World Journal of Biology Pharmacy and Health Sciences
eISSN: 2582-5542
Cross Ref DOI: 10.30574/wjbphs
Journal homepage: https://wjbphs.com/

(RESEARCH ARTICLE)

Check for updates

Drug repurposing study of selected antidepressants as anti-cancer agents by in silico

Darshan Gowda C.P *, Deepika, Darshan S and Danesh

Dayananda sagar college of pharmaceutical sciences, Bengaluru560111, Karnataka.

World Journal of Biology Pharmacy and Health Sciences, 2026, 25(03), 126-136

Publication history: Received on 29 January 2026; revised on 09 March 2026; accepted on 10 March 2026

Article DOI: https://doi.org/10.30574/wjbphs.2026.25.3.0139

Abstract

Drug repurposing offers a cost-effective and time-efficient strategy to identify new therapeutic applications for approved drugs, particularly in challenging diseases such as cancer. The present study aimed to evaluate the anticancer potential of selected antidepressants using in silico molecular docking against key cancer-associated targets. Selective serotonin reuptake inhibitors and related antidepressants, including fluoxetine, sertraline, paroxetine, fluvoxamine, citalopram, escitalopram, dapoxetine, and moclobemide, were screened against Histone Deacetylase (HDAC) and mammalian Target of Rapamycin (mTOR), two proteins critically involved in tumor growth and progression. Three-dimensional structures of ligands and proteins were retrieved from public databases and prepared for docking analysis. Molecular docking was performed using AutoDock Vina, and binding interactions were analyzed to determine affinity and stability in comparison with the standard anticancer drug temozolomide.

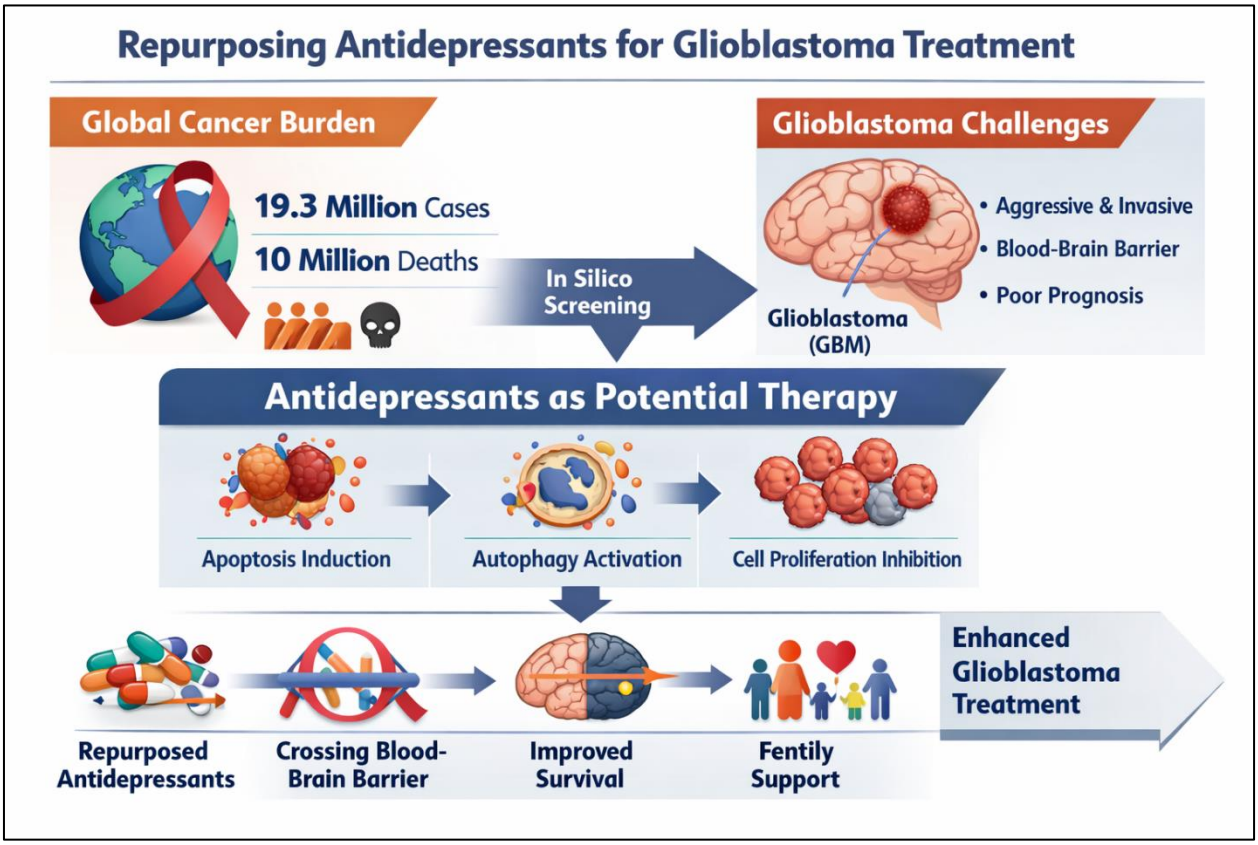
The results demonstrated that several antidepressants exhibited significant binding affinities toward both targets. Dapoxetine showed the strongest interaction with HDAC, while paroxetine demonstrated the highest affinity for mTOR, with docking scores comparable to or better than temozolomide. Key interactions included hydrogen bonding and hydrophobic contacts within the active sites of both proteins.

In conclusion, the findings suggest that selected antidepressants possess promising anticancer potential through stable interactions with HDAC and mTOR. These results support further experimental validation and highlight drug repurposing as a viable approach for developing alternative therapeutic strategies against cancer, particularly glioblastoma.

Keywords: Drug repurposing; Antidepressants; HDAC; mTOR; Molecular docking; Anticancer activity.

* Corresponding author: Darshan Gowda C.P.

Graphical Abstract



1. Introduction

Cancer continues to be one of the major public health burdens globally, with rising incidence and mortality rates despite advancements in treatment strategies. The process of developing a novel anticancer drug is often time-consuming, expensive, and marked by a high failure rate during clinical trials. Therefore, alternative strategies such as Exploring alternative therapeutic uses for previously approved drugs, known as drug repurposing, has become a prominent area of research. This approach reduces both time and cost while improving success rates due to pre-existing pharmacokinetic and safety data [1].

Among the various classes of drugs explored for repurposing, Antidepressants, particularly SSRIs, have been found to impact cancer cell growth and promote programmed cell death. Several studies have demonstrated that drugs like fluoxetine, sertraline, and paroxetine not only affect serotonin levels but also interact with various intracellular pathways associated with cancer progression [2].

SSRIs and other antidepressants were traditionally prescribed to treat major depressive disorders, anxiety, and related psychiatric conditions. However, emerging evidence suggests that many of these drugs influence mitochondrial pathways, reactive oxygen species (ROS) production, and calcium signaling in a way that overlaps with known anti-cancer mechanisms [10].

For instance, fluoxetine has been reported to inhibit cancer cell proliferation and promote apoptosis in breast and colon cancer cell lines [3]. Moreover, antidepressants have been reported to act synergistically with conventional chemotherapeutic agents. For example, in glioblastoma cells, fluoxetine has been shown enhance the efficacy of temozolomide by promoting DNA damage and inhibiting DNA repair processes. [7]

Two critical molecular targets in cancer treatment are Histone Deacetylases (HDACS) and the MTOR (mechanistic Target of Rapamycin) signaling pathway. HDACs regulate gene expression by modifying chromatin structure, and their inhibition can reactivate tumor suppressor genes leading to cancer cell death [4]. mTOR is a central regulator of cell growth, metabolism, and survival, and its dysregulation is implicated in many cancers. Inhibiting mTOR signaling has become a validated strategy in cancer therapy [5].

In terms of pharmacodynamics, many SSRIs block cellular efflux pumps and inhibit P- glycoprotein (P-gp), a common cause of chemotherapy resistance in tumors [8]. By inhibiting these transporters, SSRIs may improve drug retention in cancer cells, leading to enhanced cytotoxic effects. Additionally, they are known to modulate signaling pathways like MAPK., PI3K/Akt, and NF-kB, which play crucial roles in cell cycle progression and apoptosis [9]

Recent advances in silico techniques, such as molecular docking, allow efficient prediction of drug-target interactions at the molecular level. These computational tools can screen existing drugs against specific protein targets, thus identifying candidates with promising binding affinities that may exert anticancer effects [6]. Auto Dock Vina, Discovery Studio, and similar platforms are widely used for such purposes, helping to evaluate and visualize molecular interactions between ligands and receptors.

The current study focuses on the in-silico evaluation of selected SSRIs and related antidepressants (fluoxetine, sertraline, paroxetine, fluvoxamine, citalopram, escitalopram, dapoxetine) as potential anticancer agents by targeting HDAC and mTOR proteins. The docking results will be compared to temozolomide, a standard anti-cancer drug. This approach aims to identify possible interactions that suggest anticancer efficacy, laying a foundation for future experimental validation.

Drug repurposing, also known as drug repositioning, involves discovering new therapeutic applications for existing or previously ineffective drugs beyond their original medical purposes. This strategy has gained significant attention in modern drug development, as it bypasses the initial stages such as formulation and toxicity assessments, which are often costly and time-consuming. It is particularly advantageous in the context of complex diseases like cancer, where high mortality rates and resistance to treatment demand more rapid therapeutic solutions. This approach has garnered considerable attention in modern drug discovery, as it circumvents the lengthy and costly initial stages of drug development, such as formulation and toxicity evaluation. Drug repurposing is especially valuable for complex diseases like cancer, where rapid therapeutic interventions are crucial due to high mortality rates and resistance to existing treatments. For difficult-to-treat conditions like cancer, characterized by high death rates and resistance to therapy, drug repurposing provides a promising and expedited therapeutic strategy It also leverages existing pharmacokinetic, pharmacodynamic, and safety data, thus reducing the risk of clinical trial failure and accelerating the overall development process. [11]

The key advantages of drug repurposing include reduced development costs, shorter timelines to market, and improved success rates, particularly in comparison to de novo drug development.Since repurposed drugs have already been tested in humans, their safety profiles are well established, making them attractive candidates for rapid clinical translation in new disease contexts [12,13]. As a result, repurposing has emerged as a strategic and efficient route to expand therapeutic options for conditions with unmet medical needs, including various forms of cancer.

1.1. Rationale Behind the Study

some selective serotonin reuptake inhibitors (SSRIs), including paroxetine, sertraline, and fluoxetine, have been shown in recent studies to have possible anticancer properties in addition to their primary use in treating depression. These antidepressants have been demonstrated to cause glioma, breast, and leukemia cells, among other cancer cell lines, to undergo apoptosis, suppress cell division, and encourage autophagy. [28,29] Among them, fluoxetine has demonstrated significant cytotoxicity against glioblastoma cells by modulating key intracellular signaling nature, poor prognosis, and limited treatment options. Since antidepressants can cross the blood- brain barrier, they are particularly suitable candidates for targeting brain tumors like glioblastoma [31]. Additionally, proteins such as histone deacetylases (HDACs) and mammalian target of rapamycin (mTOR) are critical regulators of cell survival, proliferation, and gene expression in cancer progression. Inhibiting these proteins has shown to reduce tumor growth and increased sensitivity to chemotherapy, making them ideal molecular targets for in silico docking studies with repurposed drugs like SSRIs [32] Therefore, This work uses computational screening against important oncogenic targets in glioblastoma to investigate the possibility of specific antidepressants as anti-cancer drugs. athways like AMPK/mTOR, suggesting its role as a promising repurposed therapeutic agent [30].

The rationale for selecting glioblastoma as a cancer target is based on its highly aggressive

2. Materials and methods

2.1. Selection of Ligands

A wide range of natural, semi-synthetic, and synthetic compounds known for their antidiabetic potential were selected for the study. The compounds were chosen based on literature support and reported interaction with the Nrf2 pathway. The selected ligands were retrieved from public databases in SDF format, including PubChem and ChEMBL or the compounds can be drawn from chemdraw.

2.2. Protein Preparation

Preparation of protein was done using protein preparation BIOVIA -Discovery studio. The typical structure PDB may not be suitable for immediate use in molecular modelling. It may contain co-crystallized ligand, water molecules, metal ions and also co-factors. Some structure may be multimeric, hence need to be reduced to single unit. Protein prepared in 2 steps first involved, Removal of crystallographic water molecules, ions, and co-crystallized ligands to avoid interference during docking. The polar hydrogen was added in second step.

2.3. Preparation of Ligands

To prepare the ligand, first visit the PubChem website (www.pubchem.ncbi.nlm.nih.gov) and search for the required compound. Once located, download the 3D conformer of the compound in CDF format. Alternatively, the structure can be drawn using ChemSketch and saved in MDL molfile format for further use.

2.4. Molecular Docking Procedure

To load the protein and ligand into PyRx for molecular docking, begin by navigating to the 'File' menu and selecting the 'Load Molecule' option. Open the preferred folder and choose the downloaded or prepared protein file. Right-click on the selected protein and choose the 'Autodock' option, followed by selecting 'Make Macromolecule'.

Next, open Open Babel and click on 'Insert New Item' icon. From there, navigate to the folder containing the prepared ligand, and select the appropriate ligand file. Right-click on the molecular formula and select 'Minimize All' to optimize the structure. Note the energy value (E) after minimization for reference.

Once minimized, right-click again on the molecular formula and convert it to the Autodock ligand format. Proceed to the 'Vina Wizard' and click on 'Start'. Select both the ligand and the macromolecule, then click on 'Forward'. Finally, click on 'Maximize' to visualize the grid box on the display screen, indicating the docking area. A grid area was generated around the binding site of the receptor.

2.5. Visualization and Interaction Analysis

The compounds with highest binding affinity docked complexes were visualized using BIOVIA Discovery Studio Visualizer. Detailed binding interactions were analyzed based on:

- Hydrogen bonds: Identification of donor-acceptor hydrogen bonds within the active site.
- Van der Waals interactions: Evaluation of contact residues stabilizing the ligand.
- π–π and cation–π interactions: Detection of aromatic stacking interactions.

2D interaction diagrams were generated to visually represent the interactions for inclusion in results and discussion. [9]

2.6. ADME and Drug-Likeness Prediction

The SwissADME online server (http://www.swissadme.ch) was utilized to predict the pharmacokinetic profiles and drug-likeness of the selected steroidal drugs. The canonical SMILES of each ligand were input to calculate:

- Physicochemical properties: Molecular weight, topological polar surface area (TPSA), number of hydrogen bond donors and acceptors, and rotatable bonds.
- Lipophilicity: LogP values estimated using various predictive models (iLOGP, XLOGP3, WLOGP, MLOGP, SILICOS IT).
- Water solubility: Qualitative and quantitative predictions of solubility.

- Pharmacokinetics: Gastrointestinal (GI) absorption, blood-brain barrier (BBB) permeability, P-glycoprotein substrate likelihood, and cytochrome P450 enzyme inhibition profile.
- Drug-likeness rules: Evaluation using Lipinski's Rule of Five, Ghose, Veber, Egan, and Muegge filters.
- Medicinal chemistry friendliness: Synthetic accessibility score and PAINS filter alerts.

3. Tools and software used

3.1. PubChem

PubChem is an online database that lists the molecular formula, smiles, 3D chemical structures, and other details about each chemical compound. Managed and updated by the National Center for Biotechnolog

Information (NCBI), the database is part of the National Library of Medicine, which operates under the National Institutes of Health.

3.2. Protein Data Bank

An online database called the PDB contains information on the three dimensional chemical structures of biological components such amino acids, sugar bases, phosphates, and nucleic acids. Researchers from all over the world have provided data that has been estimated using methods including X-ray crystallography, NMR spectroscopy, and in some cases cryo-electron microscopy. The Worldwide Protein Data Bank is the entity responsible for maintaining the PDB.

3.3. BIOVIA Discovery Studio

BIOVIA, a software company based in the U.S., maintains a global presence through its offices in Europe and Asia. It offers software for chemical, materials, and bioscience research for the chemical manufacturing, industries, pharmaceutical, biotechnology, packaged products, aerospace, and energy industries.

3.4. Chemsketch

A molecular modeling program called Chemsketch is used to create and alter representations of 2D chemical structures. It is also a piece of software used to comprehend the structure offunctional groups and chemical bonds.

3.5. Autodock 4.2

Designed for molecular modeling, AutoDock 4.2 is particularly effective for protein-ligand docking studies. The software is freely available under the GNU General Public License and is widely cited in the scientific literature.

4. Result and Discussion

The study was conducted to assess whether selected antidepressants exhibit anticancer effects through computational drug repurposing, focusing on their interactions with two critical cancer- associated proteins—HDAC (Histone Deacetylase) and mTOR (mechanistic Target of

Rapamycin Using in silico molecular docking, the antidepressants were screened for their binding affinity and interaction profiles, compared against the standard anticancer drug temozolomide, which is commonly used in the treatment of glioblastoma.

Molecular Docking with HDAC:

The docking analysis revealed that several antidepressants showed significant binding affinities toward HDAC, with dapoxetine displaying the strongest interaction (docking score: -8.5) compared to temozolomide (-7.0). Key interactions involved hydrogen bonding and hydrophobic contacts with essential residues like HIS142, PHE152, GLY151, TYR306, and MET274 -residues commonly involved in the active site of HDAC.

These interactions are pharmacologically significant since HDAC inhibition is associated with chromatin remodeling, transcriptional reactivation of tumor suppressor genes, and induction of cancer cell apoptosis. The antidepressants' ability to dock at the same or overlapping binding pockets as temozolomide strongly supports their functional relevance. 4.1Molecular docking analysis

Table 1 The selected antidepressants were subjected to molecular docking analysis targeting the anticancer protein HDAC-3 (3SFF).

	Names	**Docking score**	**Ligand-Amino acids**
0.1	Standard temozolomide HDAC	-7	CYS A:153, HIS A:142, GLY A:151, PHE A:152, HIS A:143, PHE A:208, HIS A:180, TYR A:306, GLY A:303, LYS A:33, GLY A:305, GLY A:304, TRP A:141, ILE A:34, ARG A:37.
0.2	HDAC-Citalopram	-6.1	GLY A:206, HIS A:180, HIS A:142, HIS A:143, PHE A:208, GLY A:151, PHE A:152.
0.3	HDAC- Clorgyline	-6	CYS A:153, PHE A:208, HIS A:180, TYR A:306, PHE A:152, GLY A:151, ASP A:267, HIS A:143, HIS A:142, GLY A:304, MET A:274, GLY A:303, ILE A:34, TRP A:141, ARG A:37.
0.4	HDAC-Dapoxetine	-8.5	CYS A:153, HIS A:142, GLY A:151, PHE A:152, HIS A:143, GLY A:140, GLY A:303, ASP A:267, ASP A:178, GLY A:304, ILE A:34, ARG A:37, TYR A:306, LYS A:33, TRP A:141, HIS A:180, MET A:274.
0.5	HDAC-Escitalopram	-6.6	HIS A:142, HIS A:143, GLY A:151, PHE A:208, MET A:274, PHE A:207, TYR A:306, GLY A:206, HIS A:180, PHE A:152, GLY A:304.
0.6	HDAC-Fluoxetine	-6.7	PHE A:208, HIS A:180, GLY A:151, HIS A:143, GLY A:305, GLY A:304, TYR A:306, TRP A:141, PHE A:152, PHE A:207, MET A:274.
0.7	HDAC-Fluvoxamine	-5.1	LYS A:33, ILE A:34, LEU A:31, PHE A:152, ALA A:32, TYR A:154, TRP A:141, ILE A:108, GLY A:107, TYR A:111.
0.8	HDAC-Moclobemide	-6.4	ASP A:178, HIS A:142, HIS A:143, GLY A:303, GLY A:304, CYS A:153, TRP A: 141, TYR A:306, MET A:274, HIS A:180, PHE A:208, GLY A:151, PHE A:152.
0.9	HDAC-Sertraline	-6.4	VAL A:321, LEU A:292, GLY A:324, LYS A:289, ILE A:322, VAL A:133, PRO A:16, LEU A:14, LYS A:132, GLN A:295
10	HDSC-Paroxetine	-6.2	GLY A:151, MET A:274, HIS A:143, GLT A:304, TYR A:306, HIS A:180, PHE A:152, PHE A:208

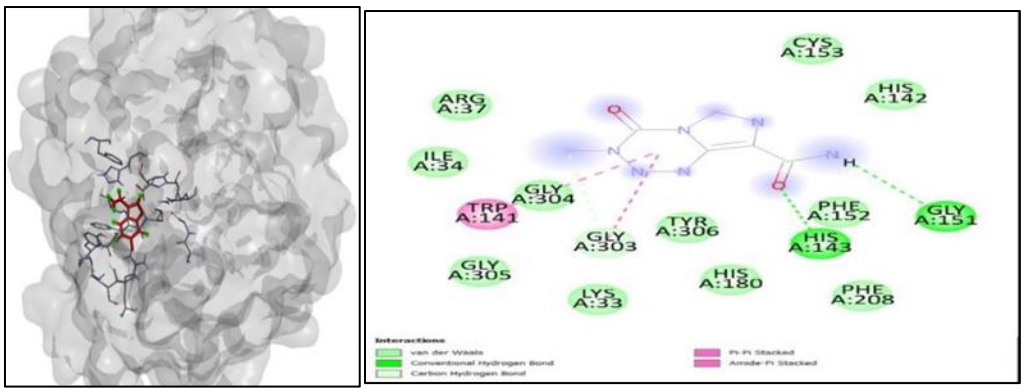


Figure 1 2D&3D interactions of temozolomide with the protein HDAC-3SFF

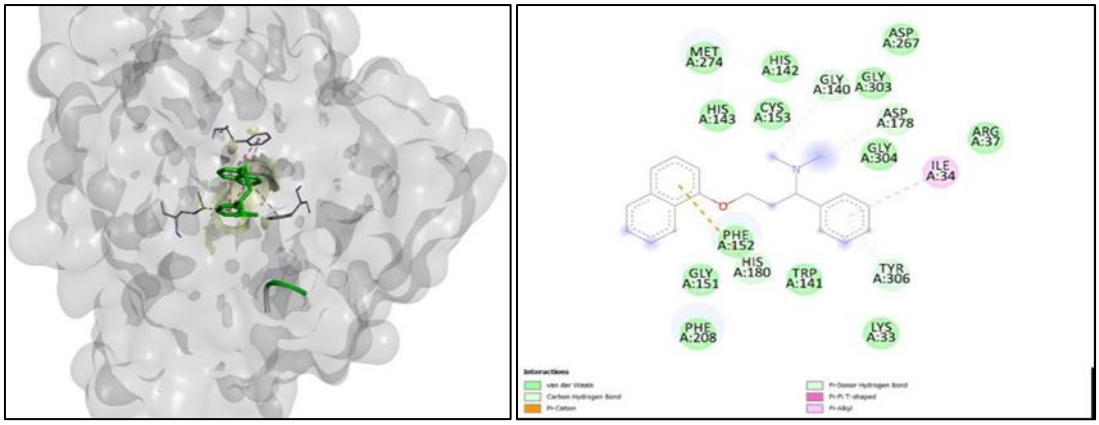


Figure 2 2D&3D interactions of Dapoxetine with protein HDAC-3SFF

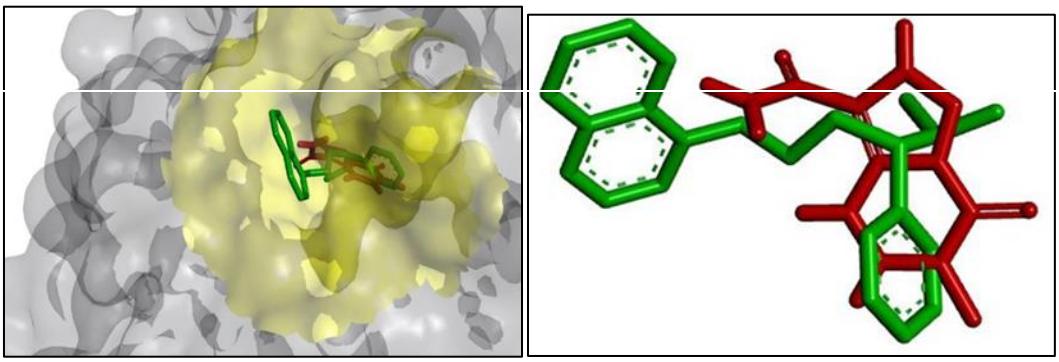


Figure 3 Both standard and test drugs are overlapped with each other in same pocket of protein HDAC-3SFF

4.1. Molecular docking analysis

Table 2 Molecular docking analysis of the selected anti-depressant compounds against anti-cancer protein Mtor-4DRH

Sl. no	Names	Docking score	Ligand -Amino acids
0.1	Standard Temozolomide mTOR	-5.6	ILE D:87, VAL D:86, PHE D:77, TYR D:57, PHE D:67, PRO D:120, ASP D:68, ILE D:122, TYR D:113, PHE D:130, TRP D:90
0.2	mTOR-Citalopram	-6.2	ILE D:87, VAL D:86, TYR D:57, ASP D:68, PHE D:130, ASP D:68, TYR D:113, SER D:118, PRO D:120, ILE D:122, LYS D:121, PHE D:67, TRP D:90.
0.3	mTOR-Clorgyline	-5.0	TYR D:57, PHE D:130, PHE D:77, TRP D:90, ILE D:87, VAL D:86, TYR D:113, GLB D:85, LYS D:88, GLY D:84
0.4	mTOR-Dapoxetine	-7.2	PHE D:77, PHE D:130, VAL D:86, GLN D:85, TYR D:113, TRP D:90, ILE D:87, GLY D:84, LAL D:112, LYS D:88.
0.5	mTOR-Escilatopram	-6.5	TYR D:57, VAL D:86, TRP D:90, PHE D:77, ILE D:87, TYP D:113, SER D:118, PRO D:120, ILE D:122, LYS D:121, PHE D:67, ASP D:68.

0.6	mTOR-Fluoxetine	-6.4	ASP D:68, PHE D:67, TYR D:113, ILE D:122, SER D:118, PRO D:120, TYR D:57, LEU D:119, ILE D:87, VAL D:86, PHE D:130, TRP D:90, PHE D:77, GLN D:85.
0.7	mTOR-Fluvoxamine	-5.3	TRP D:90, ILE D:87, TYR D:113, PHE D:67, ILE D:122, SER D:118, LEU D:119, PRO D:120, ASP D:68, HIS D:71, TYR D:57, PHE D:77, VAL D:86, PHE D:130.
0.8	mTOR-Moclobemide	-6.0	PRO D:120, ASP D:68, SER D:118, PHE D:67, ILE D:122, PHE D:130, TYR D:57, ILE D:87, VAL D:86, TRP D:90, TYR D:113, HIS D:71.
0.9	mTOR-Paroxitine	-7.7	VAL D:86, PHE D:77, TRP D:90, ILE D:87, TYR D:113, SER D:118, LEU D:119, PRO D:120, LYS D:121, ILE D:122, PHE D:67, TYR D:57, ASP D:68.
10	mTOR-sertraline	-6.9	VAL D:86, GLN D:85, PHE D:77, TYR D:57, PHE D:130, ASP D:68, TRP D:90, PHE D:67, TYR D:113, ILE D:122.

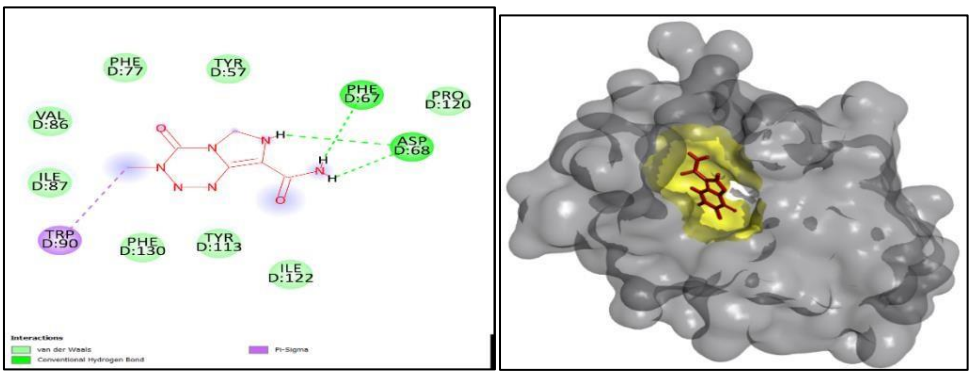


Figure 4 2D&3D interactions of temozolomide with the protein of mTOR- 4DRH

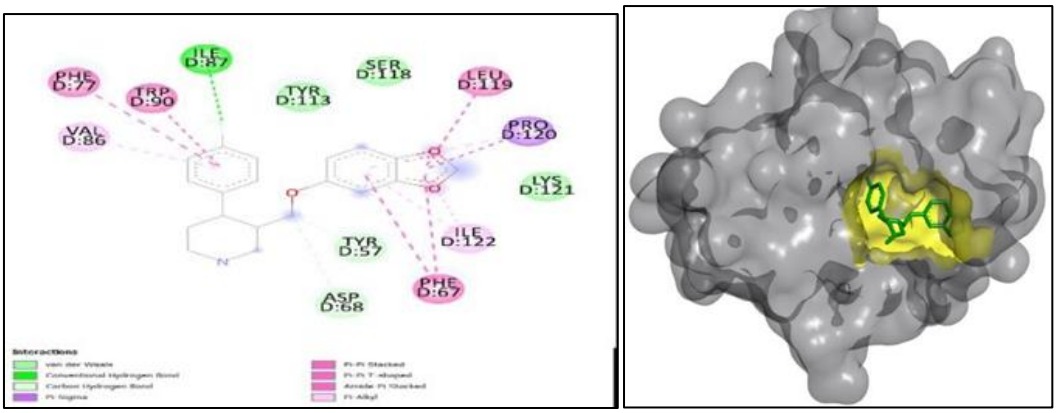


Figure 5 2D&3D interactions of Paroxitine with the protein of mTOR-4DRH

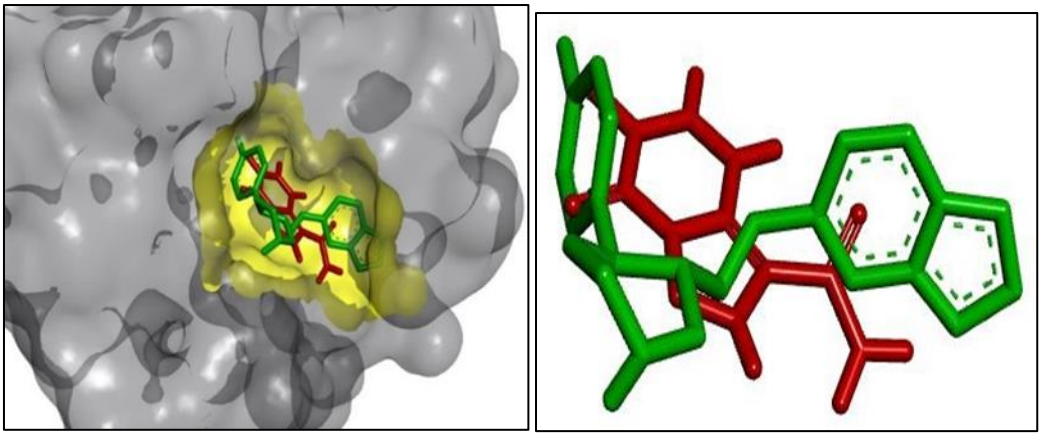


Figure 6 Both standard and test drugs are overlapped with each other in same pocket of protein mTOR-4DRH

5. Conclusion

This in silico study provides strong computational evidence that selective serotonin reuptake

- Inhibitors (ssris) and other antidepressants exhibit promising anticancer potential, particularly against glioblastoma-relevant targets such as HDAC and mtor. The binding affinities and
- Molecular interactions observed were comparable to or superior to the standard chemotherapy drug temozolomide, reinforcing the rationale for repurposing these CNS drugs for cancer treatment.

Key highlights of the findings include:

- Dapoxetine and paroxetine showed the highest docking affinity toward HDAC and mTOR, respectively.
- The interactions involved critical catalytic site residues, suggesting strong and specific binding.

The binding conformations of test compounds significantly overlapped with that of temozolomide, indicating similar mechanistic action.

These antidepressants may offer dual benefits—psychological support and direct anticancer action—especially valuable in cancer patients with comorbid depression.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

References

[1] Ashburn TT, Thor KB. Drug repositioning: identifying and developing new uses for existing drugs. Nat Rev Drug Discov. 2004;3(8):673–683.

[2] Jeon SM. Use of antidepressants for cancer treatment. Biomed Pharma other. 2019; 109:1350– 1359.

[3] Xia D, Zhang YT, Xu GP, et al. Fluoxetine induces apoptosis in human breast cancer cells through downregulation of Bcl-2. Oncol Lett. 2016;11(1):299–304.

[4] Bolden JE, Peart MJ, Johnstone RW. Anticancer activities of histone deacetylase inhibitors. Nat Rev Drug Discov. 2006;5(9):769–784.

[5] Saxton RA, Sabatini DM. mTOR signaling in growth, metabolism, and disease. Cell. 2017;168(6):960–976.

[6] Trott O, Olson AJ. AutoDock Vina: improving the speed and accuracy of docking with a new scoring function. J Comput Chem. 2010;31(2):455–461

[7] Lupu L, Kirmizis A, Papadopoulou LC. SSRIs and chemotherapy: synergistic effects of fluoxetine with temozolomide. J Neurooncol. 2020;147(1):77–86.

[8] Munoz M, Coveñas R. Antidepressants and cancer: where do we go from here? Curr Med Chem. 2020;27(25):4163–4176.

[9] Kannen V, Hintzsche H, Zanette DL, et al. Antidepressant drugs modulate the MAPK/ERK pathway in cancer cells. Mol Carcinog. 2015;54(10):1125–1135.

[10] Munoz M, Rosso M. The antidepressant fluoxetine induces apoptosis in human breast cancer cells. Cell Mol Life Sci. 2010;67(6):1111–1124.

[11] Pushpakom S, Iorio F, Eyers PA, Escott KJ, Hopper S, Wells A, et al. Drug repurposing: progress, challenges and recommendations. Nat Rev Drug Discov. 2019;18(1):41–58.doi:10.1038/nrd.2018.168

[12] Li J, Zheng S, Chen B, Butte AJ, Swamidass SJ, Lu Z. A survey of current trends in computational drug repositioning. Brief Bioinform. 2016;17(1):2–12. doi:10.1093/bib/bbv020

[13] Nosengo N. Can you teach old drugs new tricks? Nature. 2016;534(7607):314–6. doi:10.1038/534314a

[14] Sung H, Ferlay J, Siegel RL, Laversanne M, Soerjomataram I, Jemal A, et al. Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancer in 185 countries. CA Cancer J Clin. 2021;71(3):209–49.doi:10.3322/caac.21660

[15] Fitzmaurice C, Abate D, Abbasi N, Abbastabar H, Abd-Allah F, Abdel-Rahman O, et al. Global burden of cancer, 1990–2017: A systematic analysis for the Global Burden of Disease Study. JAMA Oncol. 2019;5(12):1749–68.doi:10.1001/jamaoncol.2019.2996

[16] Holohan C, Van Schaeybroeck S, Longley DB, Johnston PG. Cancer drug resistance: an evolving paradigm. Nat Rev Cancer. 2013;13(10):714–26. doi:10.1038/nrc3599

[17] Ostrom QT, Cioffi G, Gittleman H, Patil N, Waite K, Kruchko C, et al. CBTRUS Statistical Report: Primary brain and other central nervous system tumors diagnosed in the United States in 2012–2016. Neuro Oncol. 2019;21(Suppl 5):v1–100. doi:10.1093/neuonc/noz150

[18] Louis DN, Perry A, Wesseling P, Brat DJ, Cree IA, Figarella-Branger D, et al. The 2021 WHO Classification of Tumors of the Central Nervous System: a summary. Neuro Oncol. 2021;23(8):1231–51. doi:10.1093/neuonc/noab106

[19] Rees JH. Diagnosis and management of brain tumours. Postgrad Med J. 2001;77(909):663– 70 doi:10.1136/pmj.77.909.663

[20] D'Alessandris QG, Biffoni M, Martini M, Runci D, Buccarelli M, Cenci T, et al. The clinical value of drug repurposing in glioblastoma. Front Oncol. 2018;8:461.doi:10.3389/fonc.2018.00461

[21] Louis DN, Perry A, Reifenberger G, von Deimling A, Figarella-Branger D, Cavenee WK, et al. The 2016 World Health Organization Classification of Tumors of the Central Nervous System: a summary. Acta Neuropathol. 2016;131(6):803–20.doi:10.1007/s00401-016-1545-1

[22] Stupp R, Mason WP, van den Bent MJ, Weller M, Fisher B, Taphoorn MJ, et al. Radiotherapy plus concomitant and adjuvant temozolomide for glioblastoma. N Engl J Med. 2005;352(10):987–96. doi:10.1056/NEJMoa043330

[23] Omuro A, DeAngelis LM. Glioblastoma and other malignant gliomas: a clinical review. JAMA. 2013;310(17):1842–50. doi:10.1001/jama.2013.280319

[24] Brennan CW, Verhaak RG, McKenna A, Campos B, Noushmehr H, Salama SR, et al. The somatic genomic landscape of glioblastoma. Cell. 2013;155(2):…

[25] serotonin reuptake inhibitors directly signal for apoptosis in biopsy-like Burkitt lymphoma cells. Blood. 2003;101(8):3212–9. doi:10.1182/blood-2002-05-1440

[26] Cloonan SM, Williams DC. The antidepressants maprotiline and fluoxetine induce Type II autophagic cell death in drug-resistant Burkitt's lymphoma. Int J Cancer. 2011;128(2):376–85. doi:10.1002/ijc.25330

[27] Xia D, Zhang YT, Xu GP, Yan WW, Pan XR, Tong JH, et al. Fluoxetine induces apoptosis and autophagy in glioma cells through modulation of the AMPK/mTOR pathway. Biochem Biophys Res Commun. 2017;492(3):373–9. doi:10.1016/j.bbrc.2017.08.061

[28] Omuro A, DeAngelis LM. Glioblastoma and other malignant gliomas: a clinical review. JAMA. 2013;310(17):1842–50. doi:10.1001/jama.2013.280319

[29] West AC, Johnstone RW. New and emerging HDAC inhibitors for cancer treatment. J Clin Invest. 2014;124(1):30–9. doi:10.1172/JCI69738

[30] Laplante M, Sabatini DM. mTOR signaling in growth control and disease. Cell. 2012;149(2):274–93. doi:10.1016/j.cell.2012.03.017