

## Synthesis, characterisation and Docking studies of 6-(4-fluorophenyl)-8-(5-(4-nitrophenyl)furan-2-yl)-[1,2,4]triazolo[3,4-b][1,3,4]thiadiazepines

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### Abstract:

A series of 6-(4-fluorophenyl)-8-(5-(4-nitrophenyl)furan-2-yl)-[1,2,4]triazolo[3,4-b][1,3,4]thiadiazepines were synthesised and screened these molecules for antimicrobial activity and it was tested for cytotoxicity test and Docking scores for all the compounds are quite good against all the proteins. Among them, compounds 1 and 2 show best activities, having either the highest or second highest docking scores among the molecules. Compounds 1 and 2 can be potential leads as anti bacterials.

### Introduction :

Traditional interest in pyrazoles stemmed from their use as drugs, dyes and anaesthetics. Pyrazoles themselves can be used as antioxidants in fuels, but their major practical applications have been in medical and agriculture fields. Pyrazole derivatives have been widely used as bacteriostats, bacteriocides, insecticides, fungicides, amoebicides, hypoglycemic, sedative, anticarcinogens, hypnotic, trichomonacidal and psychopharmacological agents.

Several books and reviews on pyrazoles and their derivatives have appeared. A recent one is that of Grimmett [1] in 'Comprehensive organic chemistry'. Jacobs' review [2] was the leading reference for many years and a permanent source of research ideas. Applications of pyrazoles derivatives as pharmaceuticals, agrochemicals, dyestuffs, analytical reagents and as plastics was reviewed by Elguero ins [3] 1984. Some of the most important pyrazoles with biological activity are shown in the table. Pyrazole itself and several N- substituted pyrazoles are inhibitors and deactivators of liver alcohol dehydrogenase [4-7] .

### 1. Materials and methods

Here we synthesised chalcones by using aromatic ketones and substituted aldehyde in the presence of Acid as a catalyst ,we obtained propenones, again on debromination in the presence of drybenzene and triethylamine we obtained Acetylinic ketone ,and it is made to react with triazole in the presence of alcohol medium to obtain thiazadapines .

### Experimental section :

Thin layer chromatography was used to analyse the reaction progress and purity of the compounds synthesized. Melting points were determined in open glass capillary methods and were uncorrected. IR spectra were obtained in KBr discs on a Shimadzu- 8400 IR spectrophotometer, <sup>1</sup>H NMR spectra were recorded on Bruker spectrometer (400 MHz) in DMSO-d<sub>6</sub>/CDCl<sub>3</sub> using TMS as an internal standard, Mass spectra were recorded on Agilent 6320 Ion Trap method

## Procedure for synthesis of propenones (1)

A solution of 5-(p-halo-phenyl)-2-furfuraldehyde (0.01mol) and an appropriate acetophenone (0.01 mol) in ethanol (20ml) was cooled to 5-10°C in ice bath. The cooled solution was treated with dropwise addition of aqueous sodium hydroxide (5ml, 50%) the reaction mixture was magnetically stirred for 30 minutes and allowed to stand at room temperature for 24 hours. The precipitated crystals of propenones were collected by filtration, washed with ethanol, dried and recrystallized from alcohol.

## 2. Synthesis of dibromopropenones (2)

propen-1-ones (0.01mol) was dissolved in glacial acetic acid (10ml) by gentle warming. A solution of bromine in glacial acetic acid was added to it with constant stirring until the yellow colour of bromine persisted. The reaction mixture was kept aside at room temperature for overnight. Crystals of dibromo propenone separated were collected by filtration and washed with ethanol. It was dried and recrystallised from Alcohol.

## 2. Synthesis of thiazadapines by using acetylenic ketone (3)

Triazole (0.01mol), acetylenic ketone (0.01mol) and concentrated sulphuric acid in the presence of ethanol (25ml) were refluxed on a water bath for 1-2 hours. Yellow crystals separated on cooling were collected by filtration and recrystallised from dioxane.

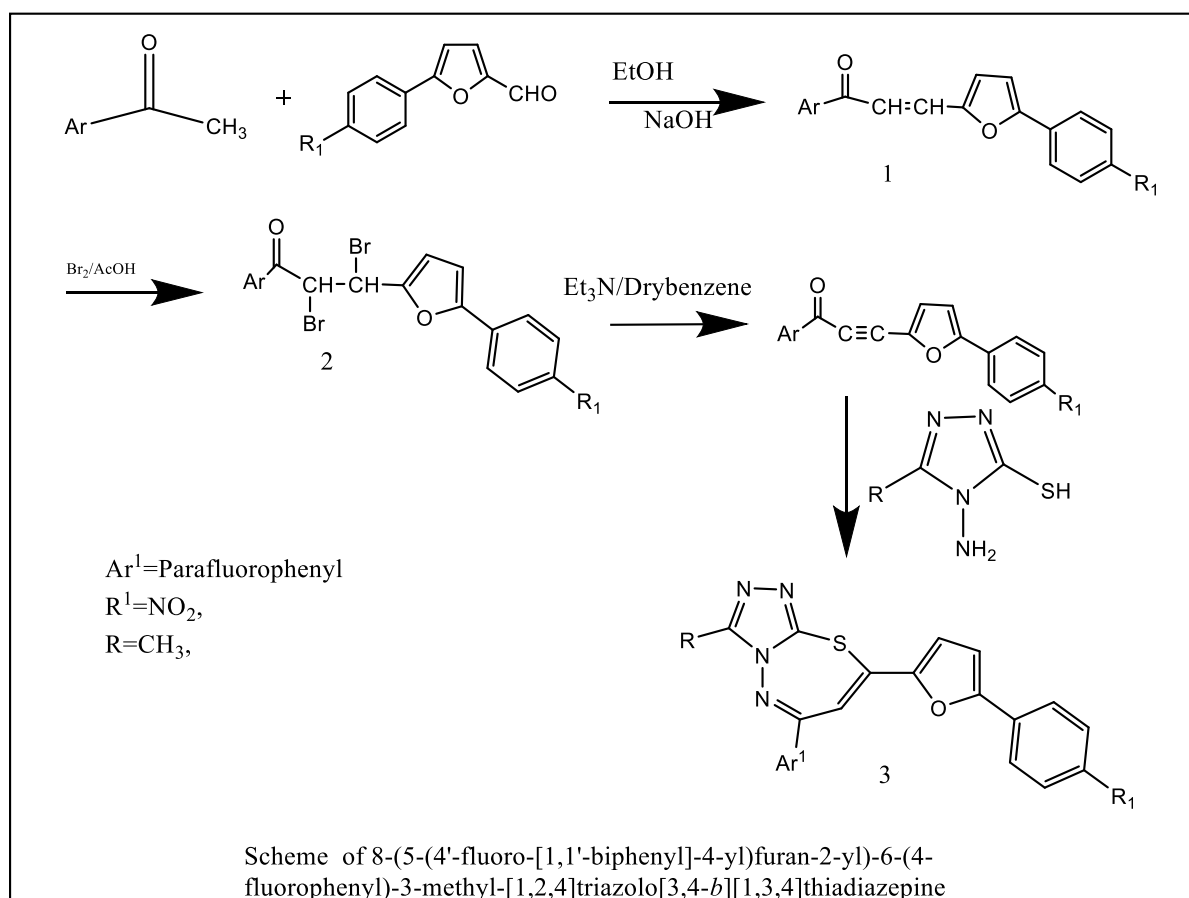


Figure1: scheme of Synthesis of thiazadapines by using acetylenic ketone

Table 1: Percentage yield and molecular weight of compounds

compound No,	R	Ar <sup>1</sup>	R <sup>1</sup>	Yield % m.pt in <sup>o</sup> C	Colour of crystals	Mol wt/ mol formula
1	methyl	4-fluoro-phenyl	4-fluoro 1	60 146 <sup>o</sup> C	Yellow powder	420 C <sub>22</sub> H <sub>14</sub> N <sub>4</sub> SOF <sub>2</sub>
2	methyl	4-fluoro-phenyl	4-chloro	73 132 <sup>o</sup> C	Yellow crystals	436.5 C <sub>22</sub> H <sub>14</sub> N <sub>4</sub> SOCIF
3	methyl	4-fluoro-phenyl	4-bromo -	75 110 <sup>o</sup> C	Yellow crystals	481.0 C <sub>22</sub> H <sub>14</sub> N <sub>4</sub> SOBrF
4	methyl	4-fluoro-phenyl	4-nitro-	69 200 <sup>o</sup> C	Light orange crystals	447 C <sub>22</sub> H <sub>14</sub> N <sub>5</sub> SO <sub>3</sub> F
5	ethyl	4-fluoro-phenyl	4-fluoro	81 202 <sup>o</sup> C	Yellow crystals	434 C <sub>23</sub> H <sub>16</sub> N <sub>4</sub> SOF <sub>2</sub>
6	ethyl	4-fluoro-phenyl	4-chloro-	55 102 <sup>o</sup> C	Yellow flakes	450.5 C <sub>23</sub> H <sub>16</sub> N <sub>4</sub> SOCIF

#### Spectral values of synthesised compounds

##### Compound 1

**H<sup>1</sup> NMR (400 MHz,)** : $\delta$  8.39 – 7.66 (m), 7.66 – 7.55 (m), 6.7-6.45 (m) 4.44 – 4.37 (m), 2.72-2.53 (m), 1.13 – 0.18 (m).

**m/z**=420(M<sup>+</sup>+1)

##### Compound 2:

**H<sup>1</sup>NMR:**  $\delta$  8.37 – 7.64 (m), 7.62 – 7.50 (m), 6.75-6.44 (m) 4.46 – 4.374(m), 2.73-2.51 (m), 1.10 – 0.14 (m).

**m/z**=436.5(M<sup>+</sup>+1)

##### Compound 3:

**H<sup>1</sup>NMR:**  $\delta$  8.28 – 7.52 (m), 7.69 – 7.48 (m), 6.66-6.42 (m) 4.48 – 4.34(m), 2.69-2.49 (m), 1.08 – 0.09 (m).

**m/z**=481(M<sup>+</sup>+1)

##### Compound:4

**H<sup>1</sup>NMR:**  $\delta$  8.21 – 7.48 (m), 7.64 – 7.43 (m), 6.64-6.38 (m) 4.43 – 4.31(m), 2.65-2.45 (m), 1.06 – 0.08 (m).

**m/z**=447(M<sup>+</sup>+1)

##### Compound 5:

**H<sup>1</sup>NMR:**  $\delta$  8.28 – 7.52 (m), 7.69 – 7.48 (m), 6.66-6.42 (m) 4.48 – 4.34(m), 2.69-2.49 (m), 1.08 – 0.09 (m).

$m/z=434(M^++1)$

### Compound 6:

**$^1H$ NMR:**  $\delta$  8.06 – 7.46 (m), 7.62 – 7.41 (m), 6.62-6.39 (m) 4.42 – 4.31(m), 2.62-2.43 (m), 1.06 – 0.07 (m).

$m/z=450.5(M^++1)$

### Biological Activity

#### Evaluation of antibacterial activity.

Determination of minimum inhibitory concentration by tube dilution method [8]

Antibacterial activity as MIC is evaluated by tube dilution method. Double strength Nutrient broth was prepared and autoclaved. Prepared various concentration of stock solution using serial dilution method (100- 1.56 mcg/ml).

Each 2.5ml of this solution double strength nutrient broth 2.5ml is added.

Microorganism was inoculated (E. coli) in all test tubes were incubated at 37°C for 48h

Table 2: Minimum Inhibitory Concentration of compounds

Compounds	Minimum Inhibitory Concentration (mcg/ml)
1	12.5
2	12.4
3	24
4	45
5	48
6	25

The given compounds showed promising antimicrobial activity. The minimum

inhibitory concentration achieved by the compounds was in the range of 12.5 to

50 mcg/ml. Compound 1 and 2 exhibited maximum activity with minimum inhibitory concentration (mic) of 12.5 mcg/ml.

#### Determination of zone of inhibition by cup-plate method. [9]

In this technique, melted agar inoculated with microorganisms is poured into Petri dishes. Wells were made in the agar plate and a specific volume of the antimicrobial substances were placed in them; plates were incubated at 37°C for the specified time. The antimicrobial substance diffuses through agar around its well and produces a clear zone of inhibition. The diameter of this zone gives an estimation of the degree of activity of the antimicrobial substance.

Table 3: Zone of inhibition.

**Std:Ciprofloxacin**

Compounds	Std (ciprofloxacin 5mcg)	C1	C2	C3	C4	C5	C6
Zone of inhibition (mm)	32mm	31.0±0.033	29.07±0.106	19.26±0.12	12.00±0.135	10.74±0.031	22.06±0.65

All the six samples at MIC concentration exhibited antimicrobial activity in the zone of inhibition studies carried out. Compound 1 and 2 showed maximum activity which was comparable to the standard drug ciprofloxacin (5mcg).

### Docking Studies:

#### Introduction

Molecular docking is used as a useful in silico tool to identify possible leads as useful drugs. [8] The proteins selected for molecular docking are common anti-bacterial targets [9], found across many bacterial families. Penicillin Binding Proteins are a set of proteins which are active targets of common penicillins. They are involved in the cross linking of peptidoglycans during cell division [10]. All penicillins like piperacillin, benzylpenicillin etc., and ceftazidime bind to these proteins. Dihydrofolate reductase (DHFR) catalyses the hydrogenation of dihydrofolate to tetrahydrofolate [11]. It is an important enzyme in the biosynthetic pathway of folate synthesis. Trimethoprim is a useful DHFR inhibitor [12]. Tyrosine tRNA ligase is an aminoacyl tRNA ligase, which is important in protein synthesis [13]. A number of new inhibitors for this protein have been developed, as the bacterial and human tyrRS enzymes are quite different [14]. Glutamine Synthetase is involved in the synthesis of glutamine from glutamic acid and ammonia, and is involved in many important cellular processes [15]. New antibacterials developed are important GS targets. [16,17]

### Materials and Methods

#### Ligand Preparation

The ligands Comp1-6 were drawn using Discovery Studio Visualiser 2021.11 and saved as SDF files. The structures were minimised using the MMFF94 forcefield using OpenBabel, for 10000 steps using steepest descent algorithm [12]. The ligands were saved as SDF files and converted to Autodock PDBQT files using OpenBabel. Polar Hydrogens and charges were added while converting to PDBQT. The ligand files were visualised and checked for errors using Discovery Studio 2021.

#### ADME and Toxicology Calculations

To predict the Absorption, Distribution, Metabolism and Excretion properties of the ligands, SwissADME13 web tool was used. The Toxicology studies were taken from pkCSM webserver [14].

#### Protein Preparation

The proteins were downloaded from the RCSB PDB website<sup>15</sup>. The PDB files were visualised using Discovery Studio, and then loaded into the PyRx software, which automatically converted the PDB files to PDBQT files, with polar Hydrogens and Kollmann Charges added. The substrates/known inhibitors of the proteins were downloaded from PubChem database<sup>16</sup>.

### Molecular Docking

The Autodock Vina<sup>17</sup> module in PyRx was used for molecular docking of all proteins, one by one, against its own substrate/inhibitor and the nine ligands. The docking was performed at the active sites of each of the proteins, with an exhaustiveness of 16. The Inhibitory constant  $K_i$  was calculated as  $K_i = \exp(\Delta G/RT)$ , where  $\Delta G$  is the Binding Affinity obtained as Vina Score,  $R$  is the universal gas constant ( $=1.987 \times 10^{-3} \text{ kcal mol}^{-1} \text{ K}^{-1}$ ) and  $T$  is the absolute temperature (298.15K). All the computational studies and visualisations were done using Discovery Studio Visualiser 2021.

## Results and Discussion

Table 4: Protein Structures

PDB ID	Protein Name	Function	Organism	Inhibitor/Substrate
<b>3ocn</b>	Penicillin Binding Protein 3	Cell wall Synthesis	<i>P. aeruginosa</i>	Piperacilin(PIP), Ceftazidine(CTJ)
<b>3srw</b>	Dihydrofolate Reductase	Folic acid metabolism	<i>S. aureus</i>	Trimethoprim
<b>1vbm</b>	Tyrosine tRNA Ligase	Aminoacyl tRNA synthesis	<i>E. coli</i>	Ligand-SB219383
<b>4s0r</b>	Glutamine Synthetase	Amino acid metabolism	<i>B. subtilis</i>	Glutamine

Table 5: Description of the proteins used for molecular docking

### ADMI

Molecule	Comp1	Comp2	Comp3	Comp4	Comp5	Comp6
#Heavy atoms	30	30	30	32	31	31
#Aromatic heavy atoms	22	22	22	22	22	22
#Rotatable bonds	3	3	3	4	4	4
#H-bond acceptors	6	5	5	7	6	5
#H-bond donors	0	0	0	0	0	0

<b>Molecular Refractivity</b>	114.58	119.64	122.33	123.45	119.39	124.44
<b>Topological Polar Surface Area</b>	81.51	81.51	81.51	127.33	81.51	81.51
<b>MLOGP</b>	4.55	4.66	4.76	3.26	4.76	4.87
<b>ESOL Log S</b>	-6.05	-6.48	-6.8	-5.95	-6.32	-6.76
<b>ESOL Solubility (mg/ml)</b>	0.000376	0.000143	7.67E-05	0.000507	0.000207	7.86E-05
<b>ESOL Solubility (mol/l)</b>	8.94E-07	3.28E-07	1.59E-07	1.13E-06	4.76E-07	1.74E-07
<b>ESOL Class</b>	Poorly soluble	Poorly soluble	Poorly soluble	Moderately soluble	Poorly soluble	Poorly soluble
<b>GI absorption</b>	High	High	High	Low	High	High
<b>BBB permeant</b>	No	No	No	No	No	No
<b>Pgp substrate</b>	No	No	No	No	No	No
<b>CYP1A2 inhibitor</b>	Yes	Yes	Yes	Yes	Yes	Yes
<b>CYP2C19 inhibitor</b>	Yes	Yes	Yes	Yes	Yes	Yes
<b>CYP2C9 inhibitor</b>	Yes	Yes	Yes	Yes	Yes	Yes
<b>CYP2D6 inhibitor</b>	No	No	No	No	No	No
<b>CYP3A4 inhibitor</b>	No	No	No	No	No	No
<b>Skin Permeability(log Kp (cm/s))</b>	-5.19	-4.92	-5.15	-5.55	-4.97	-4.7
<b>Lipinski #violations</b>	1	1	1	0	1	1
<b>Bioavailability Score</b>	0.55	0.55	0.55	0.55	0.55	0.55
<b>PAINS #alerts</b>	0	0	0	0	0	0

Table 6: ADME Prediction of the compounds 1-6.

**Toxicity Prediction**

<b>Compound</b>	<b>Unit</b>	<b>Comp 1</b>	<b>Comp 2</b>	<b>Comp 3</b>	<b>Comp 4</b>	<b>Comp 5</b>	<b>Comp 6</b>
<b>AMES toxicity</b>	Categorical (Yes/No)	No	No	No	Yes	No	No
<b>Max. tolerated dose (human)</b>	Numeric (log mg/kg/day)	0.248	0.144	0.149	0.466	0.427	0.33
<b>hERG I inhibitor</b>	Categorical (Yes/No)	No	No	No	No	No	No
<b>hERG II inhibitor</b>	Categorical (Yes/No)	Yes	Yes	Yes	Yes	Yes	Yes

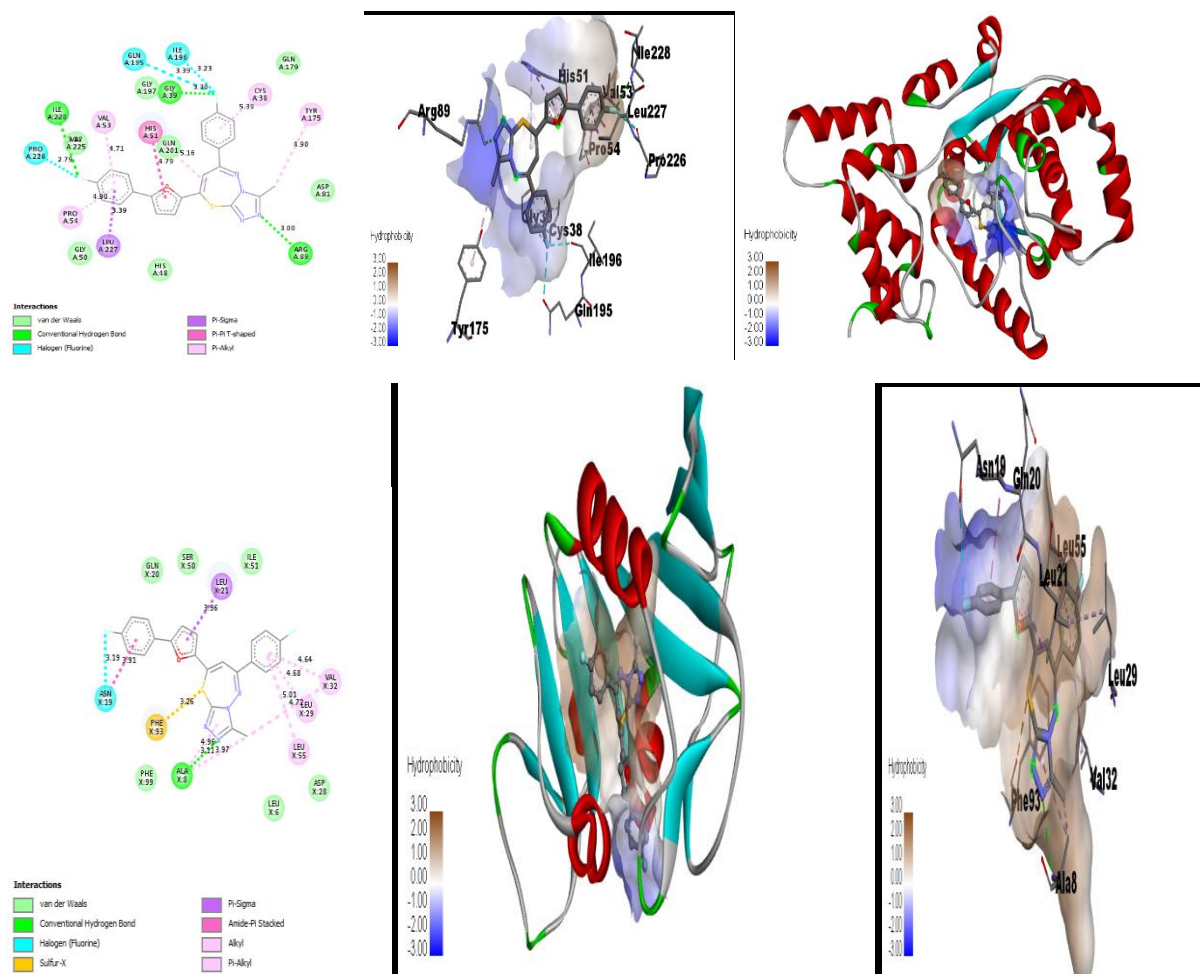
<b>Oral Acute Toxicity (LD50)</b>	<b>Rat</b>	Numeric (mol/kg)	2.64	2.578	2.584	2.968	2.797	2.72
<b>Oral Chronic Toxicity (LOAEL)</b>	<b>Rat</b>	Numeric (log mg/kg_bw/day)	0.926	0.811	0.801	0.767	0.774	0.66
<b>Hepatotoxicity</b>		Categorical (Yes/No)	No	No	No	No	No	No
<b>Skin Sensitisation</b>		Categorical (Yes/No)	No	No	No	No	No	No
<b>T.Pyriformis toxicity</b>		Numeric (log ug/L)	0.29	0.292	0.292	0.286	0.29	0.292
<b>Minnow toxicity</b>		Numeric (log mM)	-2.102	-2.65	-2.796	-3.689	-2.053	-2.601

Table 7: Docking Results

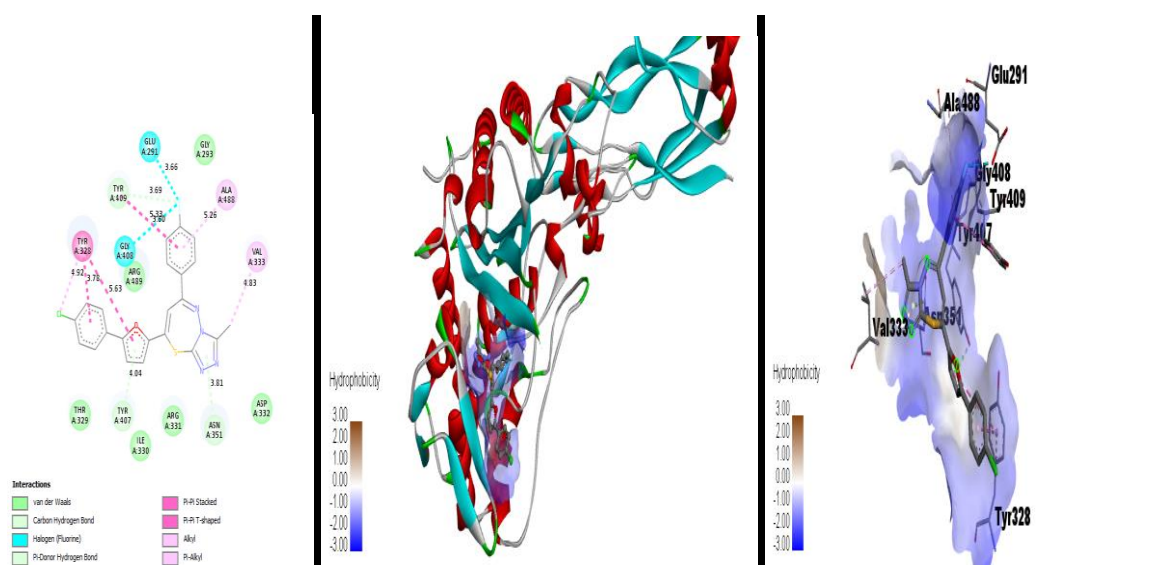
Ligand	Proteins							
	1vbm		3ocn		3srw		4s0r	
	Binding Energy (kcal/mol)	Inhibitory Constant Ki(nM)	Binding Energy (kcal/mol)	Inhibitory Constant Ki(nM)	Binding Energy (kcal/mol)	Inhibitory Constant Ki(nM)	Binding Energy (kcal/mol)	Inhibitory Constant Ki(nM)
<b>Comp1</b>	-10.6	16.96	-9.7	77.47	-11.4	4.39	-8.4	695.22
<b>Comp2</b>	-10.4	23.77	-9.8	65.44	-11.2	6.16	-8.4	695.22
<b>Comp3</b>	-10.4	23.77	-9.8	65.44	-11.0	8.63	-7.7	2266.11
<b>Comp4</b>	-10.3	28.14	-9.6	91.71	-11.3	5.20	-8.5	587.24
<b>Comp5</b>	-10.0	46.69	-9.7	77.47	-11.4	4.39	-8.2	974.41
<b>Comp6</b>	-9.9	55.27	-9.7	77.47	-11.2	6.16	-8.2	974.41
<b>LigSB</b>	-8.6	496.03	-	-	-	-	-	-
<b>CTJ</b>	-	-	-8.2	974.41	-	-	-	-
<b>PIP</b>	-	-	-9.5	108.58	-	-	-	-
<b>TRI</b>	-	-	-	-	-7.5	3176.12	-	-
<b>GLN</b>	-	-	-	-	-	-	-5.7	66289.01

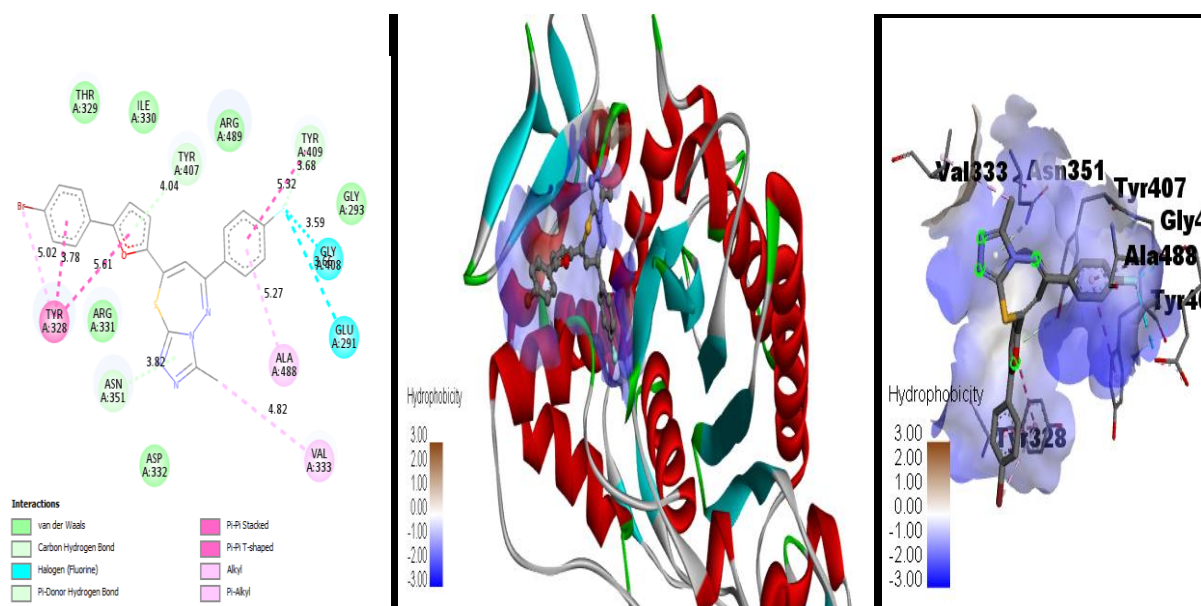
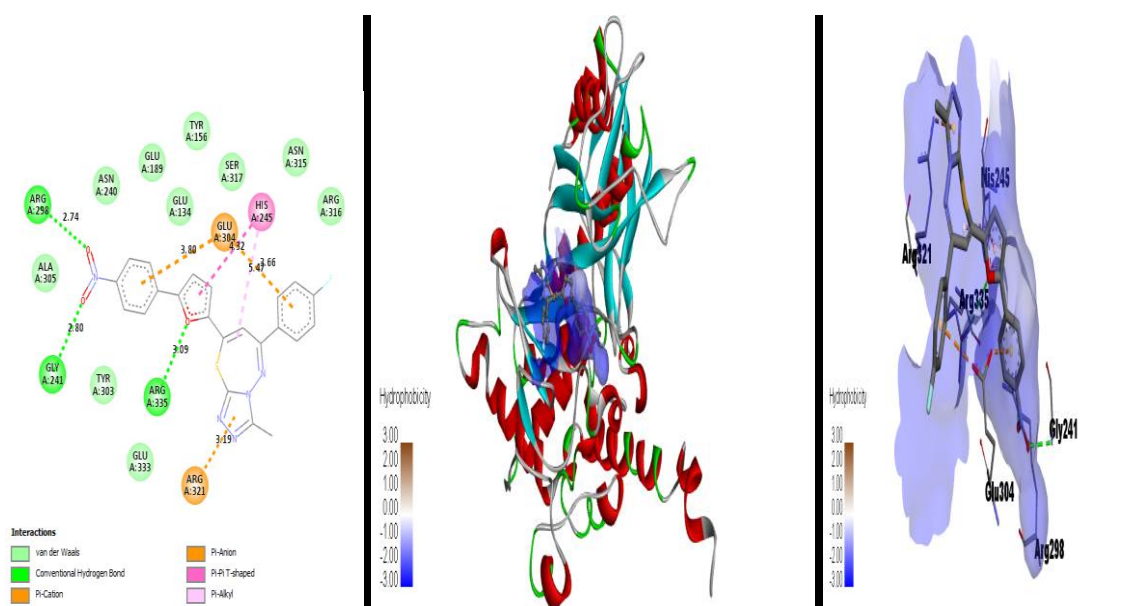
Compound:1

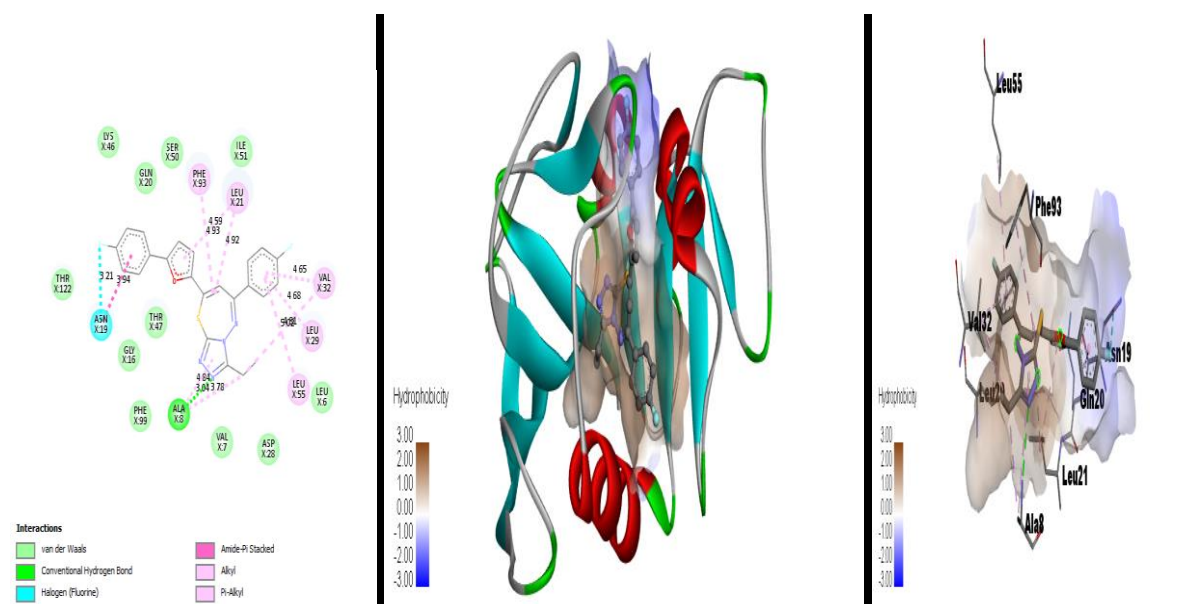




## Compound:2



**Compound:3****Compound:4**

**Compound:5****Result and discussion:**

A series of 6-(4-fluorophenyl)-8-(5-(4-nitrophenyl) furan-2-yl)-[1,2,4] triazolo[3,4-b][1,3,4]thiadiazepines were synthesised and screened these molecules for antimicrobial activity and it was tested for cytotoxicity test and Docking scores for all the compounds are quite good against all the proteins. Among them, compounds 1 and 2 show best activities, having either the highest or second highest docking scores among the molecules. Compounds 1 and 2 can be potential leads as anti bacteria. From spectral studies we confirmed the structures by Mass as well as from NMR values all showed nearly same values in aromatic region.

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**Conflict of interest:**

No conflict of interests

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