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## The Biological Activities, Molecular Docking Studies, and Anticancer Effects of 1-Arylsulfonylpyrazole Derivatives

Parham Taslimi<sup>1\*</sup>, Yavuz Erden<sup>2</sup>, Sabir Mamedov<sup>3</sup>, Lala Zeynalova<sup>3</sup>, Nina Ladokhina<sup>3</sup>, Recep Tas<sup>1</sup>, Burak Tuzun<sup>4\*</sup>, Afsun Sujayev<sup>3</sup>, Nastaran Sadeghian<sup>5</sup>, Saleh H. Alwasel<sup>6</sup>, Ilhami Gulcin<sup>5</sup>

<sup>1</sup>Department of Biotechnology, Faculty of Science, Bartin University, 74100 Bartin, Turkey

<sup>2</sup>Department of Molecular Biology and Genetics, Faculty of Science, Bartin University, 74100 Bartin, Turkey

<sup>3</sup>Laboratory of Faine Organic Synthesis, Institute of Chemistry of Additives, Azerbaijan National Academy of Sciences, 1029, Baku, Azerbaijan

<sup>4</sup>Department of Chemistry, Faculty of Sciences, Cumhuriyet University, 58140, Sivas, Turkey

<sup>5</sup>Department of Chemistry, Faculty of Sciences, Ataturk University, 25240, Erzurum, Turkey

<sup>6</sup>Zoology Department, College of Science, King Saud University, Riyadh, Saudi Arabia

\*Address for Correspondences: Dr. Burak Tüzün, Faculty of Science, Department of Chemistry, Sivas Cumhuriyet University, 58140-Sivas, Turkey. E-mail: Theburaktuzun@yahoo.com;

\*Parham Taslimi Ph.D., Department of Biotechnology, Faculty of Science, Bartin University, 74100 Bartin, Turkey. Email: parham\_taslimi\_un@yahoo.com; ptaslimi@bartin.edu.tr

### ABSTRACT

This work is devoted to definition of the direction of reaction between 1-benzenesulfonylimino pyridinium chloride and  $\alpha$ - or  $\beta$ -halo-containing sulfamides, chloroacetic acid, 1-chloro-2,3-dihydroxypropane, etc. The optimal conditions for the synchronous reaction of heterocyclization are determined. Benzenesulfonyliminopyridinium chloride was obtained to form pyrazolopyridines with 1,2-polarophiles, and pyridazine pyridines with 1,3-polarophiles. These novel derivatives were found as effective inhibitors of the  $\alpha$ -glycosidase with  $K_i$  values in the range of  $13.66 \pm 2.63$ - $60.63 \pm 12.71$  nM. The molecules (**II-X**) against enzyme were compared theoretically with the help of molecular docking to compare biological activities. The results were compared with the numerical values of the parameters obtained from molecular docking calculations and found to be in great agreement with the experimental results. However, ADME analysis of molecules was performed. Also, the compounds exhibited significant anticancer effect depending on the doses administered.

**Key words:** Pyrazolopyridines; pyridazine pyridines; anticancer; enzyme inhibition; molecular docking

## 1. INTRODUCTION

Creation of the new physiological active compounds with desired biological properties, as well as determination of the link between the chemical structure of synthesized compounds and their biological activity, and expansion of the range of their actions is among the most important problems of organic chemistry today. Among condensed heterocycles, pyrazolo- or pyridazopyridines, which have a wide spectrum of biological activity, occupy a special place. Condensed pyridines have a pronounced inhibitory effect of cholinesterase and are widely used in pharmacy and medicine. Among them, pyridostigmine bromide, quinotilin, and alloxime are the most known ones. Pyrazolo-pyridines are very strong inhibitors of  $\gamma$ -secretase (Ye et al., 2013) and dihydropyrazolopyridinyl sulfamides have an autoimmune property (Herrey et al., 2004). Pyridazonyl sulfamide derivatives exhibit strong antimicrobial activity. As can be seen from the examples given above, urea and tiourea fragments contain different application areas. New synthesized compounds and active heterocycle rings show that it is necessary to examine their various properties. Moreover, there is no systematic study of the effect of cyclic chains and different functional groups on the chemical properties of the compounds containing the ring in the literature in relation to various side effects with different side effects (Mohamed, 2007). On the basis of the synthesized sulphamides obtain functionally substituted pyrazolin-, pyrazolidone-, -imidazole- and pyrimidine sulfonamides. It is revealed that reaction of arylsulfochlorides with alkyldiamines with high yield give only bis- sulphamides, and with carbamyl guanidine only monosulphamide. Synthesized polyamine sulphamides and their derivatives were tested in different areas. Regularities between structure, composition and properties are defined (Mamedov, 2007; Farzaliev 2010).

Carbohydrate digestive enzymes are found in the brush border of the intestine and break down the long-chain polysaccharides into simple absorbable monosaccharide units including glucose. Indeed,  $\alpha$ -glycosidase enzymes play a key role in the lysis of  $\alpha$ -glucopyranoside bond in disaccharides and oligosaccharides to release monosaccharide molecules, which then get absorbed in the body and thus regulate glucose availability and the degree of postprandial hyperglycemia. Hence, the inhibition of  $\alpha$ -glycosidase is recorded as a prime aim to develop and discover novel potent and less toxic antidiabetic drugs (Demir et al., 2019; Bilgicli et al., 2019; Kaya et al., 2019; Çağlayan et al., 2019). Theoretical calculations have become widespread. One of the main reasons for this is that it is possible to make a clearer comparison of theoretical calculations in less time. The theoretical method used in this study is molecular docking. Molecular docking studies compare biological activities of molecules with enzymes (Tüzün 2020; Tüzün and kaya 2018; Mamedova et al., 2019).

In this study, we performed the design, biological evaluation of some of 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridine (**I-X**) which compounds (**II-X**) were as effective  $\alpha$ -glycosidase inhibitors. Also anticancer studies were performed on these compounds. Another goal of this work, is compared their inhibitory results with control compounds like acarbose. Lastly, the biological activity of molecules (**II-X**) against  $\alpha$ -glycosidase enzyme, ID 1R47, was compared. ADME (Absorption, Distribution, Metabolism and Excretion) analysis (Mermer et al., 2019; Sari et al., 2019; Şener et al., 2019; Altındağ et al., 2019; Singh and Bast 2014; Sağlık et al., 2019; Tao et al., 2013) of the molecules was carried out so that the molecules can be used as drugs in the future. As a result of this analysis, if the numerical values of the obtained parameters fall within certain ranges, the molecule is said to be a drug.

## 2. EXPERIMENTAL

### 2.1. General chemistry

For synthesis of 1-benzenesulfonamide-2-R-3-Z-1,2-dihydropyrazolo[1,5-a]pyridines (**I-III**) 0.001 mol of N-benzenesulfonamidepyridinium chloride and 0.001 mol of dipolar (1,2-dichloro-3-benzenesulfamide, chloroacetic acid,  $\beta$ -bromopropionic acid, 1-chloro-2,3-dihydroxypropane) were dissolved in 50 ml of ethanol. To the solution was added dropwise a solution of NaOH (0.002 mol) in ethanol. It was boiled until complete precipitation of NaCl or NaBr (5.5 - 6.0 hour). It was cooled and filtered, then, the filtrate was evaporated to half the volume, cooled and the precipitated crystals were recrystallized from ethanol.

For synthesis of 6,6-dimethyl-4-oxycyclohexane-2,3-pyrazolo-1-phenylsulfamido [1,5-a] pyridine (**IV**) 4.2 g (0.03 mol) of dimedone and 8.12 g (0.03 mol) of pyridinimine were dissolved in 20 mL of ethanol. With stirring, a 7% alkali solution (1.5 g of NaOH in 40 mL of ethanol) was added dropwise. Then the mixture was heated for 5-6 hours, half the volume of the alcohol was distilled off, cooled, 20 mL of water was added and the crystals obtained were filtered. Then they were recrystallized in ethanol. The method of obtaining is similar to the method of synthesis of compounds (**V-X**). However, 0.15 mmol of morpholine is taken, instead of alkali. The structure of all substances was confirmed by modern physical and chemical analysis (Tao et al., 2013).

### 2.2. Enzymes studies

#### 2.2.1. $\alpha$ -Glycosidase enzyme assay

$\alpha$ -Glycosidase inhibitory efficacy of novel 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridine (**II-X**) was performed using p-nitrophenyl-D-glycopyranoside (p-NPG) as the substrate,

according to the procedure of Tao et al. (2013) as described previously (Gulcin et al., 2019; Burmaoglu et al., 2019). The samples were prepared by dissolving 10 mg in 10 mL (EtOH:H<sub>2</sub>O). First, 100 µL of phosphate buffer was mixed with 20 µL of the enzyme solution in phosphate buffer (0.15 U/mL, pH 7.4) and 10-100 µL of the sample. Multiple solutions in phosphate buffer were prepared in case of getting full enzyme inhibition. Then, it was pre-incubated at 35 °C for 15 min previous by adding the p-NPG to the initiation of the reaction. Also, after preincubation, 50 µL of p-NPG in phosphate buffer (5 mM, pH 7.4) was added and re-incubated at 37 °C. The absorbances of samples were spectrophotometrically measured at 405 nm (Maharramov et al., 2019; Eruygur et al., 2019; Aktaş et al., 2019). The IC<sub>50</sub> values were calculated from activity (%) versus novel 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridine (**II-X**) concentration plots. Lineweaver-Burk graphs were used to determine the K<sub>i</sub> values (Aktas et al., 2020; Bal et al., 2020;).

### **2.3. Anticancer studies**

#### **2.3.1. Proliferation of cells**

Human prostate (PC-3, ATCC) and breast (MCF-7, ATCC) cancer cell lines were used to determine the anticancer properties of the tested compounds. Cells were first extracted from liquid nitrogen and then cultured in 75 cm<sup>2</sup> culture flasks. Cultured PC-3 cells were prepared with RPMI-1640 (Sigma-Aldrich R8758, USA) medium (prepared by adding 10% FBS, 100 U/mL Penicillin and 0.1 mg/mL Streptomycin), and MCF-7 cells were DMEM (Gibco 41965039, UK) medium (prepared by adding 10% FBS, 100 U/mL Penicillin and 0.1 mg/mL Streptomycin, 10 µg/mL insulin). The media of the cells were changed twice a week and the cells were incubated at 37 °C (Thermo Forma II CO<sub>2</sub> Incubator, USA) with CO<sub>2</sub> (5%) in all steps. Cells that were confluent at the base of the flask were removed from the flasks using trypsin-EDTA (Gibco 25300054, UK) and stained with 0.4% trypan blue followed by cell counts under an inverted microscope (Optec BDS400, China). Experimental studies were initiated when cell viability was 90% or more (Koyunoglu et al., 2013).

#### **2.3.2. Cell Viability (MTT assay)**

The effect of test compounds on viability in human prostate and breast cancer cells was determined by the 3- (4,5-dimethylthiazol-2-yl)-diphenyltetrazolium bromide (MTT) method, which is widely used in the assessment of cell viability. Cells of which viability levels were determined were cultured in 96-well plates with 15x10<sup>3</sup> cells per well. The plates were incubated for one day in CO<sub>2</sub> medium and then the test compounds were treated with concentrations of 1,

5, 25, 50 and 100  $\mu\text{M}$  prepared in DMSO for 24 hours. After this time, 0.5 mg/mL MTT (Sigma-Aldrich M2128, USA) working solution was prepared to determine the changes in cell viability and 100  $\mu\text{L}$  of the prepared MTT solution was added to each well and incubated for 3 hours in a  $\text{CO}_2$  incubator. At the end of incubation, the optical densities of the cells in the plates were read in the microplate reader (Thermo MultiskanGo, USA) at a wavelength of 570 nm (Mosmann 1983). Control wells (wells with cells and medium only) were recorded; the obtained mean absorbance values were accepted as 100% viable cells. The absorbance values obtained from the wells treated with vehicle control (DMSO) and test compounds were proportional to the control absorbance value and percent viability values were calculated (Tekin et al., 2015; Koran et al., 2017). The effect of compounds on cell viability was analyzed in comparison to control and solvent. These experiments were repeated 5 times independently on different days.

### 2.3.3. Statistical Analysis

Statistical analyzes were performed using GraphPad Prism 5 package program. Homogeneity of the variances was evaluated by Bartlett tests test. One-way ANOVA was used to determine the differences between the groups and Bonferroni test was used for multiple comparisons. Quantitative data were expressed as mean  $\pm$  standard error (mean $\pm$ SD) and  $p < 0.05$  was considered significant.

### 2.4. Docking Study

Bioinformatics chemistry has been greatly influenced by advances in technology and informatics. Bioinformatic chemistry has become widely used in the design of new drugs and active substances (Kaya et al., 2016). Theoretically, there are many programs for the design of new drugs and active substances in bioinformatic chemistry. Molecular docking is one of the methods developed for this. In this study, biological activity value of molecules was calculated by using molecular docking method (Bilgiçli et al., 2019; Günsel et al., 2019; Tüzün and saripinar, 2019). The molecules were first optimized using the Gaussian package program (Frisch et al., 2009). \*.pdb extension files were created using optimized structures. The enzyme  $\alpha$ -glycosidase file was obtained from the RCSB Protein Data Bank website. The RCSB Protein Data Bank builds upon the data by creating tools and resources for research and education in molecular biology, structural biology, computational biology, and beyond. Maestro Molecular modeling platform (version 12.2) by Schrödinger, LLC was used to calculate biological activity values of 1-Arylsulfonylpyrazole derivatives against enzymes (Schrodinger 2019).

### 3. RESULTS

#### 3.1. Chemistry

Our research has shown that the reaction of heterocyclization of a dipolarophile with 1-(arylsulfonyl)iminopyridine (comp. A), the nature and content of the electron-withdrawing group in their composition have little effect. For example, the reaction of compound (A) with 1,2-dichloro-3-benzenesulfonamide produces 1-benzenesulfanilamido-3-benzenesulfamidomethylpyrazolo [1,5-a] pyridine. Probably, in the presence of alkali, nucleophilic substitution of hydrogen of sulfamide nitrogen by chlorine in secondary carbon occurs, followed by substitution of pyridine hydrogen and closure of the heterocycle. In the interaction of sulfonyliminopyridinium with chloroacetic and  $\alpha$ -bromopropionic acid, 1-(benzenesulfonyl)pyrazolo [1,5-a] pyridinones are formed. Compounds **II** and **III** dissolved in 15-20% alkali, which proves the presence of keto-enol tautomerism. Sulfonyliminopyridine with cyclic diketones (Dimedone) in the presence of a base also easily reacts to heterocyclization. It was established that the reaction of sulfonyliminopyridine with chloromethyl- or nitrilaziridine sulfamides and with epichlorohydrin produces 1-(benzenesulfonyl)pyridazino- [1,6-a] pyridines. The outputs of compound **VII** are lower than those of compounds **V** and **VI**. This can be explained by the fact that when using 2-chloroxyrane, the opening of the epoxy group is difficult. Sulfamidopyridinimine in the presence of alkali enters easily into a heterocyclization reaction with diacetone alcohol and with 1-chloro-2,3-hydroxypropane. The yields of compounds **VIII**, **IX** and **X** are lower than those of other pyridazine pyridines (60-85%). Heterocyclization with benzoin takes place with brief heating (Mamedova et al., 2019). All reactions were shown in the Scheme 1.

#### 3.2. Biochemical Results

##### 3.2.1. Enzymes Results

For the  $\alpha$ -glycosidase enzyme, the novel 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridine (**II-X**) compounds had  $IC_{50}$  values in the range of 11.73–58.53 nM and  $K_i$  values in the range of  $13.66 \pm 2.63$ – $60.63 \pm 12.71$  nM (Table 1 and Figure 1). The results obviously showed that all novel 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridines (**II-X**) demonstrated efficient  $\alpha$ -glycosidase inhibitory effects than that of acarbose ( $IC_{50}$ : 22.80  $\mu$ M,  $K_i$ : 12.60  $\mu$ M) (Foroumadi et al., 2005) as a standard  $\alpha$ -glycosidase inhibitor. However, the most effective  $K_i$  values were obtained by compounds **III** and **II**, with  $K_i$  values of  $13.66 \pm 2.63$  and  $26.93 \pm 3.84$  nM, respectively.

##### 3.2.2. Anticancer results

The changes in cell viability in human prostate (PC-3) and breast (MCF-7) cancer cell lines after 24 hours of treatment with test compounds are shown in Figures 2 and 3, respectively. Accordingly, concentrations of 5  $\mu$ M and above of all compounds significantly reduced PC-3 cell viability compared to control groups ( $p < 0.05$ ; Figure 2).

There was no significant change in MCF-7 cell viability after treatment with compound MS72 as compared to control groups. Although all the concentrations of compound MS50 reduced MCF-7 cell viability compared to the control group ( $p < 0.05$ ), no significant difference was found compared to the solvent control. All other compounds were found to reduce MCF-7 cell viability, especially concentrations of 25  $\mu$ M and above compared to control groups ( $p < 0.05$ ; Figure 3).

### 3.2.3. Docking result

Many parameters were obtained as a result of docking study of 1-arylsulphonylpyrazole derivatives against enzyme  $\alpha$ -glycosidase, which is ID: 1R47. The biological activities of the molecules are compared using the numerical values of these parameters. This parameter provides guidance for experimental studies in designing new drugs and active substances (Mamedova et al., 2019). The interaction of molecules with enzyme  $\alpha$ -glycosidase is the most important factor to increase the biological activity values. Interactions between molecules and enzyme are the most important factors affecting the biological activity value of molecules in Figure 4. These interactions have many interactions such as hydrogen bonds, polar and hydrophobic interactions,  $\pi$ - $\pi$  and halogen bonds (Sayın and Karakaş 2017, 2018, 2018, Sayın and Üngördü 2018, 2019, Üngördü and Sayın 2019, Tüzün and Sayın 2019, Tüzün 2020).

Molecular docking calculations were made at pH  $7.0 \pm 2.0$  ranges. The most important reason for this is that the pH of the enzyme studied is the most active in the human body at pH 7.35, which is the pH of human blood (Friesner et al., 2006). The parameters obtained as a result of the structure calculations are given in Table 2.

To examine the interactions of 1-arylsulphonylpyrazole derivatives with the proteins that make up the enzyme, it was initially prepared using the protein preparation module (Friesner et al., 2006, Schrödinger Release 2019), the  $\alpha$ -glycosidase enzyme crystalline, which is ID: 1R47. The water molecules in the enzyme were removed using this module. However, binding methods and protein loads in the enzyme structure were optimized using this module. The most active region of the enzyme was found by evaluating with the proteins that make up the enzyme. Freedom of movement was given during the interaction with 1-arylsulphonylpyrazole derivatives for the proteins in the active region of the enzyme. LigPrep module (Sastry et al., 2013, Schrödinger



Release 2019-4) was used to prepare 1-arylsulfonylpyrazole derivatives for molecular docking calculations. Then, 3D structures of 1-arylsulfonylpyrazole derivatives, correct protonation status at physiological pH and molecular geometries of 1-arylsulfonylpyrazole derivatives were obtained using this module. After the preparation of 1-arylsulfonylpyrazole derivatives, enzymes were interacted with 1-arylsulfonylpyrazole derivatives using the Glide ligand-docking (Du et al., 2019) module.

After interactions of enzymes with 1-arylsulfonylpyrazole derivatives, the possibilities of 1-arylsulfonylpyrazole derivatives to be drugs were investigated. ADME (Absorption, distribution, metabolism, excretion, and toxicity) analysis was used for this examination. The Qik-prop module (Schrödinger Release 2020-1) of Schrödinger was used to perform this analysis. Using this module, drug properties of molecules are examined. Many parameters are obtained at the end of this examination. The most important parameters among these parameters are molecular weight, QP log  $P_{o/w}$  donorHB, acptHB, rule of five, and rule of three, etc (Jorgensen and Duffy 2002, Lu et al., 2004, Lipinski et al., 2001).

#### 4. DISCUSSION

It was established that the reactions between arylsulfochlorides and polyamines are always obtained mono- and disulfonamides despite excessive double molar concentration of amine in literature (Gulçin et al., 2018). Type 2 diabetes mellitus is determined by insulin resistance, which may be combined with relatively decreased insulin secretion and lead to hyperglycemia. This disease can cause many disorders or complications, which happen in several organs causing serious health issues, often retinopathy and nephropathy (Boztas et al., 2019). One of the goals for hyperglycemia reduction is to decrease the activity of  $\alpha$ -glycosidase responsible for carbohydrates hydrolysis. The  $\alpha$ -glycosidase inhibitors delay the absorption of sugars in the intestinal tract, thus limiting the excursions of postprandial plasma glucose. Indeed, acarbose compound is an oral  $\alpha$ -glycosidase inhibitor (Taslimi and Gulçin 2017, Song et al., 2019).

Interactions of 1-arylsulfonylpyrazole derivatives with enzymes formed by proteins are examined in Figure 5. When many parameters obtained as a result of the calculations are examined, the docking score parameter is the most important parameter among these parameters (Sağlık et al., 2019, Ertaş et al., 2019, Kecel-Gunduz et al., 2020). The molecule with the most negative numerical value of this parameter has the highest biological activity. Therefore, the biological activity values of the molecules are compared according to the numerical value of this parameter. On the other hand, many parameters are obtained other than this parameter; these other parameters are used to explain the interaction of molecules and enzymes. In molecular

docking calculations, the Glide H-bond parameter is the term residue interaction per hydrogen bond. The total of individual H-bond points for H-bonds between 1-arylsulphonylpyrazole derivatives and a particular residue. If the numerical value of this parameter is more negative, it means stronger H-bond. The types of atoms in the H-bonds and the geometry of the H-bonds influence the numerical value of this parameter. Glide emodel parameter is the energy of the interaction model obtained. This parameter is the combination of the numerical value of many parameters. Glide ligand efficiency parameter is a numerical value that gives information about the effectiveness of ligand molecules. It should be well known that the most important thing affecting the biological activity of molecules is the interaction between the molecule and enzymes (Bıçak et al., 2019, Budama-Kilinc et al., 2019, Mermer et al., 2019). As these interactions increase, the biological activities of the molecules increase.

Since the interactions of molecules with enzymes are examined, it is investigated that molecules can be used as drugs in the future. In order to use a molecule as a drug, ADME analysis of the molecules was done in Table 3. The numerical values of the parameters obtained by this analysis must be within a certain range. If those parameters of the molecule are not in that range, it is thought that the molecule cannot be a drug. Experimental work in the future is not recommended. However, if the numerical values of all parameters provide the conditions, it is said that experiments are appropriate for future medication. However, no value was found in the ADME analysis of molecule V. Because the ADME analysis values of the molecule are very bad, no value could be obtained. As a result of ADME analysis, there are many parameters obtained, among these parameters, Lipinski Rule of 5 and Jorgensen Rule of 3, which are known as the Pfizer 5 rule, are the most important parameters (Bayrak et al., 2019, Karimov et al., 2020, Demir 2020, Shah et al., 2020). In the 5 rules of Lipinski, the number of hydrogen binding atoms in the molecule studied will not be more than 5 (nitrogen and oxygen atoms for one or more hydrogen atoms attached to it). In addition, the number of atoms that accept hydrogen bonds in the studied molecule are 10 (nitrogen and the number of oxygen atoms) will not exceed. In addition, its molecular weight should be under 500 Daltons and the lipophilic coefficient ( $\log p$ ) below 5. Small molecules that follow these rules are thought to have the potential to be medicines. Another parameter is Solute as Donor-Hydrogen Bonds, which is the estimated hydrogen bond sequence to be given to the aqueous solution. Another parameter is Solute as Acceptor-Hydrogen, which is the estimated number of hydrogen bonds to be accepted by the substance dissolved from water molecules in an aqueous solution (Bayindir et al., 2019, Acar et al., 2019, Menteşe et al., 2019, Türkan et al., 2019, Celik et al., 2020).

## 5. CONCLUSIONS

The effectiveness of the inhibitor action of the synthesized compounds depends not only on the composition of the functional groups, but also on the nature of the heterocycle and the location of the functional groups. Each of the studied drugs has a relatively long latent period of action. This is probably due to the difficulty of transporting the toxophore molecules through the cell walls of microorganisms to the vital centers they suppress. One of the goals of AD therapy is to enhance the level of acetylcholine in the brain by inhibiting AChE. Patients with the neurodegenerative disease treated with these inhibitors present undesirable effects like nausea, diarrhea, gastrointestinal anomalies, and hepatotoxicity.  $\alpha$ -Glycosidase inhibition is a logical process in the effective management of type 2 diabetes. Various inhibitors of this enzyme class are in clinical utilize but are riddled with potency, efficacy, and safety challenges. Additionally, novel effective  $\alpha$ -glycosidase inhibitors are under evaluation. In molecular docking studies, the parameters obtained from the interaction of molecules with enzyme showed that molecule III has the highest biological activity. The theoretical results were in great agreement with the experimental results.

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## Conflicts of interests

The authors declare that no conflicts of interests.

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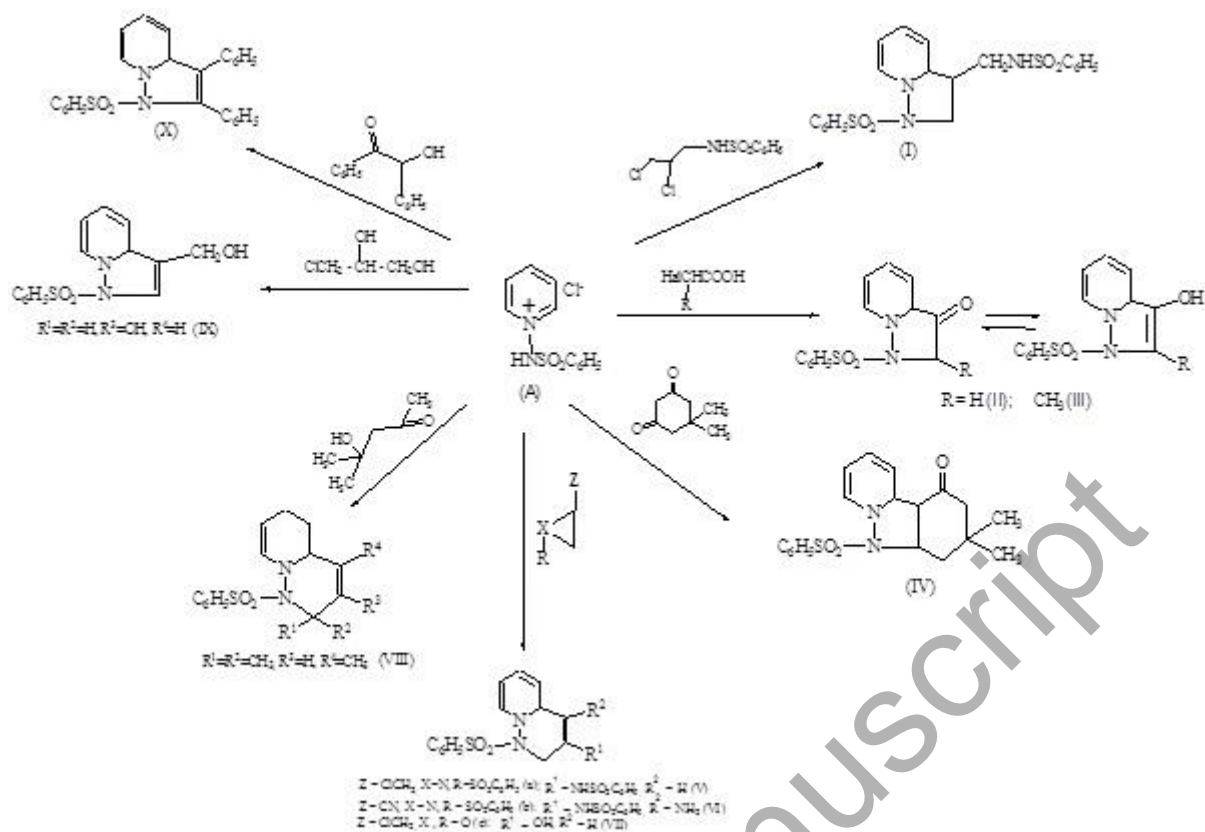
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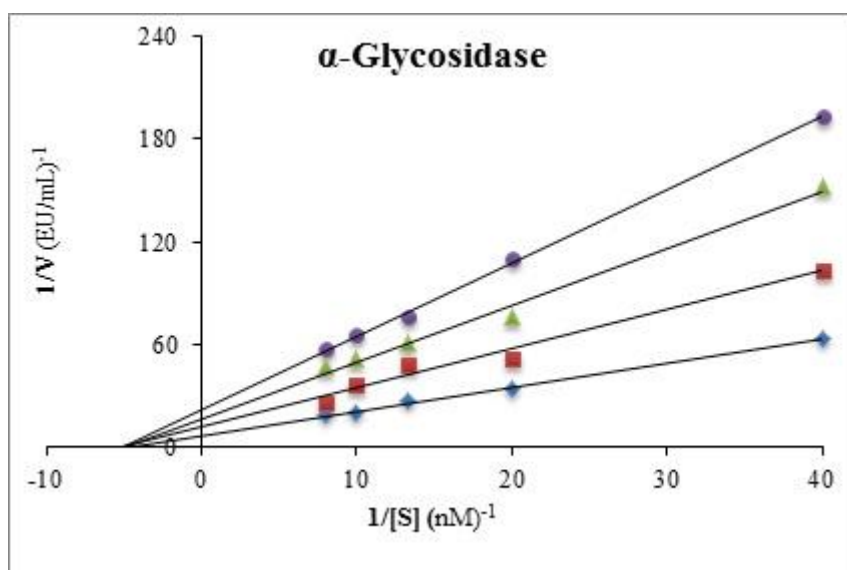
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**Scheme 1.** The heterocyclization reaction of sulfamidopyridinimine with benzoin (**I-X**)



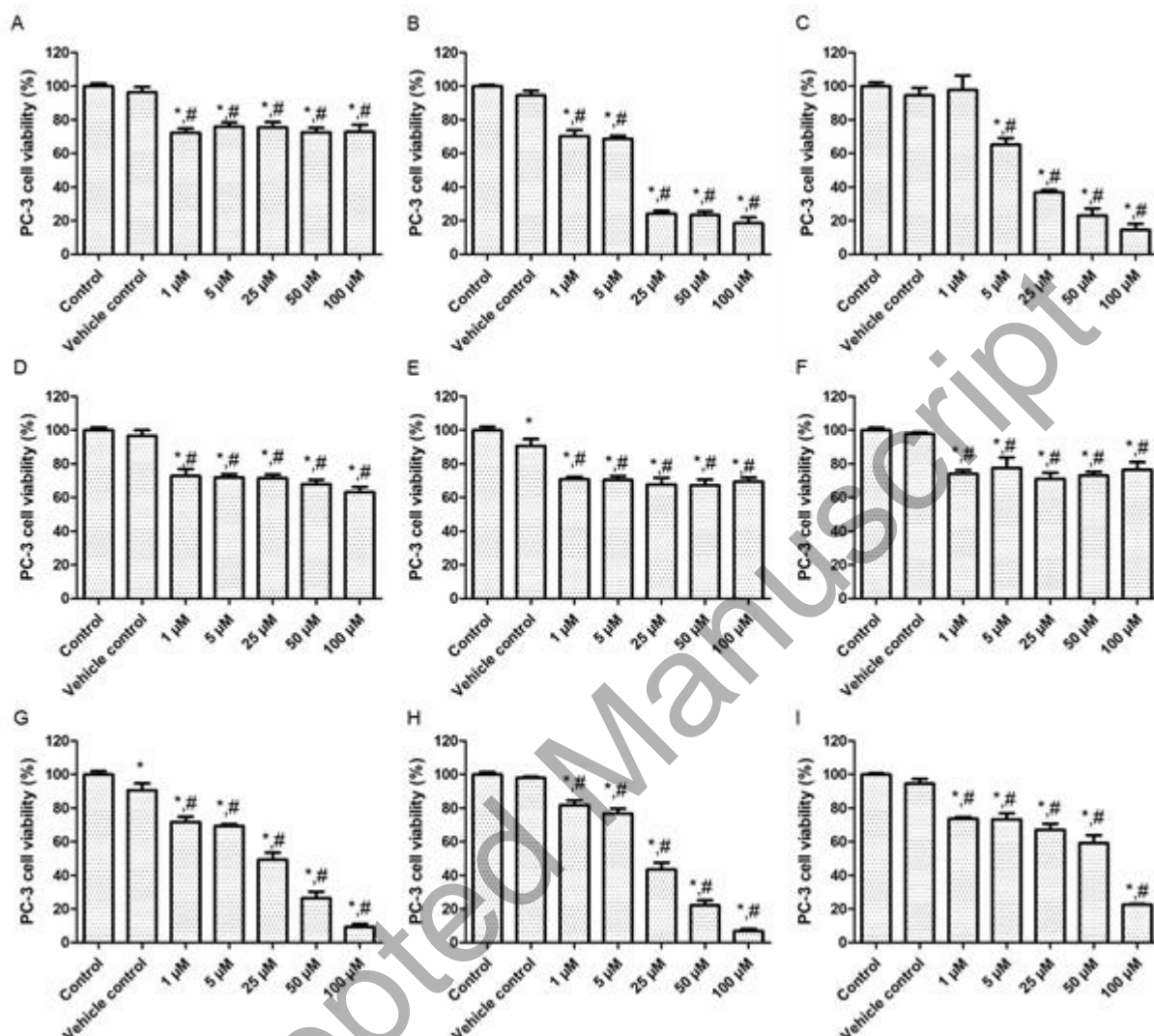
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**Figure 1.** Determination of  $K_i$  value from Lineweaver-Burk graphs for excellent inhibitor of  $\alpha$ -glycosidase enzyme (III or MS-54)

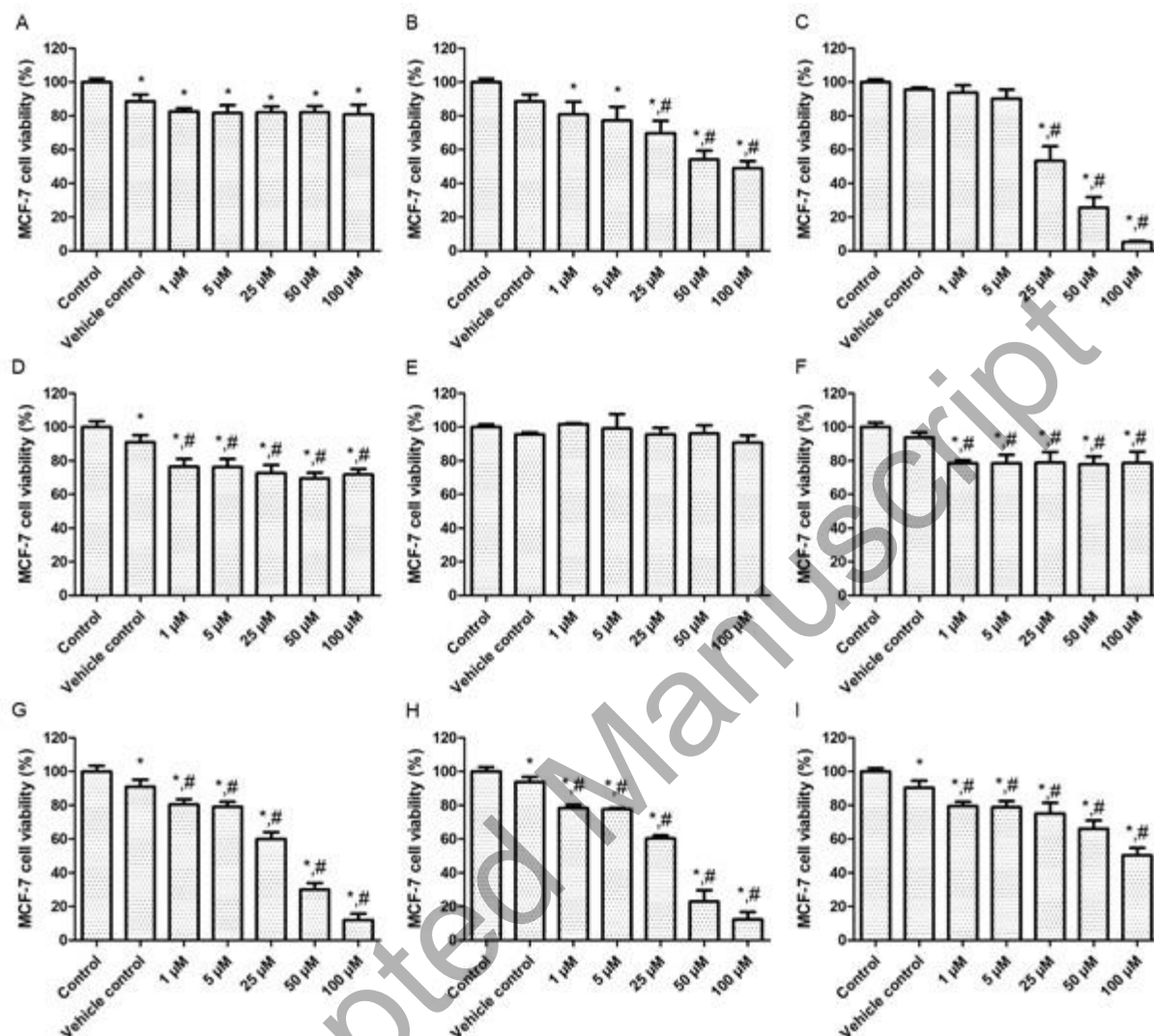


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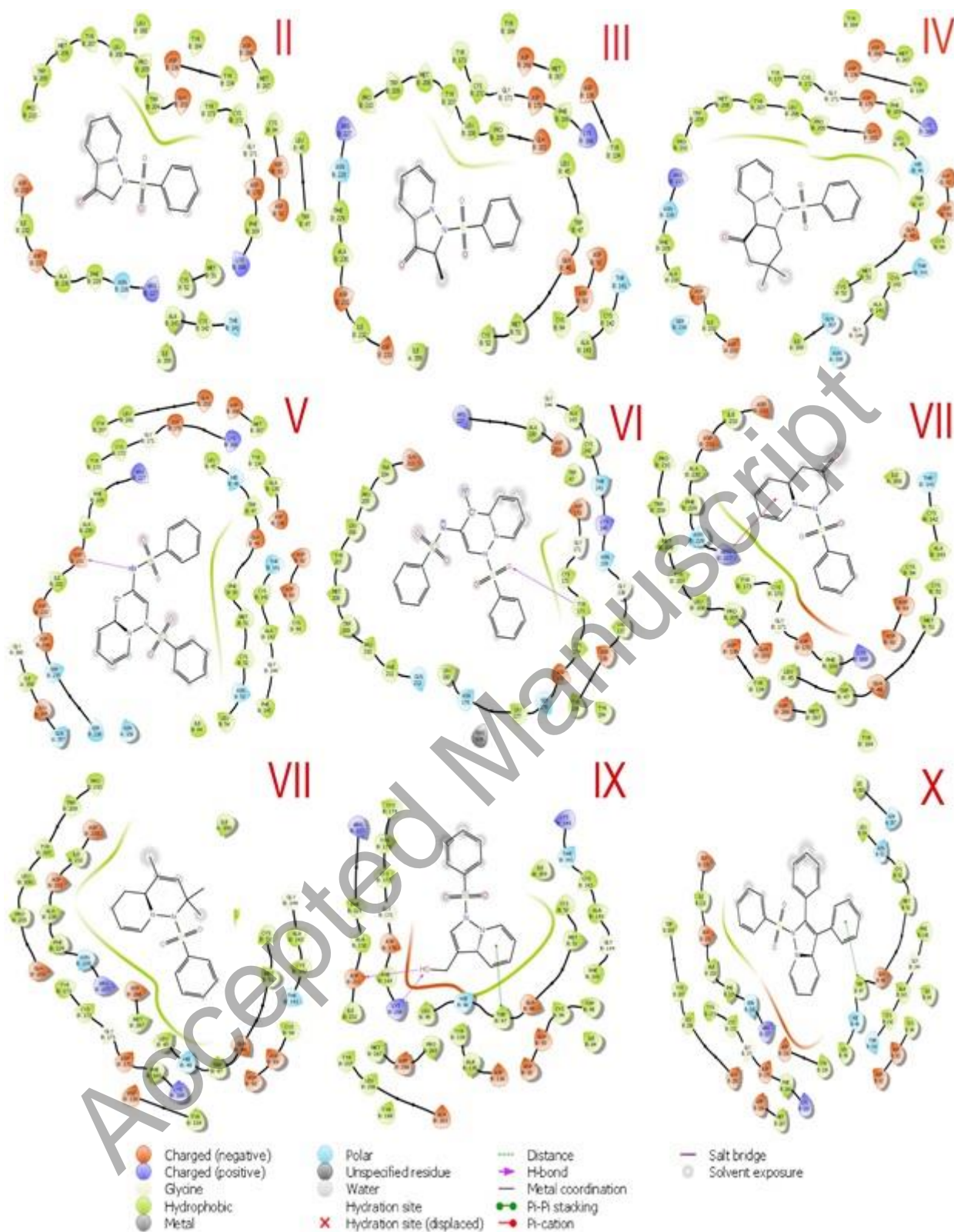
**Figure 2.** Effects of test compounds on PC-3 cell viability. Different concentrations of the compounds of MS50 (A), MS54 (B), MS56 (C), MS67 (D), MS72 (E), MS82 (F), MS116 (G), MS120 (H) and MS122 (I) for 24 hours PC-3 cells. No application was made to the cells in the control group. Cells in the solvent control group were treated with DMSO, which was used to prepare the same amount of compounds. Values were expressed as mean  $\pm$  SD. \*  $p < 0.05$  compared to control group, # $p < 0.05$  compared to vehicle control group.



**Figure 3.** Effects of test compounds on MCF-7 cell viability. Different concentrations of the compounds of MS50 (A), MS54 (B), MS56 (C), MS67 (D), MS72 (E), MS82 (F), MS116 (G), MS120 (H) and MS122 (I) for 24 hours PC-3 cells. No application was made to the cells in the control group. Cells in the solvent control group were treated with DMSO, which was used to prepare the same amount of compounds. Values were expressed as mean  $\pm$  SD. \*  $p < 0.05$  compared to control group, #  $p < 0.05$  compared to vehicle control group

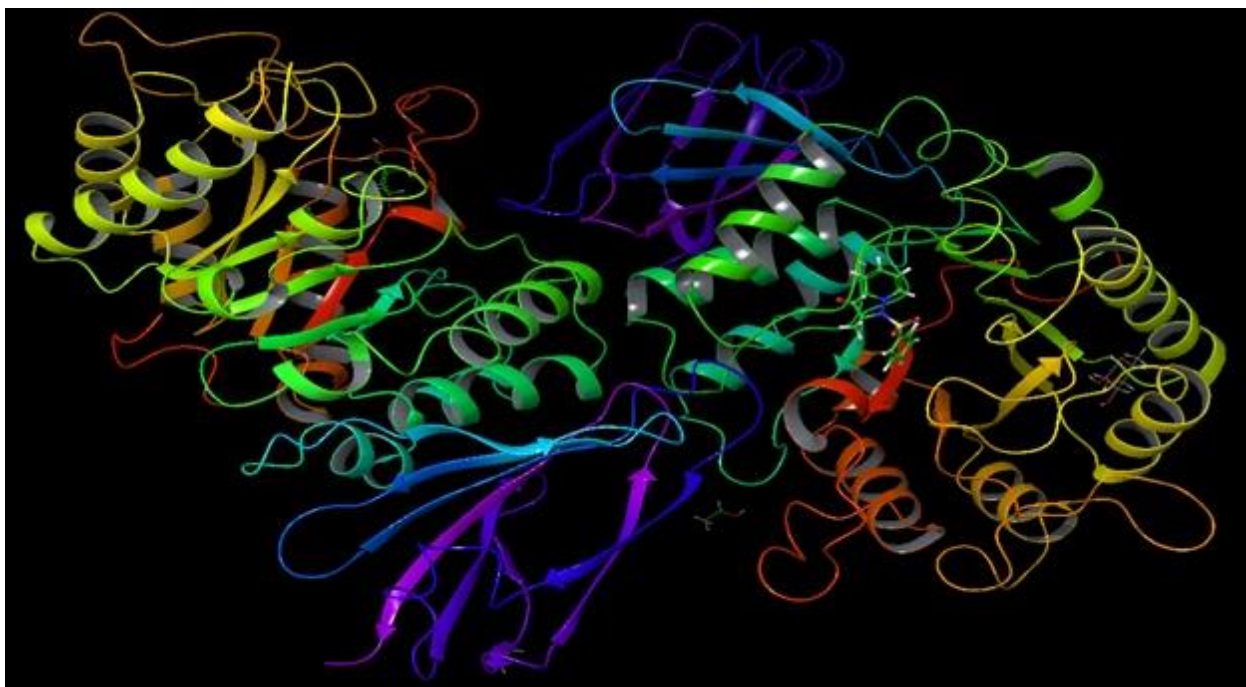


**Figure 4.** Interaction of molecules against  $\alpha$ -glycosidase enzyme





**Figure 5.** Interaction of molecule III with proteins of  $\alpha$ -glycosidase enzyme



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**Table 1.** Determination of half maximal inhibition concentration ( $IC_{50}$ , nM) and inhibition constant values ( $K_i$ , nM) of  $\alpha$ -Glycosidase enzyme inhibition effects of 1-arylsulphonylpyrazole- or pyridazin [1,5-a]-pyridine (**II-X**) compounds

Compounds	$IC_{50}$ (nM)	$r^2$	$K_i$ (nM)
(II) MS-50	23.94	0.9843	26.93±3.84
(III) MS-54	11.73	0.9692	13.66±2.63
(IV) MS-56	29.24	0.9904	33.64±6.53
(V) MS-67	58.53	0.9362	60.63±12.71
(VI) MS-72	35.33	0.9599	43.78±9.62
(VII) MS-82	28.41	0.9618	32.88±8.53
(VIII) MS-116	27.04	0.9792	30.92±4.60
(IX) MS-120	40.73	0.9930	46.83±6.05
(X) MS-122	36.95	0.9638	39.68±10.53
ACR*	22800	-	12600±78

\*Acarbose (ACR) was used as a control for  $\alpha$ -glycosidase enzyme

**Table 2.** Molecular docking data of studies molecules for  $\alpha$ -glycosidase

III	IV	V	VI	VII	VIII	IX	X
-4.68	-3.41	-2.70	-1.10	-3.62	-3.20	-4.14	-2.86
0.00	0.00	-0.08	0.00	0.00	0.00	-0.26	0.00
-31.62	-33.47	-33.63	-23.92	-34.02	-28.66	-34.14	-24.63
-0.16	-0.13	-0.09	-0.03	-0.18	-0.14	-0.20	-0.09



**Table 3.** ADME properties of molecules

	II	III	IV	V	VI	VII	VIII	IX	X	<b>Recommended</b>
Solute Molecular Weight	276	290	358	-	442	290	318	290	412	130-725
Solute Dipole Moment (D)	6.0	6.4	6.3	-	7.5	7.0	6.5	5.4	5.9	1.0-12.5
Solute Total SASA	487	500	582	-	657	495	535	517	637	300.0-1000.0
Solute Hydrophobic SASA	47	80	180	-	2	77	251	59	10	0.0-750.0
Solute Hydrophilic SASA	110	98	101	-	150	123	55	111	58	7.0-330.0
Solute Carbon Pi SASA	32.85	32.20	30.15	-	50.36	29.52	22.86	34.64	57.01	0.0-450.0
Solute Weakly Polar SASA	0.60	0.00	0.00	-	0.43	0.00	0.44	0.42	0.38	0.0-175.0
Solute Molecular Volume (A <sup>3</sup> )	837	875	1080	-	1217	878	994	889	1204	500.0-2000.0
Solute CdW Polar SA (PSA)	72	67	71	-	113	71	36	66	42	7.0-200.0
Solute as Donor-Hydrogen Bonds	0.00	0.00	0.00	-	2.00	0.00	0.00	1.00	0.00	0.0-6.0
Solute as Acceptor-Hydrogen	8.5	8.5	8.5	-	11.5	8.0	6.0	8.1	6.5	2.0-20.0
Solute Globularity (Sphere =1)	0.88	0.88	0.87	-	0.83	0.89	0.89	0.86	0.85	0.75-0.95
Solute Ionization Potential (eV)	8.5	8.5	8.3	-	8.4	8.3	8.0	8.2	8.3	7.9-10.5
Solute Electron Affinity (eV)	1.0	0.9	0.9	-	1.3	1.1	0.8	0.8	0.8	-0.9-1.7
<b>Predictions for Properties</b>										
QP Polarizability (Angstroms <sup>3</sup> )	29	30	38	-	43	30	34	30	46	13.0-70.0
QP log p for hexadecane/gas	9.1	9.4	11.1	-	14.5	9.4	9.6	9.9	13.8	4.0-18.0
QP log p for octanol/gas	14.8	15.3	17.9	-	24.6	15.2	14.9	16.2	19.6	8.0-35.0
QP log p for water/gas	11.8	11.7	11.7	-	18.6	11.1	8.4	12.7	11.4	4.0-45.0
QP log p for octanol/water	0.24	0.56	1.85	-	1.68	0.62	2.75	1.20	4.25	-2.0-6.5
QP log S aqueous solubility	-0.67	-0.92	-2.48	-	-3.34	-1.09	-2.90	-2.26	-4.59	-6.5-0.5
QP log S-conformation independent	-1.7	-2.0	-3.4	-	-4.8	-2.2	-3.7	-2.7	-6.3	-6.5-0.5
QP log K has Serum protein Binding	-1.3	-1.1	-0.6	-	-0.4	-1.0	-0.1	-0.6	-0.2	-1.5-1.5
QP log BB for brain/blood	-0.5	-0.3	-0.4	-	-1.2	-0.5	-0.0	-0.6	-0.0	-3.0-1.2
No. of Primary Metabolites	2	2	3	-	2	3	3	2	1	1.0-8.0
<b>Predicted CNS Activity (-- to ++)</b>										
HERG K <sup>+</sup> Channel blockage: log IC <sub>50</sub>	-5.0	-4.9	-5.0	-	-6.5	-4.6	-4.2	-5.3	-6.5	(concern below -5)
Apparent Caco-2 Permeability (nm/sec)	891	1157	1087	-	369	670	2968	870	2783	*
Apparent MDCK Permeability (nm/sec)	440	579	541	-	169	321	1611	427	1502	*

QP log Kp for skin Permeability Jm	-2.2	-2.0	-2.1	-	-1.9	-2.5	-1.5	-1.9	-0.3	Kp in cm/hr
Lipinski Rule of 5 Violations	0	0	0	-	0	0	0	0	0	Maximum is 4
Jorgensen Rule of 3 Violations	0	0	0	-	0	0	0	0	0	Maximum is 3
% Human Oral Absorption in GI (+20%)	3	3	3	-	3	3	3	3	3	<25% is poor
Qual. Model for Human Oral Absorption	81	85	92	-	82	81	100	86	100	>80% is high

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