



Research article

Pyrazole derivatives as antileishmanial agents: Biological evaluation, molecular docking study, DFT analysis and ADME prediction

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ABSTRACT

Leishmaniasis is a parasitic disease that is commonly found in tropical and sub-tropical regions. Currently, there is no protective antileishmanial vaccine, and the available clinical drugs have serious side effects. On the other hand, due to the emergence of multidrug-resistant strains of the causative pathogens, the study and design of novel antileishmanial agents is urgently needed. Accordingly, fourteen previously synthesized pyrazole and pyrano [2,3-c] pyrazole derivatives (P₁-P₁₄) were evaluated for antileishmanial efficacy against the protozoan parasite, *Leishmania major*. Among the tested compounds, seven derivatives including P₁, P₃, P₅, P₈, P₁₂, P₁₃, and P₁₄ exhibited promising antileishmanial activity with IC₅₀ values in the range of 34.79–43.55 µg/mL, compared to the standard drug (Glucantime) with an IC₅₀ value of 97.31 µg/mL. In the case of pyrazole derivatives, P₁, P₅, and P₈ exhibited significant antileishmanial activity with IC₅₀ values of 35.53, 36.79, and 37.40 µg/mL, respectively. The most potent antileishmanial activity is belong to P₁₂ and P₁₄, with IC₅₀ values of 34.79 and 38.51 µg/mL, respectively. Molecular docking outputs presented that P₁₂ and P₁₄ formed favorable interactions with key residues in the active site of the 14-alpha demethylase enzyme, which is an important target for antileishmanial agents. Various DFT parameters were also calculated for compounds P₁ and P₁₂, which were the most and least active compounds, respectively. The outputs indicated that compound P₁ was more thermodynamically stable than P₁₂. Additionally, P₁ had higher hardness and a higher energy gap, resulting in greater stability. In addition, these compounds showed satisfactory theoretical ADME properties. The present results indicate that the investigated pyrazole and pyrano [2,3-c] pyrazole derivatives can be considered as promising agents for the development of antileishmaniasis treatments.

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1. Introduction

Leishmaniasis is a highly prevalent and chronic intracellular infectious disease caused by the protozoan parasites of the genus *Leishmania*, which can lead to a wide range of symptoms in humans, from asymptomatic infection to serious problems with visceral, cutaneous, and mucocutaneous symptoms [1-3]. Leishmaniasis is recognized by the World Health Organization (WHO) as the second most important tropical protozoan disease, following malaria [4-7]. The disease is endemic in the tropical and subtropical regions of 98 countries across four continents [8]. The clinical forms of leishmaniasis include Cutaneous (CL), Mucocutaneous (MCL), Visceral (VL) Post-Kala-Azar Dermal (PKDL), and Diffuse Cutaneous (DCL) leishmaniasis. More than 90 % of CL cases is present in Iran, Afghanistan, Nepal, Syria, Saudi Arabia, and Peru [9]. Leishmaniasis, as one of the most significant tropical diseases that puts approximately 350 million people at risk of infection, has been neglected in terms of drug discovery [1,2]. Currently, there is no approved vaccine available for humans, and the treatment of this disease is limited to miltefosine, pentamidine, paromomycin, liposomal amphotericin B, and pentavalent antimonials like sodium stibogluconate [2,4,10]. Furthermore, the drugs used to treat cutaneous and visceral leishmaniasis are associated with severe toxicity and side effects, and the emergence of resistance limits their use [11-13]. Consequently, the pursuit of novel, cost-effective, and safe pharmacological agents with minimal adverse effects for the treatment of leishmaniasis are a significant challenge for researchers on a global scale.

Heterocyclic compounds with a cyclic ring system have different biological potential, special in the inhibition of numerous infections [14]. Nitrogen-containing heterocyclic compounds have predominantly been documented as bioactive agents that exhibit different biological potential, such as antimalarial, antibacterial, antileishmanial, antifungal, anticonvulsant, anti-inflammatory, anthelmintic, analgesic, and anticancer properties [15-19]. Among heterocyclic compounds, azoles are inhibitors of the 14-alpha demethylase enzyme, which is a promising target for the treatment of both leishmaniasis and fungal diseases. *Leishmania*, similar to fungi, has 24-substituted sterols like ergosterol as a crucial component in its membrane structure. Preventing the production of leishmanial ergosterol can lead to the disruption of membrane stability and the death of *Leishmania* [20-22].

Pyrazole derivatives are a significant category of bioactive azole compounds [23-31]. Previous studies have shown that pyrazole derivatives can inhibit ergosterol biosynthesis. Ergosterol is an attractive target for the treatment of leishmaniasis. In recent years, some pyrazole derivatives have been reported as antileishmanial agents [32-37]. Accordingly, in this study we investigated the antileishmanial effects of pyrazole and pyrano [2,3-c] pyrazole derivatives.

Recently, different derivatives of 1,2,4-trioxolane-pyrazole and 1,2,4,5-tetraoxane-pyrazole (Structure I) were examined as anti-leishmanial agents. The biological evaluation of these hybrids showed that some of the compounds had promising activity against *L. tropica* [38]. The *in vitro* antileishmanial activities of hydrazine-coupled pyrazole derivatives were examined. The results revealed that some of the compounds showed superior antipromastigote activity ($IC_{50} = 0.018 \mu\text{g/mL}$) (Structure II) (Fig. 1) [39].

So, in view of important biological activities of pyrazole moiety as antileishmanial agents, we reported the synthesis and biological evaluation of some pyrazole and pyrano [2,3-c]pyrazole compounds in our previous studies [40,41]. Herein, we aimed to investigate the *in vitro* antileishmanial activity of a series of pyrazole and pyrano [2,3-c]pyrazole derivatives against *Leishmania major* promastigotes (MRHO/IR /75/ER) using the MTT assay. Furthermore, molecular docking study, DFT analysis, and the theoretical investigation of ADME properties were performed to obtain structural information related to the antileishmanial activity of these compounds.

2. Results and discussion

2.1. *In vitro* antileishmanial activity

The pyrazole and pyrano [2,3-c] pyrazole derivatives **P₁-P₁₄**, which were evaluated in this study, were previously synthesized by our research group according to the synthetic method outlined in Fig. 2 [40,41].

The *in vitro* antileishmanial activities of all pyrazole and pyrano [2,3-c] pyrazole derivatives **P₁-P₁₄** were evaluated against *Leishmania major* promastigotes (MRHO/IR/75/ER) using the MTT assay. The obtained IC_{50} values for all compounds, defined as the concentration that reduces 50 % of cell growth, are depicted in Fig. 3. In this assay, Glucantime, an antileishmanial drug, was used as a positive control.

Based on the obtained biological results, the tested compounds **P₁-P₁₄** showed different levels of antileishmanial activities with IC_{50} ranging from 34.79 to $>288 \mu\text{g/mL}$. Among all the tested compounds, **P₁**, **P₃**, **P₅**, **P₈**, **P₁₂**, **P₁₃**, and **P₁₄** exhibited the highest activities

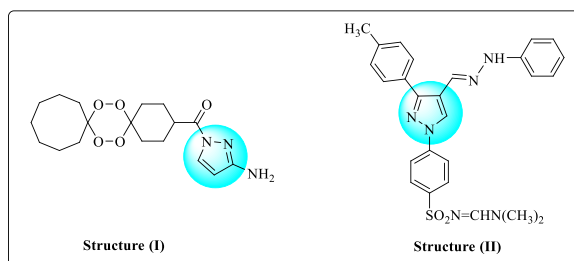


Fig. 1. Structures of some reported antileishmanial agents.

as antileishmanial agents with IC_{50} values of 34.79–43.55 $\mu\text{g/mL}$, which were 2–3 times more effective than Glucantime, as the control drug. Other compounds including **P**₂, **P**₄, **P**₆, **P**₇, **P**₉, **P**₁₀, and **P**₁₁ were inactive with $IC_{50} > 288 \mu\text{g/mL}$.

Compound **P**₁, bearing a pyrazole ring without any substitution on the phenyl ring, showed an IC_{50} value of 35.53 $\mu\text{g/mL}$. Compound **P**₁₂, containing a pyrano [2,3-*c*] pyrazole ring with 2,4-di-Cl substituents on the phenyl ring at C-4 position, exhibited an IC_{50} value of 34.79 $\mu\text{g/mL}$. Additionally, compounds **P**₃, **P**₅, **P**₈, **P**₁₃, and **P**₁₄ showed similar activity to compounds **P**₁ and **P**₁₂.

It was observed that both pyrazole and pyrano [2,3-*c*] pyrazole scaffolds are effective for antileishmanial activity and the nature and position of the substituents placed on these scaffolds significantly affect their activity. In the case of pyrazole derivatives, it was found that the presence of a chlorine group at the C-4 position of the pyrazole ring (**P**₃ vs **P**₄) or on the phenyl ring (**P**₈) is favorable for antileishmanial effects. In addition, the presence of 4-Br group (**P**₂ vs **P**₁) on the phenyl ring diminish the activity of pyrazole derivatives. In the case of pyrano [2,3-*c*] pyrazole derivatives placing a phenyl ring with 2,4-di-Cl or 2,4-di-OH substituents (**P**₁₂ and **P**₁₃), as well as placing a furan group (**P**₁₄) at C-4 position of pyrano [2,3-*c*] pyrazole ring is suitable for the effect of these compounds (Fig. 4).

Taken together, the comparison of our results with other reported antileishmanial agents showed that pyrazole and pyrano [2,3-*c*] pyrazole derivatives are promising scaffolds for development as antileishmanial agents for future studies (Table 1).

2.2. Molecular docking study

For molecular docking studies, the CYP51 enzyme from *L. infantum* with PDB ID: 3L4D was used. The active site of this enzyme is evident as a channel composed of amino acids with hydrophobic side chains that provides access to the heme group, where the catalytic activity occurs. It has been found that interaction with the heme group in the CYP51 enzyme, especially coordination with the iron, is important for blocking its activity. The reliability of docking protocol was evaluated with redocking procedure and the RMSD value was obtained 0.93 Å which confirmed the validation of the docking protocol.

The molecular docking results (Figs. 5–9 and Table 2) revealed that compounds **P**₁–**P**₁₄ were located in the active site of CYP51, and the binding free energy of all compounds was in the range of –6.0 to –9.5 kcal/mol, which was more favorable than that of the positive control (Glucantime, –5.1 kcal/mol).

Hydrogen bonds are essential factors to assess the structure of proteins and nucleic acid. They also play a crucial role in the specificity of enzyme catalysis, biological information transfer, and enzymatic reaction rate [48]. As seen in Table 2, all compounds had strong hydrogen bond interaction due to their distances ($\leq 3.1 \text{ \AA}$) except **P**₈ and **P**₁ [49]. Hydrogen bonds also have a great impact on the stabilization of enzyme-ligand complexes. Three hydrogen bonds was seen between Glucantime and the residue in the active site of CYP51 enzyme (Fig. 5).

The molecular docking results indicated that most of the studied compounds formed hydrogen bonds with the enzyme active site [50–52]. The target compounds also made additional interactions such as π -sulfur, π - π stacking, and π -sigma interactions, which led to strong interactions with the receptor. Met357 and Phe48 were the key amino acids that formed π -sulfur and π - π stacking interactions in

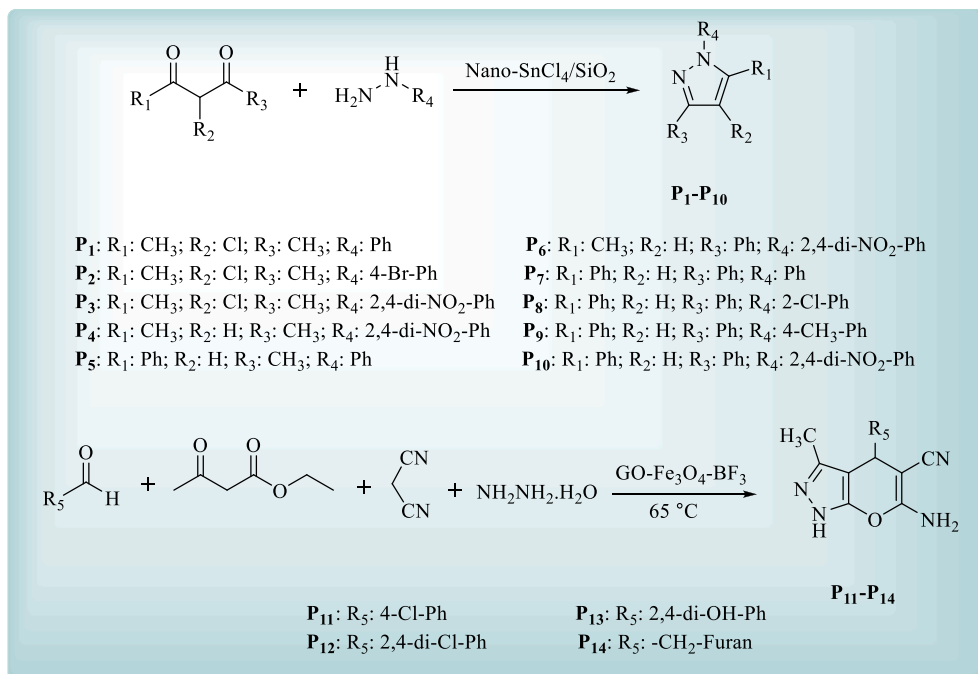


Fig. 2. Synthesis procedure of studied pyrazole and pyrano [2,3-*c*] pyrazole derivatives.

most of the compounds. **P**₁ and **P**₁₂, as the most potent compounds, exhibited one and two hydrogen bonds, respectively, with Cys422, Tyr456, and Thr458 residues, and the binding affinity values of -7.4 and -7.9 kcal/mol, respectively. In addition, **P**₁ and **P**₁₂ established π -sulfur, π - π stacking, amide π -stacking, and π -alkyl interactions with Phe415, Ala290, Phe48, Phe213, and Met357 residues located within the active site of the CYP51 receptor. Compounds **P**₃, **P**₅, **P**₈, **P**₁₃, and **P**₁₄, as the relatively active compounds, made hydrogen bonds, π -sulfur, π - π stacking, π -sigma, π -anion, π -cation, and π -alkyl interactions with critical residues such as Val356, Met357, His293, Thr294, His420, Phe48, Cys422, Met359, and Glu204 (Figs. 6–7).

Compounds **P**₂, **P**₄, **P**₆, **P**₇, **P**₉, **P**₁₀, and **P**₁₁ had weaker interactions with the active site of the enzyme (Figs. 8–9).

2.3. DFT calculations

DFT calculations help to obtain useful information about the structure of the studied molecules and their reactivity. Calculation of the highest unoccupied molecular orbital (LUMO), the lowest occupied molecular orbital (HOMO), and the energy gap between them

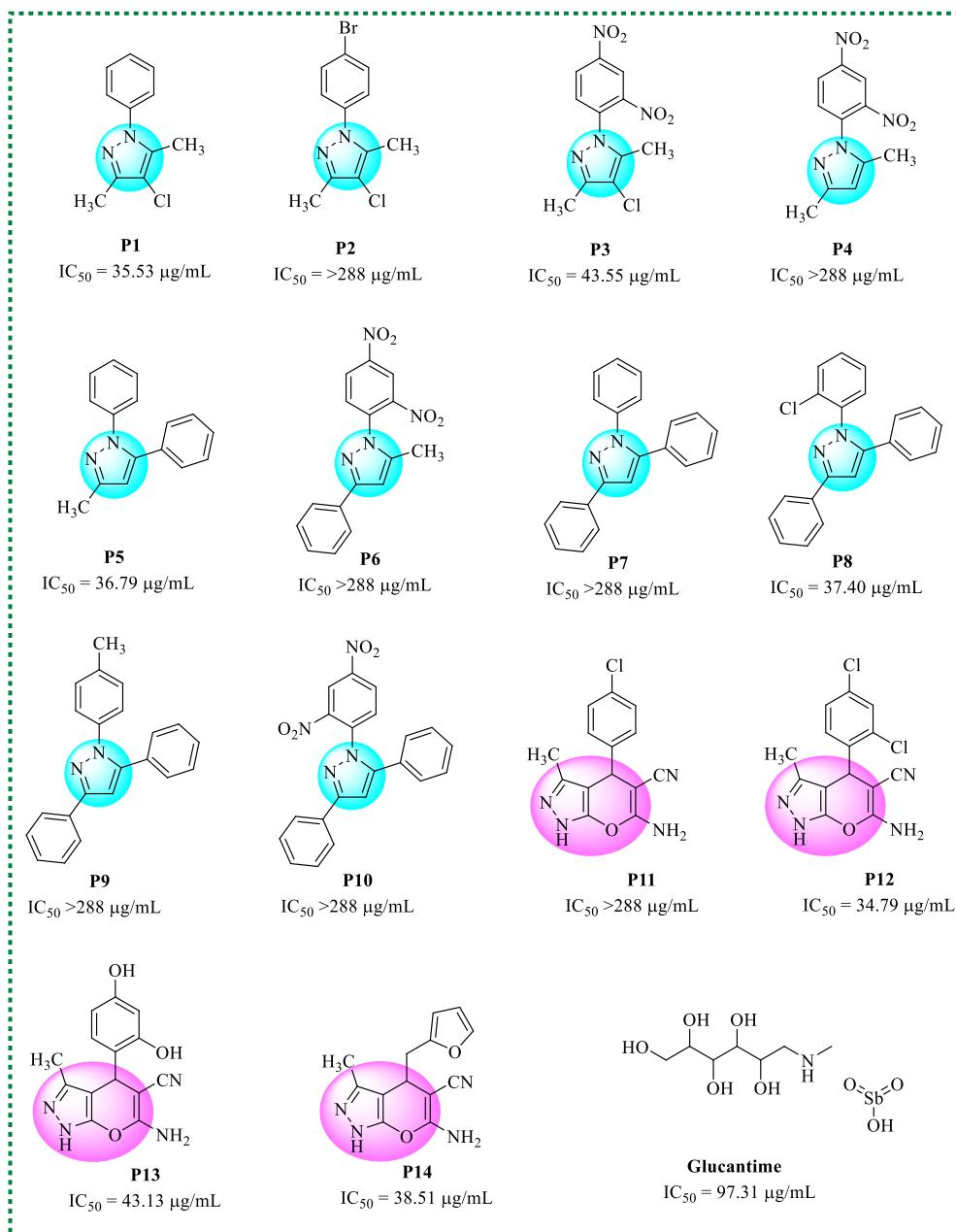


Fig. 3. The chemical structures and antileishmanial activity of the tested compounds **P**₁-**P**₁₄.

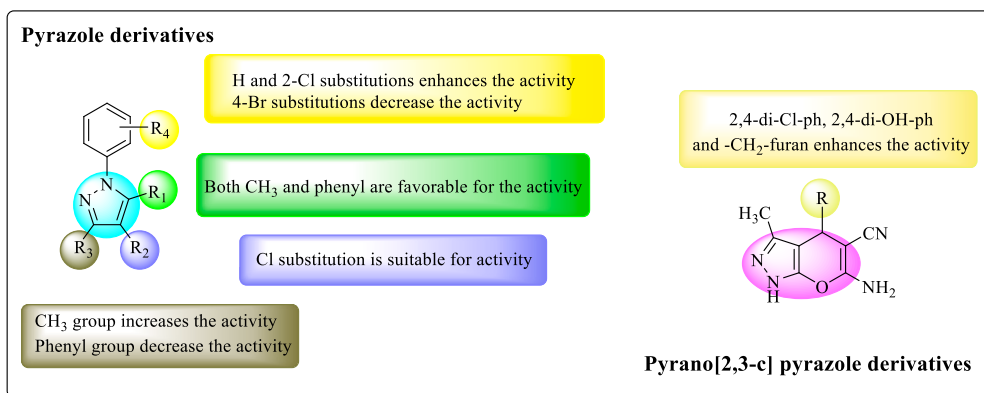


Fig. 4. The schematic SAR of pyrazole and pyrano [2,3-c] pyrazole scaffolds as antileishmanial agents.

Table 1

A comparative study of the inhibition activity of the other reported scaffolds against Leishmanial disease.

Compounds	Antileishmanial activity; IC ₅₀ (μg/mL or μM)	Compounds	Antileishmanial activity; IC ₅₀ (μg/mL or μM)
	95.5 μg/mL [4]		180.0 μM [2]
	2.1 μg/mL [42]		0.04 μM [43]
	21.4 μM [44]		41.9 μM [45]
	1.49 μg/mL [46]		0.6 μM [47]

is one of the parameters that predicate the reactivity and stability of the compounds. DFT analysis was done at the B3LYP/6-31 + G** level of theory for **P₁** and **P₁₂**, as the best molecules according to the biological results using Gaussian 09 software.

The HOMO and LUMO orbitals, their energies, and locations on the studied molecules are shown in Fig. 10. For compound **P₁₂** (Fig. 10b), the LUMO orbital covers the entire molecule, and the HOMO orbital is occupied in all parts of the molecule except for a part of the dichlorophenyl ring. In addition, for molecule **P₁** (Fig. 10a), the HOMO and LUMO orbitals are distributed throughout the molecule, indicating that all parts of the molecule can be targeted by electrophilic and nucleophilic compounds. The energy gap between HOMO and LUMO was calculated to be 5.44 and 4.75 eV for **P₁** and **P₁₂**, respectively. A higher energy gap indicates more stability, while a lower energy gap indicates more reactivity. Therefore, according to the energy gap values of the two compounds, compound **P₁**, with a larger energy gap, is more stable.

The nucleophilic and electrophilic sites of compounds were determined by the electrostatic potential map (ESP). Fig. 11 showed the ESP maps of **P₁₂** and **P₁** derivatives. Red spheres indicate preferred sites for electrophilic attack, while blue spheres are

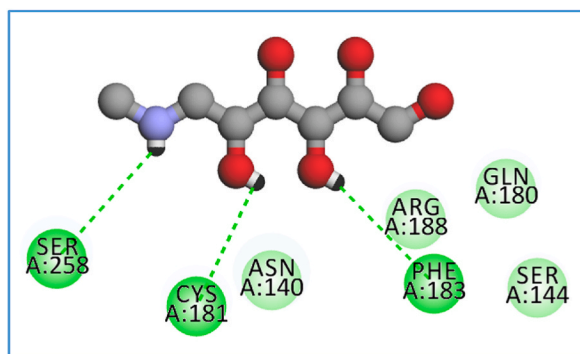


Fig. 5. Interactions of Glucantime in the active site of CYP51 receptor.

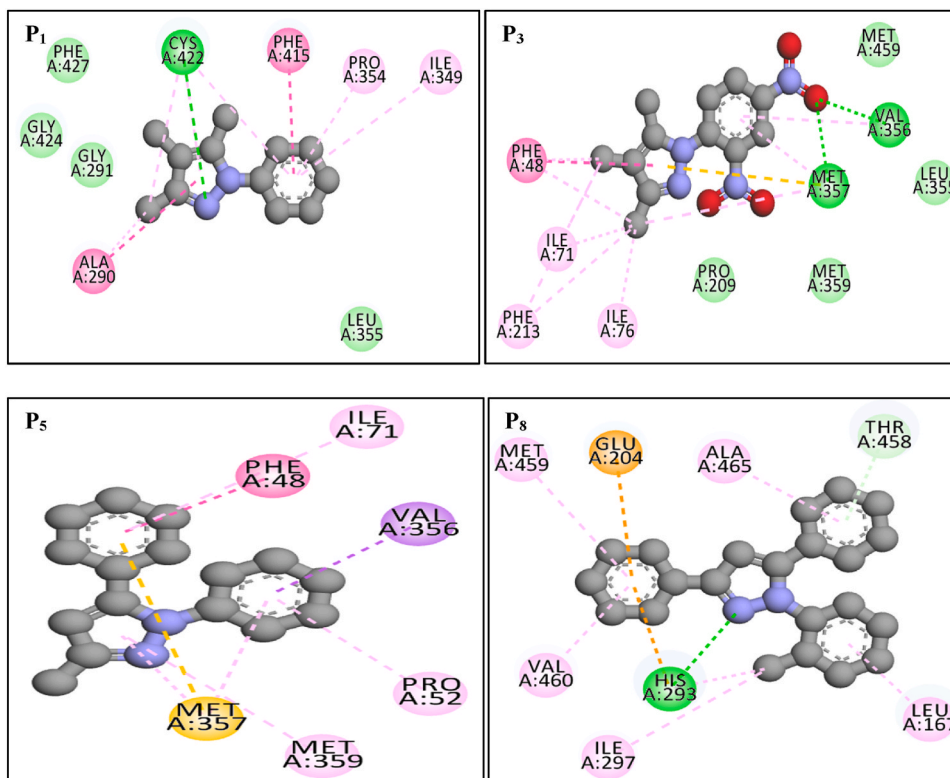


Fig. 6. The two-dimensional interactions of the active compounds P_1 , P_3 , P_5 , and P_8 within the active site of the CYP51 receptor. The interactions are categorized as follows: green represents van der Waals forces, light green denotes carbon-hydrogen bonds, dark green indicates hydrogen bonds, dark pink corresponds to π - π interactions, light pink signifies alkyl and π -alkyl interactions, purple reflects π -sigma interactions, and orange illustrates π -sulfur interactions.

suitable sites for nucleophilic attack.

The thermochemistry parameters for P_1 and P_{12} are given in Table 3. The obtained values of total energy (E), enthalpy (H°), and Gibbs free energy (G°) presented that P_1 was more thermodynamically stable than P_{12} . Chemical hardness (η) expresses the molecular resistance against the deformation of the electron cloud, which is related to the stability of the compound. The hardness parameter is measured through the energy gap between HOMO and LUMO orbitals. The harder the molecule, the wider the HOMO-LUMO gap, and the more stable the molecule. As can be observed in Table 3, compound P_1 has higher chemical hardness compared to compound P_{12} , therefore, it is more stable and less reactive. The electron affinity parameter (A) is also given in Table 3. The calculated values showed the greater tendency of compound P_{12} to participate in electrophilic reactions.

The theoretical IR spectrum of compounds P_1 and P_{12} is shown in Fig. 12. The IR peaks of C=C, C-O, C-N, C-Cl, and C-H (aliphatic and aromatic) are well visible and comparable with experimental results.

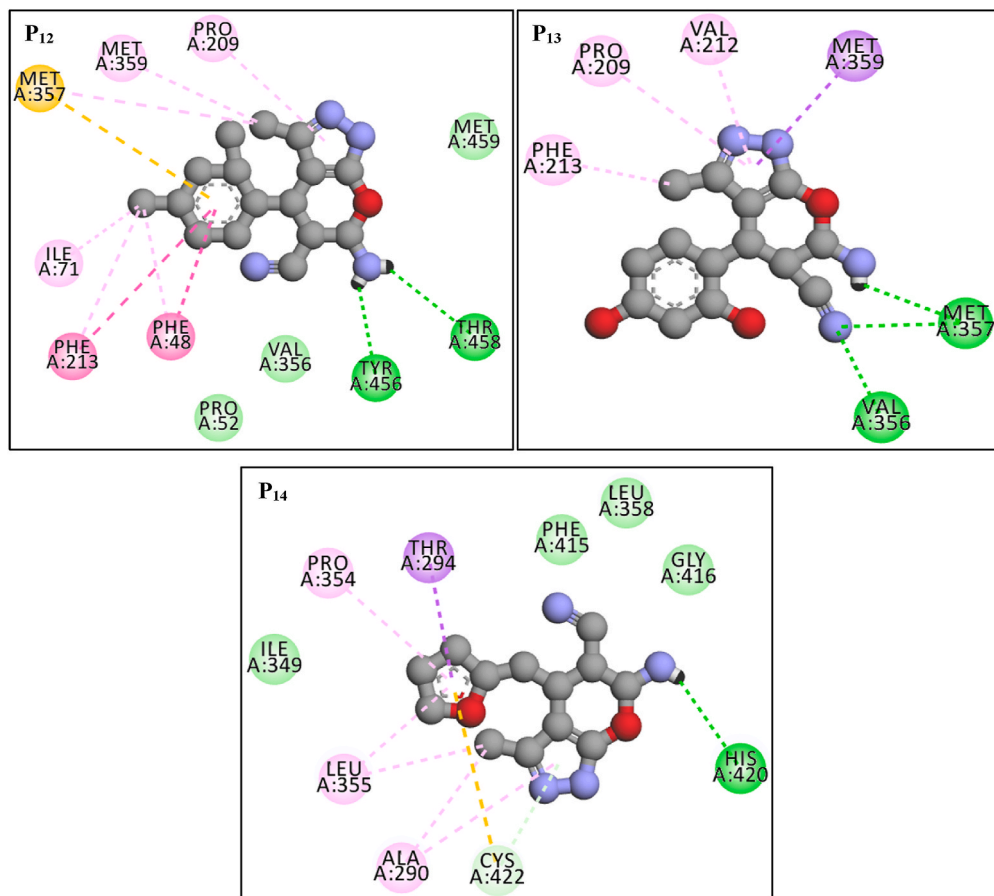


Fig. 7. 2D interactions of the active compounds **P₁₂**, **P₁₃**, and **P₁₄** within the active site of the CYP51 receptor. The interactions are categorized as follows: green represents van der Waals forces, light green denotes carbon-hydrogen bonds, dark green indicates hydrogen bonds, dark pink corresponds to π - π interactions, light pink signifies alkyl and π -alkyl interactions, purple reflects π -sigma interactions, and orange illustrates π -sulfur interactions.

2.4. ADME profile prediction

The drug-likeness properties of the tested compounds displayed that all the tested derivatives passed Lipinski's rule of five. Compounds **P₁**, **P₂**, **P₅**, **P₇**, **P₈**, and **P₉** with TPSA (Topological Polar Surface Area) values less than 60 \AA^2 , can be completely absorbed, while the absorption of other compounds with $\text{TPSA} > 60 \text{ \AA}^2$ is predicted to a lesser degree. Research shows that increasing lipophilicity leads to an increase in the antileishmanial effects of designed compounds [53]. Among all the tested compounds, **P₁** and **P₁₂** exhibited the expected LogP values (2.87 and 2.28). Furthermore, compounds **P₁**, **P₃**, **P₄**, **P₈**, **P₁₁**, and **P₁₂** exhibited high permeability, while the other compounds showed low permeability. In addition, all compounds had a negative value of the *in vitro* skin permeability parameter (LogKp), indicating that these derivatives had not skin toxicity. Compound **P₁₂** as the most potent compounds showed more negative value of LogKp and the lowest skin toxicity. All compounds except **P₁₃** and **P₁₄** showed plasma protein binding (PPB) value of more than 90 %. Compounds **P₁** and **P₁₂** as the most potent compounds indicated acceptable toxicity profile. The pharmacokinetic and drug-likeness profiles of these compounds were reported in supporting information file.

3. Experimental

3.1. Chemistry

The selected synthesized compounds were obtained from our previous study [40,41].

3.2. Parasite culture

The strain of *L. major* (MRHO/IR/75/ER) was prepared in Shiraz University of Medical Sciences, Iran. After adaptation in biphasic medium transferred to RPMI 1640 supplemented with penicillin (200 IU/mL), streptomycin (100 $\mu\text{g/mL}$) and 15 % heat-inactivated

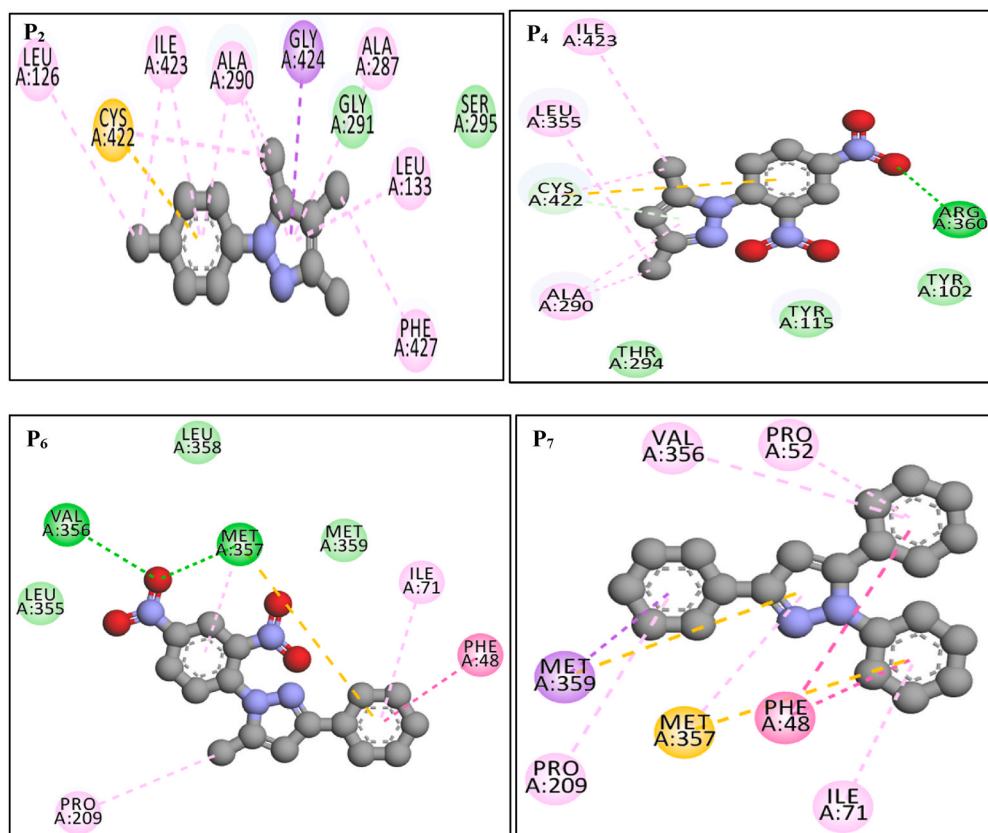


Fig. 8. 2D interactions of compounds **P**₂, **P**₄, **P**₆, and **P**₇ with the CYP51 receptor. The interactions are categorized as follows: green represents van der Waals forces, light green denotes carbon-hydrogen bonds, dark green indicates hydrogen bonds, dark pink corresponds to π - π interactions, light pink signifies alkyl and π -alkyl interactions, purple reflects π -sigma interactions, and orange illustrates π -sulfur interactions.

fetal calf serum (FCS) for mass cultivation. The *L. major* promastigote cell viability due to the addition of the pyrazole derivatives were determined using the colorimetric MTT assay. The live promastigotes are able to produce the purple formazan crystals with mitochondrial dehydrogenases enzyme.

3.3. Antileishmanial activity

50 μ L of a suspension of mass cultivated promastigotes of *L. major* at a density of 10^6 parasites/mL in stationary phase were seeded in culture plates (50,000 parasites/well). For control and blank wells, the same number of promastigotes with solvent and RPMI was applied. Amphotericin B was used in positive control wells and stock solutions of selected synthesized compounds solubilized in DMSO. All four solutions and amphotericin B were sterilized by syringe filters. Different dilutions of compounds were prepared in culture media. Fifty μ L of pyrazole compounds diluted in growth medium were added in triplicate. The various concentrations of compounds (5.0, 10.0, 25.0 and 50.0 μ g/mL) was prepared and the concentrations of 0.25, 1.0, 2.5 and 10.0 μ g/mL was examined for amphotericin B. The applied concentration for DMSO (0.25 %) doesn't harmful to the parasites. 80 μ L of the media were aspirated and 80 μ L of MTT solution (0.5 mg MTT/well) was treated to each well after 48 h. Afterwards, 200 μ L of DMSO was added to each well to solubilize the purple precipitate and the CurveExpert software, version 1.3 was used to determine of IC_{50} s values of all compounds.

3.4. DFT calculations

Density functional theory (DFT) was calculated for compounds **P**₁ and **P**₁₂ with the highest biological activity at the B3LYP/6-31 + G** level of theory. Optimization of compounds in the gas phase was conducted using the B3LYP model with a 6-31 + G** basis set in the Gaussian 09 program, assisted by Gauss View 6.0, without imposing any symmetry restrictions. Molecular structures were visualized using Avogadro software. After optimization, the HOMO and LUMO energies were obtained and applied to determine molecular properties such as electron affinity (A), chemical hardness (η), and softness (σ).

$$E = E_t + E_r + E_v + E_e$$

$$H^\circ = E + kBT$$

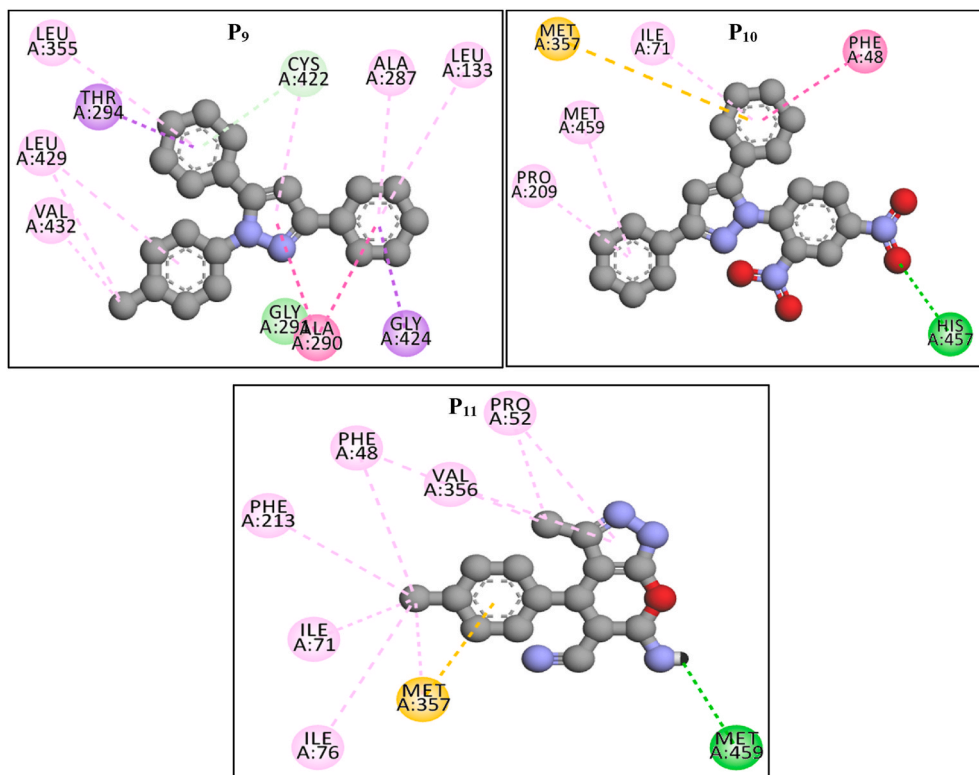


Fig. 9. 2D interactions of compounds **P₉**, **P₁₀**, and **P₁₁** with the CYP51 receptor. The interactions are categorized as follows: green represents van der Waals forces, light green denotes carbon-hydrogen bonds, dark green indicates hydrogen bonds, dark pink corresponds to π - π interactions, light pink signifies alkyl and π -alkyl interactions, purple reflects π -sigma interactions, and orange illustrates π -sulfur interactions.

$$G^{\circ} = H^{\circ} - TS$$

$$S = S_t + S_r + S_v + S_e$$

$$\sigma = 1/\eta$$

$$\eta = \frac{1}{2} (E_{\text{HOMO}} - E_{\text{LUMO}})$$

$$A = -E_{\text{LUMO}}$$

The vibrational frequencies were also calculated using the B3LYP/6-31 + G** method at the theoretical level. In this regard, electrostatic surface potential (ESP) and some DFT parameters like total energy, enthalpy, entropy, and Gibbs free energy were calculated [54].

3.5. Molecular docking study

The 3D structure of Lanosterol 14 α -demethylase (CYP51) was downloaded from the RCSB protein data bank site (PDB ID: 3L4D). From the extracted PDB file, water, ions, internal ligands, and non-polar hydrogens were removed, while polar hydrogens were added. Partial charges were calculated, and the protein was saved in pdbqt format. The size of grid box was set as 40 \times 40 \times 40 Å dimensions. In the following, the ligands under study were optimized and converted to PDBQT format, and then docked onto the 3L4D using AutoDock Vina (1.1.2) software. The interactions and orientations of pyrazole and pyra no [2,3-c] pyrazole derivatives was visualized by Discovery studio 2016 client.

3.6. ADME study

The physicochemical and drug-likeness profile of all derivatives were attained from SwissADME online platform (<http://www.swissadme.ch/>) in accordance with Lipinski's rules.

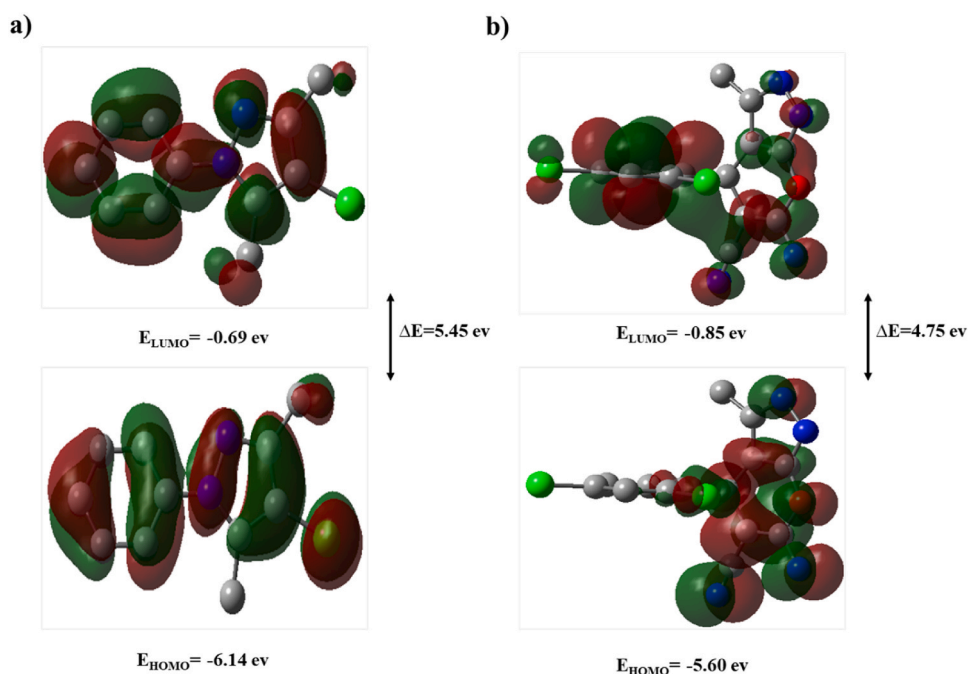
Table 2
Binding energy (kcal/mol) and interactions of pyrazole and pyrano [2,3-c] pyrazole derivatives with sterol 14 α -demethylase utilizing AutoDock Vina.

Entry	Amino Acid	Ligand involved moiety	Type of interaction and distanced of hydrogen bond interaction (Å)	B.E (kcal/mol)
P ₁	Cys 422	Pyrazole ring	Hydrogen Bond (3.45)	-7.4
	Phe 415	Phenyl ring	π - π Stacked	
	Ala 290	Pyrazole ring	Amide π -stacked	
	Ala 290, Ile 349, Pro 354, Cys 422	Pyrazole and phenyl ring, methyl group	Alkyl and π -Alkyl	
P ₂	Gly 291, Leu 355, Gly 424, Phe 427	-	Van Der Waals	-7.2
	Gly 424	Pyrazole ring	π -Sigma	
	Cys 422	Phenyl ring	π -Sulfur	
	Leu 126, Leu 133, Ala 287, Ala 290, Cys 422, Ile 423, Phe 427	Methyl, Chlorine, Bromine, Phenyl and pyrazole ring	Alkyl and π -Alkyl	
P ₃	Gly 291, Ser 295	-	Van Der Waals	-7.6
	Val 356, Met 357	NO ₂ group	Hydrogen Bond	
	Met 357	Pyrazole ring	Val 356(2.30), Met 357(2.05)	
	Phe 48	Pyrazole ring	π -Sulfur	
P ₄	Phe 48, Ile 71, Ile 76, Phe 213, Val 356, Met 357	Methyl, Chlorine and phenyl ring	Alkyl and π -Alkyl	-6.8
	Pro 209, Leu 355, Met 359, Met 459	-	Van Der Waals	
	Arg 360	NO ₂ group	Hydrogen Bond	
	Cys 422	Pyrazole ring	π -Sulfur	
P ₅	Cys 422	Pyrazole ring	π -Donor Hydrogen Bond (2.04)	-8.1
	Ala 290, Leu 355, Cys 422, Ile 423	Methyl and Pyrazole ring	Alkyl and π -Alkyl	
	Tyr 102, Tyr 115, Thr 294	-	Van Der Waals	
	Val 356	Phenyl ring	π -Sigma	
P ₆	Met 357	Phenyl and pyrazole ring	π -Sulfur	-8.8
	Phe 48	Phenyl ring	π - π Stacked	
	Pro 52, Ile 71, Met 357, Met 359	Phenyl and pyrazole ring	π -Alkyl	
	Val 356, Met 357	NO ₂ group	Hydrogen Bond	
P ₇	Met 357	Phenyl ring	Val 356 (1.98), Met 357 (2.90)	-6.3
	Phe 48	Phenyl ring	π -Sulfur	
	Ile 71, Pro 209, Met 357	Methyl and Phenyl ring	π - π Stacked	
	Leu 355, Leu 358, Met 359	-	Van Der Waals	
P ₈	Met 359	Phenyl ring	π -Sigma	-9.5
	Met 357, Met 359	Phenyl and pyrazole ring	π -Sulfur	
	Phe 48	Phenyl ring	π - π Stacked	
	Phe 48	Phenyl ring	π - π T-shaped	
P ₉	Pro 52, Ile 71, Pro 209, Val 356, Met 357	Phenyl and pyrazole ring	π -Alkyl	-7.2
	His 293	Pyrazole ring	Hydrogen Bond (2.57)	
	His 293	Phenyl ring	π -Cation	
	Glu 204	Phenyl ring	π -Anion	
P ₁₀	Thr 458	Phenyl ring	π -Donor Hydrogen Bond	-6.7
	Leu 167, His 293, Ile 297, Met 459, Val 460, Ala 465	Chlorine and phenyl ring	Alkyl and π -Alkyl	
	Thr 294, Gly 424	Phenyl ring	π -Sigma	
	Cys 422	Phenyl ring	π -Donor Hydrogen Bond (2.35)	
P ₁₁	Ala 290	Phenyl and pyrazole ring	Amide π -stacked	-7.4
	Leu 133, Ala 287, Leu 355, Cys 422, Leu 429, Val 432	Methyl group Phenyl and pyrazole ring	Alkyl and π -Alkyl	
	Gly 291	-	Van Der Waals	
	His 457	NO ₂ group	Hydrogen Bond (2.39)	
P ₁₂	Met 357	Phenyl ring	π -Sulfur	-7.9
	Phe 48	Phenyl ring	π - π Stacked	
	Ile 71, Pro 209, Met 459	Phenyl ring	π -Alkyl	
	Met 459	Amine group	Hydrogen Bond (2.14)	
P ₁₃	Met 357	Phenyl ring	π -Sulfur	-7.4
	Phe 48, Pro 52, Ile 71, Ile 76, Phe 213, Val 356, Met 357	Chlorine and methyl groups	Alkyl and π -Alkyl	
	Pyrazole ring	Pyrazole ring	π - π Stacked	
	Tyr 456, Thr 458	Amine group	Hydrogen Bond	
P ₁₃	Met 357	Phenyl ring	Tyr 456 (2.04), Thr 458 (2.49)	-7.4
	Phe 48, Phe 213	Phenyl ring	π -Sulfur	
	Phe 48, Ile 71, Pro 209, Phe 213, Met 357, Met 359	Methyl, pyrazole, and Cl moiety	π - π Stacked	
	Pro 52, Val 356, Met 459	-	Alkyl and π -Alkyl	
P ₁₃	Val 356, Met 357	NO ₂ and CN groups	Van Der Waals	-7.4
			Hydrogen Bond	
			Val 356 (2.09), Met 357 (2.06)	

(continued on next page)

Table 2 (continued)

Entry	Amino Acid	Ligand involved moiety	Type of interaction and distanced of hydrogen bond interaction (Å)	B.E (kcal/mol)
P ₁₄	Met 359	Pyrazole ring	π -Sigma	-7.2
	Pro 209, Val 212, Phe 213	Methyl and pyrazole ring	π -Alkyl	
	His 420	Amine group	Hydrogen Bond	
	Thr 294	Furan ring	π -Sigma	
	Cys 422	Furan ring	π -Sulfur	
	Cys 422	Furan ring	π -Donor Hydrogen Bond (2.42)	
	Ala 290, Pro 354, Leu 355	Methyl group, pyrazole and furan rings	Alkyl and π -Alkyl	
Glucantime	Ile 349, Leu 358, Phe 415, Gly 416	-	Van Der Waals	-5.1
	Amine and hydroxy group	Cys 181, Phe 183, Ser 258	Hydrogen bond	
	-	Asn 140, Ser 144, Gln 180, Arg 188	Van Der Waals	

Fig. 10. LUMO, HOMO, and their energies diagram for P₁ (left) and P₁₂ (right) at the B3LYP/6-31 + G** level of theory.

3.7. Implications of findings and suggestions for future researches

Zoonotic cutaneous leishmaniasis is a neglected tropical infectious disease caused by an important species of the genus *Leishmania*, known as *L. major* that has affected many parts of tropical and subtropical regions [14]. Considering the lack of an effective vaccine so far and the limitation of drug treatments due to the occurrence of resistance or the presence of harmful side effects, the need for comprehensive investigations to obtain new drugs is quite noticeable. In this study, different derivatives of pyrazoles were first checked in terms of cytotoxicity in the cell culture environment and the effect of their non-toxic doses on the parasite was investigated in the *in vitro* environment.

It is apparent that the presence chloro group at position 4 of pyrazole moiety is more favorable and also, introducing nitro groups at phenyl ring resulted in enhancement the activity. On the other hand, in compounds that don't featuring chloro substitutions, the incorporation of at least two phenyl motif is necessary. Fortunately, one of the derivatives that showed more thermochemical resistance showed good lethality on promastigotes. It is necessary to enter this compound into an animal study on Balb/c inbred mice in the next step and if we get the right results, we will design a clinical trial to examine its effect on patients.

4. Conclusion

In summary, a new set of pyrazole and pyrano [2,3-*c*] pyrazole derivatives were evaluated for their antileishmanial activity. Among of all tested compounds, P₁, P₃, P₅, P₈, P₁₂, P₁₃, and P₁₄ were found to possess a promising antileishmanial activity with IC₅₀ values in a range of 34.79–43.55 $\mu\text{g}/\text{mL}$, which were 2–3 times more effective compared with Glucantime, the control drug (IC₅₀ = 97.31 $\mu\text{g}/\text{mL}$).

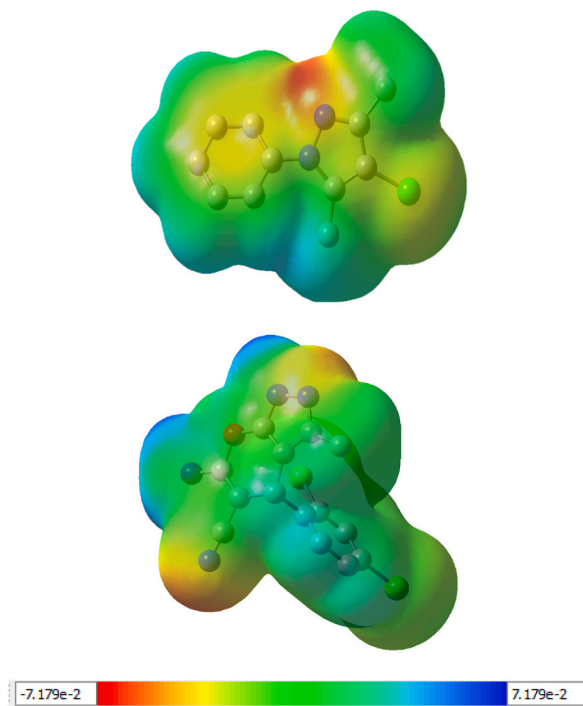


Fig. 11. Electrostatic potential maps for P_1 (left) and P_{12} (right) at B3LYP/6-31 + G (d,p) level of theory.

Table 3

The some DFT indices of P_1 and P_{12} at B3LYP/6-31 + G** level of theory.

Entry	E_{tot}^a	$H^{\circ a}$	$G^{\circ a}$	S^b	η^c	σ^d	A^c
P_1	-1744.84	-1744.84	-1744.91	140.76	2.72	0.36	0.69
P_{12}	-990.12	-990.12	-990.17	112.24	2.52	0.39	0.85

^a in Hartree/particle.

^b in cal/mol.K.

^c in ev.

^d in ev^{-1} .

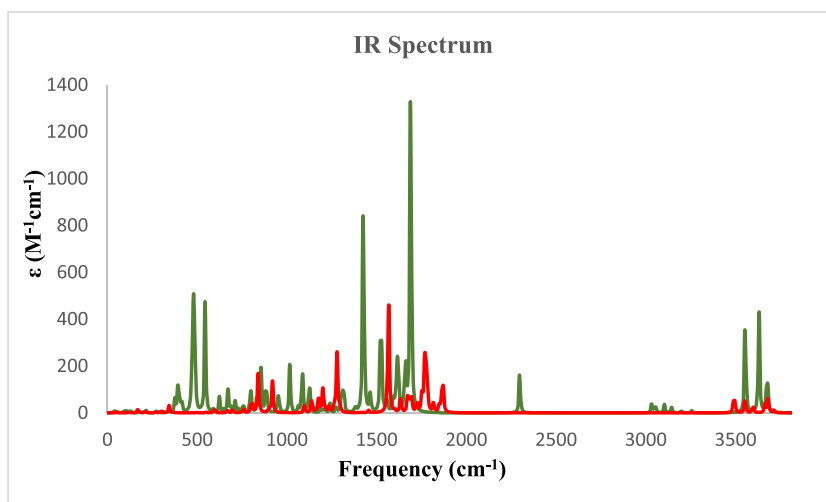


Fig. 12. Calculated IR spectra for P_1 (red) and P_{12} (green) at B3LYP/6-31 + G** level of theory.

mL). The SAR studies highlighted the significant role of chloro substitution at the C-4 position of pyrazole moiety and the phenyl moiety toward antileishmanial activity. Molecular docking studies also, showed possible binding interaction of the tested derivatives in the active site of CYP51 enzyme, an important target for antileishmanial agents. DFT analysis was performed on the most active compounds, P₁ and P₁₂. The DFT parameters such as energy gap HOMO and LUMO, hardness and softness parameters displayed that P₁₂ had greater stability and lower reactivity than P₁. The theoretical and experimental IR spectra for both compounds showed good agreement. Furthermore, *in silico* ADME properties demonstrated promising physicochemical and pharmacokinetic results for the active compounds. In overall, pyrazole and pyrano [2,3-c] pyrazole compounds are valuable lead scaffolds for further study in order to achieve new antileishmanial agents.

CRediT authorship contribution statement

Razieh Sabet: Project administration. **Gholamreza Hatam:** Project administration. **Leila Emami:** Writing – original draft. **Elaheh Ataollahi:** Writing – original draft, Software. **Fateme Zare:** Writing – original draft. **Leila Zamani:** Methodology. **Behnaz Kazemi:** Investigation. **Masood Mohabati Jahromi:** Investigation. **Sara Sadeghian:** Writing – review & editing. **Soghra Khabnadideh:** Supervision.

Ethics approval and consent to participate

All applicable international, national, and/or institutional guidelines for the care and use of live vertebrates were followed. All procedures performed in studies involving live vertebrates were in accordance with ethical standards of the institution or practice at which the studies were conducted. Procedures involving live vertebrates and their care were done under the ethical guidelines approved by Shiraz University of Medical Sciences, Shiraz, Iran.

Data availability statement

The used and analyzed data sets during the current study are available from the corresponding author upon request. We have showed all data in the form of Tables and Figures.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Soghra Khabnadideh reports financial support was provided by Shiraz University of Medical Sciences. Soghra Khabnadideh reports a relationship with Shiraz University of Medical Sciences that includes: board membership, employment, and funding grants. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.heliyon.2024.e40444>.

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