



Received on 13 May 2025; received in revised form, 23 June 2025; accepted, 02 July 2025; published 01 November 2025

DESIGN AND EVALUATION OF SULPHONYL UREA DERIVATIVES AS THERAPEUTIC CANDIDATES FOR TYPE 2 DIABETES MELLITUS BY PERFORMING *IN-SILICO* STUDIES

M. Sri Ramachandra^{*}, R. Akshaya, V. V. Kavya, D. Reshma, T. Shiva Murthi, P. Shalem Raju and P. Kalyan

Department of Pharmacology, Dr. K. V. Subbareddy Institute of Pharmacy, Dupadu, Kurnool - 518218, Andhra Pradesh, India.

Keywords:

Diabetes mellitus, Molecular docking, Hypoglycaemic agent, AutoDock, ADME, Swiss ADME, Bioavailability, Glibenclamide, Therapeutic efficacy

Correspondence to Author:

Dr. M. Sri Ramachandra

Department of Pharmacology,
Dr. K. V. Subbareddy Institute of
Pharmacy, Dupadu, Kurnool -
518218, Andhra Pradesh, India.

E-mail: chandram143@gmail.com

ABSTRACT: Diabetes mellitus - Type 2 Diabetes Mellitus (T2DM) in particular - is a long-term inherent metabolic disorder that is seriously problematic with regards to global health. Sulfonylureas are a class of widely-used oral hypoglycemic drugs aimed at type 2 diabetes mellitus, targeting ATP-sensitive potassium channels through sulfonylurea receptor 1 (SUR1). This study intends to design and evaluate novel sulfonylurea derivatives *via in-silico* models in order to enhance both therapy potential and drug-likeness. Molecular docking studies were conducted with AutoDock 4.2.6 against the protein 4EM9 (PPAR γ). This is a critical target for T2DM, along with the most established relative glibenclamide for comparison. Docking scores indicated that all derivatives (1a-1d) had strong binding affinities but ligand 1a showed the most affinity with a value of -7.48 kcal/mol. ADME profiling via Swiss ADME gave good pharmacokinetics and bioavailability data, while the suitability of drug likeness got confirmed by Molinspiration and PASS prediction. All this helps in proving the sulfonylurea derivatives-another promising one being 1a-as important drug candidates to treat T2DM.

INTRODUCTION: Diabetes mellitus is a complex group of metabolic disorders linked to insulin deficiency, leading to high blood sugar levels. Long-term high blood sugar can cause damage to small blood vessels, affecting peripheral nerves, kidneys, or the retina. Psychosocial factors are crucial for effective diabetes management, influencing self-care practices more than metabolic measures like complications or blood tests. Diabetes is characterized by high blood sugar and issues with protein and fat metabolism, occurring when the pancreas makes insufficient insulin or when cells don't use insulin properly^{1, 2, 3}.

Diabetes comes in three forms:

1. Type 1 - Insulin-dependent diabetes mellitus (IDDM)
2. Type 2 - Noninsulin-dependent diabetes mellitus (NIDDM)
3. Gestational Diabetes

Type I- Insulin-dependent diabetes mellitus (IDDM): Juvenile diabetes is also called during the first stages of the onset of diabetes. This includes destruction of the, mainly, insulin-producing cells known as β cells in the pancreas due to autoimmune reactions (type IA) in most cases. Some other cases are idiopathic (type IB), with no antibodies detected. The insulin levels are low in a person affected by type I diabetes, thus posing a higher risk for ketosis. This type is said to be rare and has a low genetic predisposition. The points of destruction of insulin-secreting cells, age of onset,

QUICK RESPONSE CODE 	DOI: 10.13040/IJPSR.0975-8232.16(11).2985-93 This article can be accessed online on www.ijpsr.com DOI link: https://doi.org/10.13040/IJPSR.0975-8232.16(11).2985-93
---	--

and hallmark symptoms such as polydipsia, polyphagia, and polyuria are emphasized. Life-long insulin must be given at present. There are still many aspects of type I diabetes that require the attention of researchers ⁴.

Type II- Noninsulin-dependent Diabetes Mellitus (NIDDM): Type 2 diabetes has also been described as maturity onset diabetes mellitus. It is a rapidly spreading health-related problem associated with obesity and is considered to predispose individuals to microvascular complications such as retinopathy and nephropathy, as well as macrovascular disorders including heart disease. Type 2 diabetes has a heritable basis, generally becomes manifest after middle age, involves little loss of β cells, varies in insulin production, and does not have detected anti- β -cell antibodies; in fact, it accounts for about 90% of cases of diabetes. Some of the possible causes are errors in glucose response by β cells, impaired insulin action in tissues, and obese conditions leading to outright insulin shortages.

Gestational Diabetes: Gestational diabetes occurs between 24 and 28 weeks of pregnancy when blood sugar levels increase due to inadequate insulin production. While it usually goes away after the child is delivered, it raises the risk of type 2 diabetes in the future. Common risk factors include obesity, a family history of diabetes, being older than 25, prior births of large babies, and certain ethnicities. Treatment includes dietary modifications, exercises, possibly insulin injections, and regular monitoring of blood glucose levels. Unmanaged gestational diabetes may yield preterm birth and higher chances of the child becoming obese or type 2 diabetic ⁵.

Sulphonyl Urea Receptors: It stimulates the pancreas to produce more insulin. Reduces the blood glucose levels, and the latter effects include hypoglycaemia. The mechanism includes Binding of the sulfonylurea receptors on beta cells of the pancreas, which results in ATP-dependent potassium channels becoming closed on the beta cell membrane, causing depolarisation and calcium influx; thereupon, insulin is released into the bloodstream due to the increase in intracellular calcium that triggers the exocytosis of insulin-containing granules ⁶.

E.g.: Glimepiride, Glibenclamide

Chemical Structure:

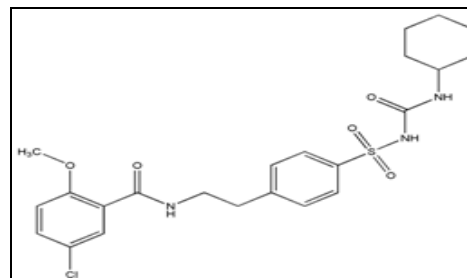


FIG. 1: STRUCTURE OF GLIBENCLAMIDE

Compound Name: Glibenclamide

IUPAC Name: 5-ChloroN- [2- [4-(Cyclohexyl carbamoyl sulfamoyl) phenyl] ethyl]-2-methoxybenzamide.

Mechanism of Action: Triggers release of insulin from pancreatic beta cells by binding to and closing ATP-sensitive potassium (KATP) channels and causing depolarization of the cell and influx of calcium. Also increases peripheral insulin sensitivity and decreases hepatic glucose production ⁷.

Pharmacokinetics ^{8,9}:

- Absorption: well absorbed orally; T_{max} ~4 hours
- Bioavailability: ~50% due to hepatic first-pass metabolism
- Distribution: >99% protein bound (albumin)
- Metabolism: Hepatic (primarily CYP2C9); inactive or weakly active metabolites
- Elimination: Urine (50%) and feces (50%)
- Half-life: 4–10 hours; prolonged in renal/hepatic dysfunction.

The above said is a standard drug, the structurally derivative compounds (1a, 1b, 1c, 1d) on the basis of the SAR of Sulphonyl urea are conducted docking for predict binding energy and binding scores against the defined protein structure where the ligands are shown in results and discussion.

Molecular Docking: Molecular docking is a computational technique that allows the prediction of non-covalent interactions between molecules

such as a protein receptor and a ligand. The methodology provides the predicted conformation and binding affinities of the small molecule in its lowest energy state and is used to screen a plethora of compounds. It helps understand drug interaction mechanisms. With the improved docking technique, it assesses the fitting of molecules and binding strength. A number of the software available include AutoDock and AutoDock Vina. When performing a docking study, a 3D structure of the protein is necessary and may be obtained from the Protein Data Bank. If the 3D structure is not available, this can be predicted by computational methods^{10, 11}.

Searching Algorithms: The docking algorithm concentrates on new lead molecules or various conformations that must be found faster and accurately by particular guidelines. Docking algorithms are basically categorized into rigid-body docking and flexible docking, as per the flexibility of the receptor and the ligand. Though rigid body docking detects ligand binding sites, it has a trade-off with accuracy because it doesn't account for flexibility changes. The results from simulation docking can then be compared to crystallographic structures using Root Mean Square Deviation (RMSD). Initially, screening is via small molecules in a database. Flexible docking is processing a more than one ligand and receptor conformations together and uses very intensive processing power. The conformational space is searched using such methods^{12, 13}.

1. Systematics Search algorithm
2. Random or Stochastic algorithm
3. Simulation algorithm

Types of Docking:

1. Rigid Docking
2. Flexible Docking

Rigid Docking: Rigid docking is a molecular docking method that predicts how ligands bind to receptors at the atomic level. It is the fastest method but often overlooks changes in protein shape, assuming fixed structures. The goal is to place a molecule accurately in three-dimensional space. The docking process relies on fitting the ligand into the receptor's expected position,

ensuring good interactions like hydrogen bonding and avoiding conflicts. Rigid docking also involves preparing the ligand and receptor by removing water, adding hydrogens, assigning charges, and optimizing shape.

Flexible Docking: One particular computational procedure in molecular modeling calculates how ligands and receptors bind together. Flexible docking allows for changes in shape for both the ligand and receptor, leading to better predictions of binding modes. Unlike rigid docking, it assesses molecular flexibility and confirms the presence of ligand and receptor in a complex. Flexible docking predicts binding interactions and conformational changes through conformational sampling and search methods¹⁴.

Applications: It assists in lead optimization and drug interaction identification, particularly with DNA:

- ❖ Bioremediation anticipates pollutants that are capable of degrading produced enzymes.
- ❖ Docking analyzes protein-protein interactions and screens side effects when medicines are taken in combination.
- ❖ It is used as a drug design tool and for judging geometry in complexes.
- ❖ Drug-DNA interactions correlate a drug's shape with its ability to kill cancer cells.
- ❖ Docking predicts possible biochemical interactions prior to experiments being performed¹⁵.

Softwares used in Performing *In-silico* Studies: The materials and softwares used in performing the molecular docking studies and *in-silico* studies (ADME, Molinspiration, Pass prediction) are^{16, 17, 18}:

Autodock 4, PyMol- 3D Molecular visualization, Biovia-Discovery Studio, Cactus- SMILES Translator Online, Swiss-ADME, Molinspiration Cheminformatics, Way2Drug- Pass prediction.

Methodology of Molecular Docking using Autodock:

Protein Preparation: The protein used in this docking research is 4EM9, a human PPAR gamma

with non-anionic acids, obtained from the Protein Data Bank. For preparing proteins with Auto Dock 4. 2. 6, start by configuring the preferences to your working directory. Open the purified protein, add polar hydrogens, apply Kollman charges, and save the file in PDBQT format. A color change indicates readiness for further research¹⁹.

Ligand Preparation: Ligands are available in online databases such as PubChem and Drug Bank or can be generated using software such as ChemDraw and ChemSketch. Another choice is ChemSpider for the retrieval of ligands and their 3D structures. After obtaining the 3D structure in SDF Mol format, translate it to PDB format using Discovery Studio. Save it as "sulphonyl urea derivatives. pdb". To finish ligand preparation, read molecule file, save as PDB, display in green, select for Autodock, modify hydrogens and charges, assign torsion portions to 13, and save as PDBQT for docking.

Grid Formation: Under this step, select the macromolecule first, then choose protein from the list and accept with ok. Switch to the grid view to get to the set map types function, then choose and set ligand. Set the grid box when saving the output dimensions file in GPF format²⁰.

Docking Parameters: Open a new window to specify strict filename when selecting the macromolecule in the docking interface. Input the ligand by selecting its acceptance option. Selection of search parameters is followed by selection of the genetic algorithm and acceptance of the input. The program must save output results as a DPF file using the Lamarckian output method.

Run Autogrid and Autodock: The process begins with selecting Autogrid from run and then selecting the GPF file to start the process. Verify the GLG file and map files. Select the DPF file and run Autodock using the same run command. The creation of the DLG file by selecting the DPF file will yield binding energy information for analysis.

Analysis and Interpretation: For the vision of 2D compound image open DLG file in Autodock. And set confirm highest binding energy and save the written complex PDBQT file. Discovery Studio should be initialized after opening the written complex file. Label and select an amino acid. Save

the 2D diagram, then check how many amino acids interact same by doing a comparison study with reference drug.

RESULTS AND DISCUSSION:

Molecular Docking Studies: The protein 4EM9 is employed to dock with the ligands and standard drug and the ligand interactions are represented with the various colours (traditional hydrogen bond, carbon hydrogen bond, van der Waals, alkyl, Pi-Pi stacked, Pi-alkyl bonds, etc.,)

Molecular Docking Studies: The protein 4EM9 is employed to dock with the ligands and standard drug and the ligand interactions are represented with the various colours (traditional hydrogen bond, carbon hydrogen bond, van der Waals, alkyl, Pi-Pi stacked, Pi-alkyl bonds, etc.,)

Scores and 2D poses of Standard drug:

Docking score: -5.77 kcal/mol

Ligand – interactions:

Conventional Hydrogen Bonding: GLY A-284

Vanderwal's Forces: GLU A: 259, ASP A: 260, GLY A: 258, ILE A: 249, ARG A: 280, PHE A: 287, SER A: 342

Alkyl Bonds: ARG A: 288, CYS A: 285, ILE A: 341, ILE A: 281, MET A: 348, LEU A: 255, ILE A: 281.

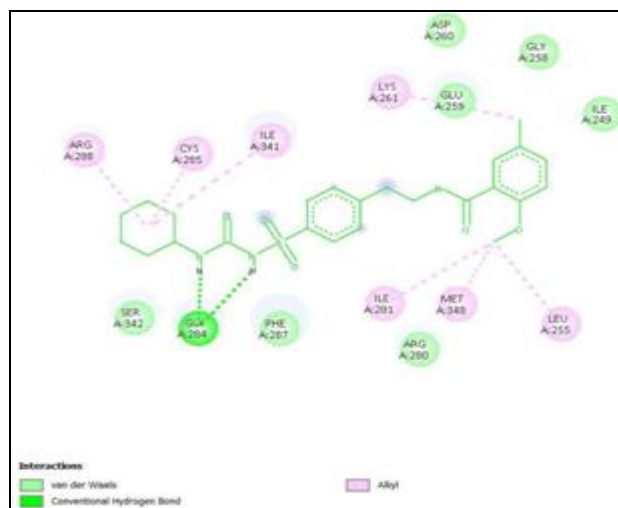


FIG. 2: STD

Scores and 2D poses of ligand 1a:

Docking score: -7.48 kcal/mol

Ligand – interactions:

Conventional hydrogen bonding: GLU, B: 291, ILE B:281

Vanderwal's forces: PHE B: 363, LEU B: 353, MET B: 348, SER B: 342, GLU B: 343, GLU B: 295

Carbon-Hydrogen Bond: GLY B: 284

Pi—Pi Stacked & Pi-Pi T shaped interactions: HIS B: 266, PHE B: 264

Alkyl and Pi-alkyl interactions: PRO, B: 227, ILE B: 345, ARG B: 288, CYS B: 285, MET B: 364

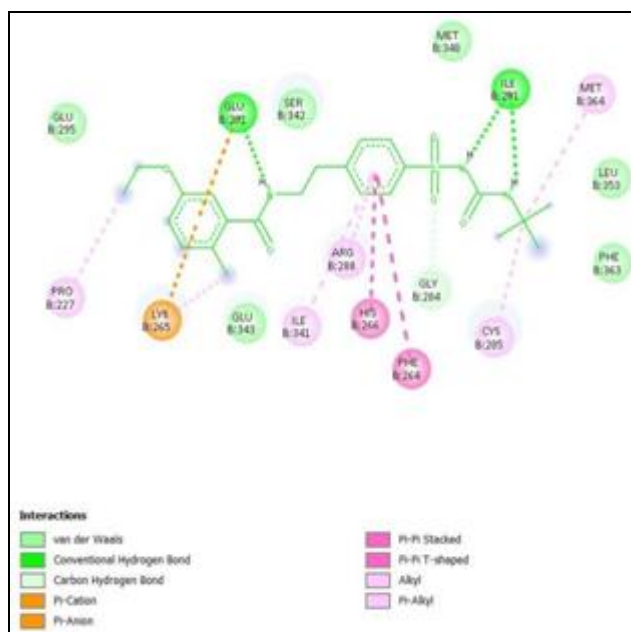


FIG. 3: 1A

Scores and 2D poses of ligand 1b:

Docking score: -6.57 kcal/mol

Ligand – interactions:

Conventional Hydrogen Bond: PHE B: 264, SER B: 342, ILE B: 281

Vanderwaals forces: HIS B: 266, MET, B: 248, ARG B: 280

Carbon-Hydrogen Bond: GLY B: 284

Alkyl and Pi-alkyl interactions: LYS, B: 265, ILE B: 341, LEU B: 330, CYS B: 285, MET B: 364

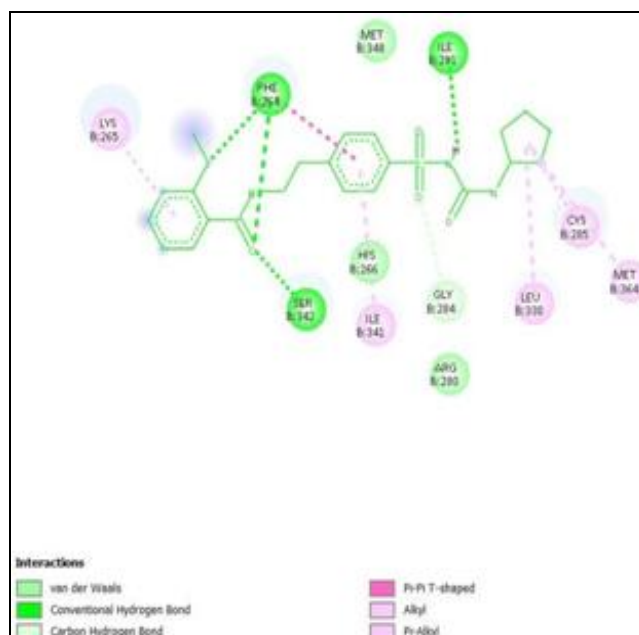


FIG. 4: 1B

Scores and 2D poses of ligand 1c:

Docking score: -6.85 kcal/mol

Ligand – interactions:

Conventional Hydrogen Bond: GLN, B: 454, LEU B: 465

Vanderwaals forces: LEU B: VAL B: 455, ILE B: 279, ILE B: 267, HIS B: 266, TYR B: 473

Pi-Sigma Bond: GLN B: 283

Alkyl and Pi-alkyl interactions: LEU, B: 469, PHE B: 287, PHE B: 360, PRO, B: 359.

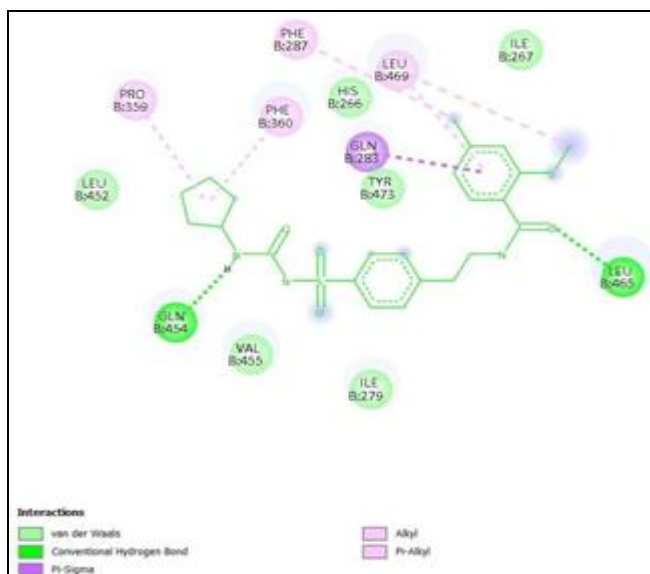


FIG. 5: 1C

Scores and 2D poses of ligand 1d:

Docking score: -6.85 kcal/mol

Ligand – interactions:

Vanderwaals forces: LEU A: 333, SER A: 289, SER A: 342, GLY A: 284, ARG A: 280, LEU A: 255, ASP A: 260, SER A: 342, LYS A: 261, GLU A: 259, GLY A: 258

Carbon-Hydrogen & Pi-Donor Bond:

CYS A: 285, ILE A: 281

Pi-Sigma Bond: LEU A: 330

Pi-Sulfur Bond: MET A: 348

Alkyl and Pi-alkyl interactions: ILE, A: 326, ARG A: 288, MET A: 329, ILE.

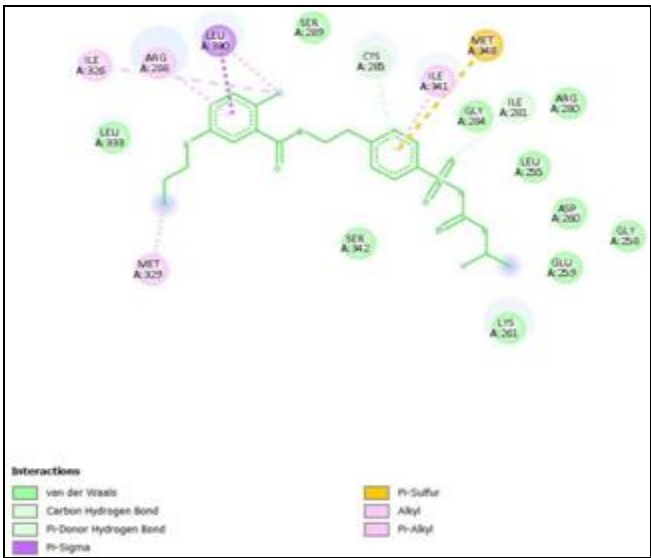


FIG. 6: 1D A: 341

The docking grid was placed accurately over the target protein's active site, focusing on key residues like GLY A: 284. The grid box size was set to 126 × 126 × 126 Å, with central coordinates at -22. 084, -9. 973, 26. 219, ensuring complete coverage of the binding pocket with 0.581Angstroms spacing.

The interactions of ligand 1a are similar to the standard drug with GLY A: 284 and GLY B: 284 respectively i.e., they bind to the same amino acid but differs in the symmetrical chain of the protein, called Homodimers.

The docking scores for sulfonyl urea derivatives were -7. 48 for 1a, -6. 57 for 1b, -6. 85 for 1c, and - 6. 85 for 1d, compared to the standard drug's score of -5. 77, indicating that protein 4EM9 has a strong binding affinity for the 1a derivative.

ADME Results: The screening for how well drugs are absorbed, distributed, metabolized, and excreted is done using the Swiss ADME online tool. The SMILES of selected ligands serve as input.

Key factors influencing absorption include water solubility, P-glycoprotein substrate, skin permeability, Gastro-Intestinal absorption, and membrane permeability. Distribution is controlled by the blood-brain barrier, while excretion relies on clearance and renal OCT2 substrate.

Different compound descriptors indicate high hydrophobicity, suggesting good membrane penetration. The ADME properties of the designed products are shown in Table 1 to 5.

TABLE 1: PHYSIOCHEMICAL PROPERTIES OF THE DESIGNED COMPOUNDS BY SWISS ADME

Code	Mol. wt.	No. of heavy atoms	No. of aromatic heavy atoms	No. of rotatable bonds	No. of H-bond Accept ors	No. of H-bond Donors	Molar Refractivity	TPSA
1a	481.99	32	12	12	5	3	123.59	121.98
1b	461.6	31	12	11	4	3	121.66	138.05
1c	496.04	32	12	11	4	3	126.67	138.05
1d	481.99	32	12	13	5	3	123.56	121.98
STD	494	33	12	11	5	3	126.25	121.98

From the above table, the ligands 1a, 1b, 1c, 1d are very similar or slight lower to the values of standard drug Glibenclamide in all physicochemical properties.

TABLE 2: LIPOPHILICITY CHARACTERISTICS OF THE DESIGNED COMPOUNDS BY SWISS ADME

Drug	iLOGP	XLOGP3	WLOGP	MLOGP	SIILICOSIT	Consensus Log PO/w
1a	2.94	3.68	4.58	2.76	3.11	3.41
1b	2.63	4.06	4.39	2.67	2.66	3.28
1c	3.06	4.69	5.05	3.15	3.32	3.85

1d	3.13	4.02	4.58	3.27	3.27	3.55
STD	2.81	4.81	4.72	2.58	3	3.58

From the above table, the ligands 1a, 1b, 1c, 1d are very similar or slight lower to the values of standard drug Glibenclamide in lipophilic characteristics.

TABLE 3: WATER SOLUBILITY CHARACTERISTICS OF THE PHYTOCONSTITUENTS OF DESIGNED COMPOUNDS

Drug	Log S	Solubility		Class
		mg/mL	mol/L	
1a	-4.63	1.12E-02	1.12E-02	Moderately soluble
1b	-4.82	6.98E-03	1.51E-05	Moderately soluble
1c	-5.42	1.88E-03	3.79E-06	Moderately soluble
1d	-4.78	7.99E-03	1.66E-05	Moderately soluble
STD	-5.48	1.65E-03	3.34E-06	Moderately soluble

From the above table, the ligands 1a, 1b, 1c, 1d are very similar or slight lower to the values of standard drug Glibenclamide in water soluble characteristics and also all the drugs are moderately soluble in water.

TABLE 4: PHARMACOKINETIC PROPERTIES AND BIOAVAILABILITY OF THE DESIGNED COMPOUNDS BY SWISS ADME

Drug	GI	BBB	Bioavailability Score
	Absorption	Permeation	
1a	Low	No	0.55
1b	Low	No	0.55
1c	Low	No	0.55
1d	Low	No	0.55
STD	Low	No	0.55

From the above table, the ligands 1a, 1b, 1c, 1d are very same to the values of standard drug Glibenclamide, there is no Blood brain barrier permeation, and also low gastrointestinal absorption because all the drugs are slightly hydrophilic in nature.

TABLE 5: DRUG LIKENESS RULES SCORE OF THE DESIGNED COMPOUNDS BY SWISS ADME

Code	Lipinski	Ghose	Veber	Egan	Synthetic Accessibility
1a	0	1	1	0	3.34
1b	0	0	1	1	3.27
1c	0	1	1	1	3.34
1d	0	1	1	0	3.35
STD	0	1	1	0	3.34

From the above table, the ligands 1a, 1b, 1c, 1d are very similar or slight lower to the values of standard drug Glibenclamide for the drug likeness rules.

Molinspiration Results: Mol inspiration helps the internet chemistry community by offering free online tools for calculating important molecular properties like Mol inspiration Log P (mi Log P), polar surface area, hydrogen bond donors (HBD), acceptors, and Lipinski's rule. The number of rotatable bonds indicates that all synthesized compounds are flexible and serves as a useful

parameter for predicting drug bioavailability. Rotatable bonds refer to individual non-ring bonds attached to non-terminal heavy atoms, while topological polar surface area helps predict drug transport by summing the surfaces of polar atoms in a molecule. The results of Molinspiration are expressed in the **Table. 6**

TABLE 6: CALCULATION OF MOLECULAR PROPERTIES USING MOLINSPIRATION V2022.08

Code	mi Log P	TPSA	No. of atoms	MW	nON	nOHNH	No. of Violations	No. of Rotatable bonds	Volume
1a	3.65	113.6	32	461.58	8	3	0	9	420.76
1b	3.44	104.36	31	461.61	7	3	0	8	403.54
1c	4.09	104.36	32	496.05	7	3	0	8	417.08
1d	3.87	113.6	32	482	8	3	0	10	418.3
STD	4.77	113.6	33	494.01	8	3	0	8	424.74

From the above table, the ligands 1a, 1b, 1c, 1d are very similar or slight lower to the values of standard drug Glibenclamide but having lesser density to all the drugs on calculating the molecular properties.

PASS Prediction: PASS (Prediction of Activity Spectra for Substances) is software designed to assess the biological activity of organic drug-like compounds. It predicts various classes of biological activity in parallel, allowing users to estimate the activity profiles of virtual molecules before their

chemical synthesis and bioassays. The software includes two probabilities: Pa predicts the likelihood of a compound being active, while Pi predicts the likelihood of a compound being inactive. Results for standard drugs and synthesized compounds are shown in **Table 7**.

TABLE 7: PREDICTED BIOLOGICAL ACTIVITIES OF STANDARD DRUGS & DESIGNED COMPOUNDS

Code	Pa	Pi	Activity
1a	0,648	0,004	CYP2C6 substrate
	0,623	0,018	CYP2C9 substrate
	0,605	0,006	Channel-conductance-controlling ATPase inhibitor
	0,555	0,005	Diuretic
	0,565	0,027	Antianginal
1b	0,698	0,001	Sulfonylureas
	0,543	0,009	Channel-conductance-controlling ATPase inhibitor
	0,468	0,028	Antidiabetic
	0,431	0,011	Potassium channel blocker
	0,455	0,066	Insulysin inhibitor
1c	0,659	0,001	Sulfonylureas
	0,524	0,010	Channel-conductance-controlling ATPase inhibitor
	0,474	0,027	Antidiabetic
	0,441	0,002	Potassium channel (Inward rectifier) blocker
	0,417	0,002	Potassium channel (ATP-sensitive) blocker
1d	0,767	0,026	Polyporopepsin inhibitor
	0,594	0,006	Channel-conductance-controlling ATPase inhibitor
	0,604	0,027	CYP2C substrate
	0,570	0,004	CYP2C6 substrate
	0,560	0,028	Antianginal
STD	0,679	0,001	Potassium channel (Inward rectifier) blocker
	0,678	0,001	Potassium channel (ATP-sensitive) blocker
	0,658	0,002	Shaker potassium channel blocker
	0,641	0,001	Sulfonylureas
	0,584	0,007	Channel-conductance-controlling ATPase inhibitor

From the above table, the ligands 1a, 1b, 1c, 1d are having very similar activities as of standard drug Glibenclamide and also shows many other activities like antianginal as well as diuretic activity for the ligand 1a on predicting the biological activities.

CONCLUSION: The Insilco screening of sulfonylurea derivatives showed that they hold promise as potential therapeutic compounds against Type 2 Diabetes Mellitus. Out of the screened compounds, ligand 1a had the most encouraging binding efficacy with the target protein 4EM9 and outcompeted the control drug glibenclamide.

ADME analysis supported the fact that the constructed compounds exhibit suitable physicochemical and pharmacokinetic properties closely following drug- likeness standards. In addition, PASS prediction and Molinspiration analysis validated their potential biological activity, especially in insulin secretagogue pathways. Overall, the findings indicate that rational

sulfonylurea scaffold modification has the potential to provide more effective and safer antidiabetic agents. In the future, in vitro and in vivo studies would be better to continue investigating the clinical applicability of the derivatives.

ACKNOWLEDGEMENTS: Nil

CONFLICTS OF INTEREST: Nil

REFERENCES:

- Sharma M, Sharma K, Gaur K and Bedi R: Socio demographic profile of Diabetic cases attended at Diabetic clinic of a tertiary hospital of western Rajasthan India 2016; 7-2: 23-28.
- Fisher EB, Arfken CL, Heins JM, Houston CA, Jeffe DB and Sykes RK: Acceptance of diabetes regimens in adults.

- Handbook of health behavior research II: Provider Determinants 1997; 189-212.
3. Glasgow RE and Osteen VL: "Evaluating diabetes education: are we measuring the most important outcomes?" *Diabetes Care* 1992; 15(10): 1423-32.
4. Rosenthal MJ, Fajardo M, Gilmore S, Morley JE and Naliboff BD: "Hospitalization and mortality of diabetes in older adults: a 3-year prospective study. *Diabetes Care*" 1998; 21(2): 231-5.
5. Testa MA and Simonson DC: "Assessment of quality-of-life outcomes. *New England Journal of Medicine*." *The New England Journal of Medicine* 1996; 13: 835-40.
6. Willms B and Ruge D: "Comparison of acarbose and metformin in patients with Type 2 diabetes mellitus insufficiently controlled with diet and sulphonylureas: a randomized, placebo-controlled study." *Diabetic Medicine* 1999; 16(9): 657-62.
7. Horowitz JD and Angus JA: "Glibenclamide and thromboxane A₂ receptors." *British Journal of Pharmacology* 1990; 101(3): 633-638.
8. Mück W, Mikus G and Läer S: "Pharmacokinetics of glibenclamide and its metabolites in diabetic patients with impaired renal function." *European Journal of Clinical Pharmacology* 1998; 54(2): 147-152.
9. Jaber LA, Wood GC and Derman RJ: "Pharmacokinetics and metabolic effects of glibenclamide and glipizide in type 2 diabetics." *European Journal of Clinical Pharmacology* 1990; 38(2): 121-125.
10. Sahu MK, Nayak AK, Hailemeskel B and Eyupoglu OE: "Exploring recent updates on molecular docking: Types, method, application, limitation & future prospects." *International Journal of Pharmaceutical Research and Allied Sciences* 2024; 13(2): 24-40.
11. Singh S, Baker QB and Singh DB: "Molecular docking and molecular dynamics simulation." In *Bioinformatics* 2022; 291-304.
12. Cheng C and Yu X: "Research progress in Chinese herbal medicines for treatment of sepsis: pharmacological action, phytochemistry, and pharmacokinetics." *International Journal of Molecular Sciences* 2021; 22(20): 11078.
13. "Youtube" KN: *Pharmaceutical Chemistry*, [Online]. Available:" [www. youtube.com/KNP Pharmaceutical Chemistry](http://www.youtube.com/KNP_Pharmaceutical_Chemistry) 2022.
14. Jin Z and Wei Z: "Molecular simulation for food protein–ligand interactions: A comprehensive review on principles, current applications, and emerging trends." *A Comprehensive Reviews in Food Science and Food Safety* 2024; 23(1): 13580.
15. Ibrahim MK, Eissa IH, Abdallah AE, Metwaly AM, Radwan MM and ElSohly MA: "Design, synthesis, molecular modeling and anti-hyperglycemic evaluation of novel quinoxaline derivatives as potential PPAR γ and SUR agonists." *Bioorganic & medicinal chemistry* 2017; 25(4): 1496-1513.
16. D. A. Good Sell, "Autodock-4," *Scriptts Research Institution* 1990. [Online].
17. L & DW: 2. P. S. L. Schrödinger, "Google - The PyMOL Version 2.3. 0," *Molecular Graphics System* 2015. [Online].
18. S. Diego, "BIOVIA, Dassault Systèmes, Discovery Studio Visualizer, 21.1.0" San Diego: Dassault Systèmes, 2021. [Online].
19. Dogulas Palleti John, Chitti Sashi Kanth and Ajay Babu P: "Virtual Screening and Molecular Docking Analysis of Zap-70 Kinase Inhibitors." *International Journal of Chemistry and Analytical Sciences* 2011; 2(9): 1208-1211.
20. Olusola Abiola Ladokun, Aminu Abiola, Durosinslorun Okikiola and Famuti Ayodeji: "GC-MS and Molecular Docking Studies of *Hunteria umbellata* Methanolic Extract as a potent Anti- Diabetic," *Informatics in Medicine Unlocked* 2018; 1-8.

How to cite this article:

Ramachandra MS, Akshaya R, Kavya VV, Reshma D, Murthi TS, Raju PS and Kalyan P: Design and evaluation of sulphonyl urea derivatives as therapeutic candidates for type 2 diabetes mellitus by performing *in-silico* studies. *Int J Pharm Sci & Res* 2025; 16(11): 2985-93. doi: 10.13040/IJPSR.0975-8232.16(11).2985-93.

All © 2025 are reserved by International Journal of Pharmaceutical Sciences and Research. This Journal licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported License.

This article can be downloaded to **Android OS** based mobile. Scan QR Code using Code/Bar Scanner from your mobile. (Scanners are available on Google Playstore)