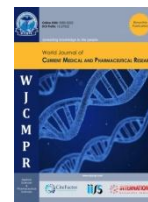




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## Insilico pharmacological evaluation of dibenzosuberone derivatives as antidepressant

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### Abstract

A new drug takes a long time and is expensive to introduce. By using *insilico* drug design, you can save time and money. Utilizing computational software, a novel Schiff's base Dibenzosuberone derivative was designed and molecular docking studies were performed using autodock software. To predict Absorption, Distribution, Metabolism, Excretion, and Molecular Properties of Dibenzosuberone derivatives, *insilico* screening was performed. It should be examined how its Dibenzosuberone derivatives interact with specific targets. The Dibenzosuberone derivatives were successfully identified as targets in this study.



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### Introduction

The new drug development is important for the pharmaceutical field. Because of the developing of new diseases, the resistance of the drug, and drugs having various side effects. A new approach is using in silico methods to develop new drugs by using various software. In silico methods, which are widely used in drug development, have significantly reduced both the cost and the time required. In silico drug discovery is based on the identification of the active target and the ligand [1].

Dibenzosuberone is a good starting point for many biologically active compounds. The 5-dibenzosuberone through different modes of functionalization of the tricyclic structure. On the central "seven-membered ring," a carbonyl ring or two double bonds modify the structure of dibenzosuberone.

Schiff's bases play an important role in pharmaceutical drug preparation. Schiff's bases are formed from primary amines and carbonyl compounds. An organic compound with the azomethine group (C = N) is referred to as a Schiff base. Schiff bases accompanying these reactions have been found to have biological activity, which is why they have been used to treat a variety of diseases. Dibenzosuberone was used with amine compounds to design new molecules. The Schiff bases of dibenzosuberone derivatives are new pharmaceutical entities [2-7].

### Methodology

#### Drug design

The drug was designed using ChemSketch software. X-ray crystallography or NMR spectroscopy plays a crucial role in the structure-based drug design process. A medicinal chemist may use interactive graphics and intuition to design candidate

drugs predicted to bind with high affinity and selectivity to the biological target based on its structure. The development of new drug entities may also be automated using various computational procedures [8-10].

#### Molecular Property Prediction

By using molinspiration, in silico molecular prediction was conducted on the new compounds. The properties such as logP, molecular weight, H-bond donors, H-bond acceptors, and rotatable bonds were assessed [11-13].

#### Molecular Docking Studies

A docking programme such as MGL Tools is used to automate the docking process. A ligand is usually a molecule that binds to a receptor (target) in a way that is most beneficial to the receptor (target). A rigid docking mode and a flexible docking mode are available. In docking, molecules are positioned, conformed, and oriented to fit perfectly into the target structure. When two molecules form an intermolecular complex, molecular docking determines how they are arranged. A ligand is typically a small molecule that binds to proteins. A binding site is an area of a protein where compounds are formed. Binding can take place in a variety of mutual conformations [14-17].

#### Autodock Procedure

The automatic docking procedure Autodock 4.2.6 determines whether ligands interact with biomacromolecular targets. In this study, a serotonin transporter with a validated experimental structure was used as a target (PDB ID: 6AWO). Through the combination of rapid grid-based energy evaluation and efficient torsional freedom search, AutoDock accomplishes these goals. AutoDock typically provides reproducible docking results for ligands that have approximately 10 flexible bonds when using the Lamarckian

Genetic Algorithm and an empirical free energy scoring function. Protein and ligand starting structures impact docking results in a significant way [18-20].

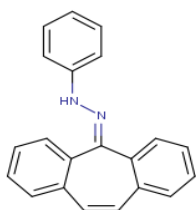
#### ADME Prediction

ChemSketch was used to draw the structures of all compounds. A Swiss ADME server is used for uploading the structures. Using the Swiss ADME server, the molecular sketcher import icon is clicked, a new window opens for selecting the structure, and then it is exported to SMILES. A further set of parameters was entered by pressing the icon "run" [21-22].

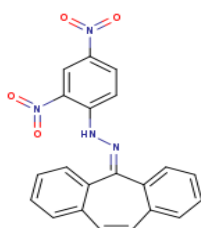
### Results & Discussion

#### Drug Design

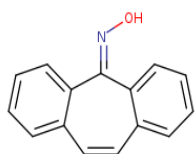
The ligands were drawn in chemsketch software and assigned to each compound with the appropriate 2D orientation. Smile Translator is used to convert the ligands into PDP format [23 & 24].



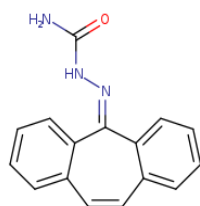
Compound -1



Compound-2



Compound-3



Compound-4

#### Calculation On Molecular Properties

The molecular properties were calculated using molecular inspiration. Lipinski's rule of five describes it. Molecule weight, hydrogen bond donor, hydrogen bond acceptor, and log P make up these five properties.[25].

**TableNo:1Molecular properties of designed compounds and reference drug**

Compound name	M.W (G/Mol)	Donor-hydrogen bonds	Acceptors-hydrogen bonds	Log P	No.of.violation
compound-1	296.37	1	1	4.66	nil
compound-2	386.36	1	5	3.78	nil
compound-3	221.25	1	2	3.19	nil
compound-4	263.29	2	2	2.48	nil
Amitriptyline	277.40	0	1	4.36	nil

#### Molecular Docking Studies

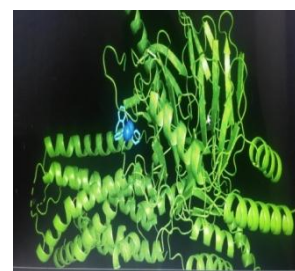
An auto-dock program was used to perform molecular docking studies efficiently.[26] Ligands bind to protein, and their binding energy has been calculated. Compound 2 has the highest protein binding energy.[28&29]. The protein is docked with all four ligands, and the results are,

**Table No: 2 Molecular docking result of designed compounds and reference drug**

Compound name	Docking interaction	(-) Binding energy (kcal mol <sup>-1</sup> )
1	6AWO	-7.37
2	6AWO	-8.31
3	6AWO	-6.72
4	6AWO	-7.13
Amitriptyline	6AWO	-6.61



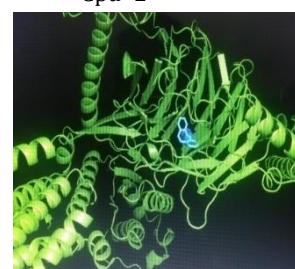
Cpd-1



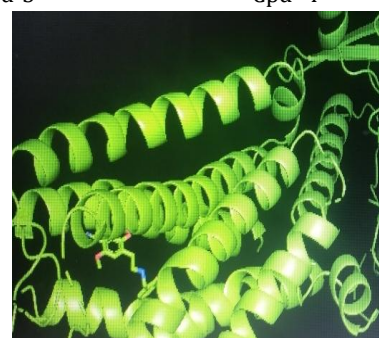
Cpd -2



Cpd-3



Cpd -4



Cpd -5

#### ADME Prediction

The ADME properties of the compounds and the reference drug amitriptyline were predicted using the SWISS ADME server, [30] and the results are recorded in Table.no.3

**TableNo: 3 ADME properties of designed compounds and reference compound**

COMPOUND NAME	M/W (g/mol)	HB A	HB D	TPSA	CONSENSUS Log Po/w	MR	GI	BB B	P-gp	Lipinski	Bioavailability	PAINS	BRE NK
1	296.37g/mol	1	1	24.39 Å	4.66	96.90	high	yes	no	Yes*	0.55	0	0
2	386.36g/mol	5	1	116.03 Å	3.78	114.54	low	no	no	Yes*	0.55	0	1
3	221.52g/mol	2	1	32.59 Å	3.19	68.80	high	yes	no	Yes*	0.55	0	2
4	263.29g/mol	2	2	67.48 Å	2.48	78.98	high	yes	no	Yes*	0.55	0	0
Amitriptyline	277.40	1	0	3.24 Å	4.36	90.96	high	yes	no	Yes**	0.55	1	0

HBA: Hydrogen bond acceptors; HBD-Hydrogen bond donors; MR-Molar Refractivity; TPSA- Topological Polar Surface Area; GI-Gastro-intestinal; BBB: Blood brain barrier; P-GP: P-Glycoprotein; \*Average of five Prediction; \*\*1 violation: MLOGP> 4.15 PAINS- Pan-Assay Interference compounds; MW: Molecular weight;

### Conclusion

Designed the new molecules from the dibenzosuberone nucleus. The design compounds possess the Lipinski rule. The compounds were studied using molecular docking, and compound-2 had a lower binding energy than the others. Based on the comprehensive virtual screening done for ADMET profiling of dibenzosuberone derivatives, it has been concluded that these molecules should be synthesized, characterized, and evaluated pharmacologically in the future based on the predicted values of physicochemical descriptors.

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### Conflicts of Interest

The authors declare no conflict of interest.

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