining was performed as previously described [51]. Each slice was taken five views for photographing at 400 X magnification for Ki67 and at 200 X magnification for CD31. Each obvious area of positive staining for CD31 was counted as a single vessel. Results were expressed as mean number of Ki67 positive cells $\pm$ SEM per high-power field (X400) or the mean number of micro vessels for CD31 $\pm$ SEM per high-power field (X200). A total of 15 high-power fields was examined and the number of micro vessels for CD31 or Ki67 positive-staining cells in each group was averaged and expressed as the number per high power field.

13. Hematoxylin & eosin (HE) staining

After being euthanized, different tissues (heart, liver, lung, kidney) from ten tumor-bearing NCG mice were fixed with 10% (v/v) formalin over 24 hours. Then all the specimens were washed, dehydrated and embedded with paraffin commonly. 5 μ m-thick viscera sections were cut randomly, fixed onto the glass slides then, stained using Hematoxylin and Eosin (H&E) (Solarbio,G1121) after being dewaxed to water, the images were taken by light microscopy with Nikon software (Melville, NY, USA) at 400 $\times$ magnification at last.

14. Statistical analysis

All measurements were performed in triplicates. The quantitative data were performed with the SPSS 20.0 software package expressed as the means $\pm$ standard

deviation (SD). The significance of the difference from the controls for each experimental test condition was assayed using unpaired t-test. ANOVAs with the post hoc Dunnett's test were used for tumor growth in comparison to the control. *P* values < 0.05 were considered statistically significant.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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why so potent?

A

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B

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