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Structure based medicinal chemistry-driven strategy to design substituted dihydropyrimidines as potential antileishmanial agents

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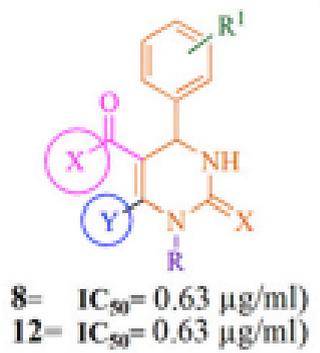
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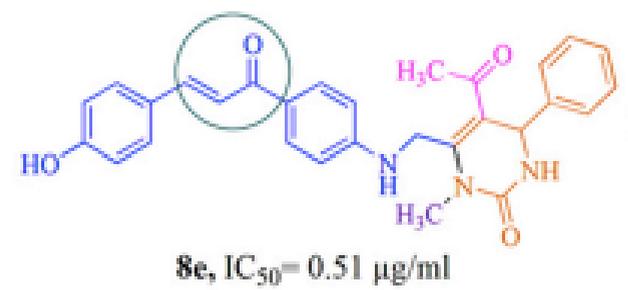
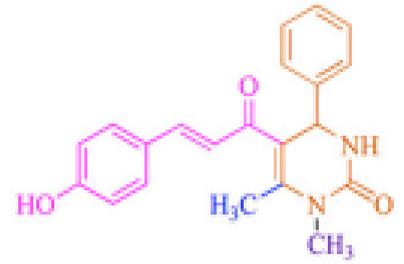




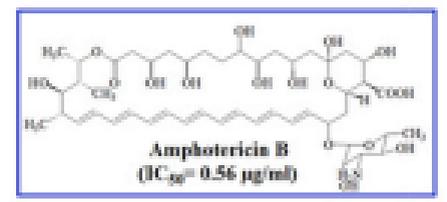
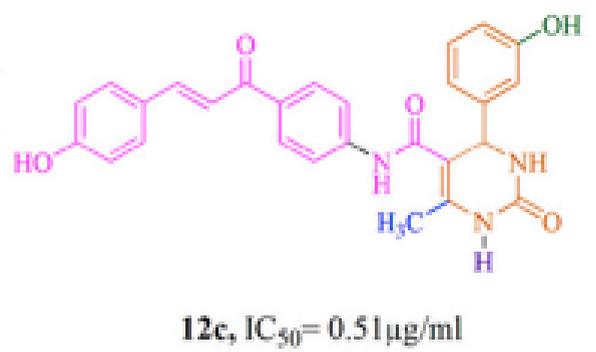
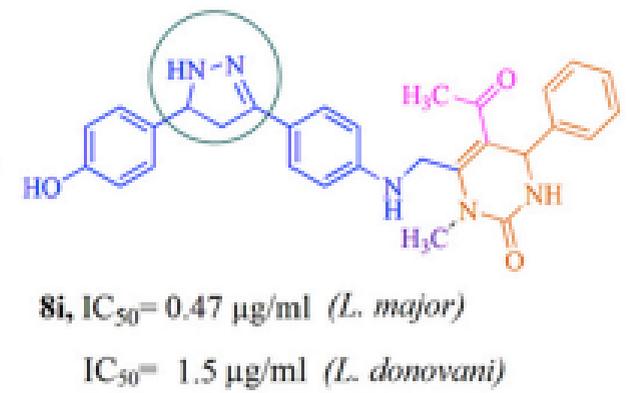
C-5 modification

C-6 modification

C-5 modification



Rigidification



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7 **Structure based medicinal chemistry-driven strategy to design substituted**
8 **dihydropyrimidines as potential antileishmanial agents**

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Abstract

In an attempt to explore novel and more potent antileishmanial compounds to diversify the current inhibitors, we pursued a medicinal chemistry-driven strategy to synthesize novel scaffolds with common pharmacophoric features of dihydropyrimidine and chalcone as current investigational antileishmanial compounds. Based on the reported X-ray structure of *Pteridine reductase 1* (PTR1) from *L. major*, we have designed a number of dihydropyrimidine-based derivatives to make specific interactions in PTR1 active site. Our lead compound **8i** has shown potent *in vitro* antileishmanial activity against promastigotes of *L. Major* and *L. donovani* with IC₅₀ value of 0.47 µg/ml and 1.5 µg/ml respectively. The excellent *in vitro* activity conclusively revealed that our lead compound is efficient enough to eradicate both visceral and topical leishmaniasis. In addition, docking analysis and *in silico* ADMET predictions were also carried out. Predicted molecular properties supported our experimental analysis that these compounds have potential to eradicate both visceral and topical leishmaniasis.

Key words: Leishmaniasis, Structure based drug design, Chalcones, Dihydropyrimidine, Docking, Rigidification

1

2 **1. Introduction**

3 Leishmaniasis is an infectious disease caused by *Leishmania* parasites belonging to genus *Leishmania* in
4 the family Trypanosomatidae. It is transmitted into host blood by the bite of female sand fly [1]. These
5 parasites can attack on mammals and human beings. When sandfly bites an infected organism parasite pass
6 from the blood of infected organism into the gut of the sandfly. These parasites grow in the gut of sandfly
7 for 8-20 days. When an infected sandfly bites a healthy organism it delivers these parasites
8 (metacyclicpromastigote) in the blood of that organism. The infected stage, metacyclicpromastigotes
9 inoculated in the rupture skin where it is phagocytosed by macrophages. The promastigotes multiplies and
10 turn into amastigotes and infect many tissues which gradually express the disease. There are more than 20
11 Leishmanial protozoan species, that are responsible for a number of clinical forms of leishmaniasis such as
12 cutaneous, diffuse cutaneous, disseminated cutaneous, mucocutaneous, visceral and post-kala-azar dermal
13 leishmaniasis (PKDL). Leishmaniasis has many symptoms, such as destructive mucosal inflammation, skin
14 lesions, ulcer and visceral infection (effects internal organs such as liver and spleen), fever and sometime
15 anemia. This disease is prevalent in 88 countries, including Asia, Africa and Latin America. Visceral
16 leishmaniasis (VL) is the most devastating and fatal form of leishmaniasis. It is caused by *L. donovani* and
17 *L. infantum*. VL patients are prone to bacterial co-infection including tuberculosis and pneumonia etc. Post-
18 kala-azar dermal leishmaniasis (PKDL), a form of dermal leishmaniasis caused by *L. donovani*, is a sequel
19 of VL and develops months to years in VL cure patients [2].

20 In recent years, a plethora of investigational compounds has been investigated for antileishmanial activity.
21 The major approved antileishmanial drugs are: pentavalent antimony drugs (meglumine antimoniate and
22 sodium stibogluconate), pentamidine, miltefosine and amphotericin B. All these available treatments are
23 not satisfactorily significant and have many draw backs such as renal dysfunction, nausea, anorexia, fever
24 etc. There are also some reports of cardiac deaths. Besides investigational drugs, natural products are
25 valuable sources in finding lead compounds. Flavonoids such as quercetin and luteolin emerged as potent
26 antileishmanial agents against *L. donovani*. Similarly, natural products like lichochalcone A, iridoids,
27 naphtoquinones, quinolone alkaloids, saponins, lignans and coumarins have shown promising
28 antileishmanial activities [3-5]. Immunotherapy is considered as best alternative for the treatment of VL.
29 Despite intense attempts to develop a prophylactic vaccine, there is no safe and efficacious vaccine against
30 leishmaniasis due to inadequate knowledge of early immune response and poor understanding of parasite
31 pathogenesis. However, Leish-111f+MPL-SE vaccine has been proved promising to control VL [6-7].
32 Apart from chemotherapy/vaccination, leishmaniasis can be controlled by taking some safety measures like
33 reservoir eradication, use of insect repellent, protective clothing and use of fine-mesh netting to prevent
34 exposure to female sand fly [8].

1 Chalcones (1,3-diaryl-2-propen-1-ones), belonging to the flavonoid family, have been reported to possess
2 many pharmacological activities. Zhai et al reported oxygenated chalcones as potent inhibitors of *L. major*
3 with IC_{50} in the range of 4.0-10.5 mM [3]. Foroumadi et al investigated chromene-based chalcones namely,
4 1-(6-methoxy-2H-chromen-3-yl)3-phenylpropen-1-ones and 3-(6-methoxy-2H-chromen-3-yl)-1-phenyl-
5 propen-1-ones for their antileishmanial activity against promastigotes form of *Leishmania major* [9]. These
6 chalcones exhibited excellent activity at non-cytotoxic concentrations. Narender et al. reported promising
7 antileishmanial activity of naturally occurring chromenochalcones [10]. 3,4-Dihydropyrimidine (DHPM) is
8 the most attractive derivative of pyrimidines for a medicinal chemist. This structural motif may also be
9 described as a derivative of cyclic urea. These non-planar heterocyclic compounds have received
10 considerable attention of the pharmaceutical industry because of their interesting multifaceted
11 pharmacological profiles. In the exploration of new and more potent antileishmanial compounds to
12 diversify the current inhibitors, it is essential to design novel and potent inhibitors. Singh et al. identified
13 potent dihydropyrimidine (DHPM) based derivatives targeting *Pteridine reductase* (PTR1) [11-12].
14 Recently, Kaur et al. reported monastrol, a dihydropyrimidine based KSP inhibitor, as a potent
15 antileishmanial agent [13].

16 In our group, a major part of our research is focused on computer-aided drug design with subsequent
17 synthesis and testing of new chemical entities as putative drugs for the treatment of various diseases [14-
18 16]. Our group recently identified a series of N-(1-methyl-1H-indol-3-yl)methyleneamines and eight new
19 3,3-diaryl-4-(1-methyl-1H-indol-3-yl)azetidin-2-ones against *Leishmania major* [17]. In another study, we
20 identified a variety of 2-aryl- and 5-nitro-2-arylbenzimidazoles as new antileishmanial agents with IC_{50}
21 values ranging from 0.62-0.92 $\mu\text{g/ml}$ [18]. In continuation of our endeavor and considering the
22 pharmacological importance of DHPM scaffold, it was planned to design and synthesize a variety of
23 DHPM-based potent antileishmanial compounds to diversify the current inhibitors.

24 2. Results and discussion

25 2.1. The Design strategy

26 Molecular docking has contributed a lot in the identification of novel small drug-like scaffolds exhibiting
27 high binding affinity and selectivity for the target. Hence, we extended our study to investigate *in silico*
28 binding orientation of the synthesized DHPMs. *Pteridine reductase* (PTR1) is an important enzyme
29 responsible for Pteridine salvage in leishmania and other trypanosomatid protozoans. PTR1 contributes to
30 antifolate resistance and is responsible for the failure of conventional therapies such as methotrexate
31 (MTX) against these protozoans [19]. In a study, Singh et al. reported DHPM analogues targeting PTR1,
32 therefore, we focused on molecular docking studies to investigate PTR1 (from *L. major*) as a possible
33 target for our newly synthesized DHPM derivatives. Crystal structure of PTR1 (PDB ID 1E7W, from *L.*
34 *major*) with MTX as the co-crystallized ligand was selected for these studies [20]. Docking experiments
35 were performed *via* Molecular Operating Environment (MOE) docking program [21].

1 **Table 1** enlists the 50% inhibitory concentration (IC_{50}) values of dihydropyrimidines (**1-13**). Compounds
2 **1-13** showed varying degrees of antileishmanial activities with IC_{50} values ranging between 0.61 and 0.99
3 $\mu\text{g/ml}$ as compared to standard amphotericin B ($IC_{50} = 0.56 \mu\text{g/ml}$). Compound **3** ($IC_{50} = 0.61 \pm 0.01$), **4**
4 ($IC_{50} = 0.67 \pm 0.04 \mu\text{g/ml}$), **8** ($IC_{50} = 0.63 \pm 0.02 \mu\text{g/ml}$), **12** ($IC_{50} = 0.63 \pm 0.01 \mu\text{g/ml}$), **13** ($IC_{50} = 0.65 \pm 0.04$
5 $\mu\text{g/ml}$) and were found to show good *in vitro* activity against the promastigote form of *L. Major*.
6 Compounds **6** ($IC_{50} = 0.71 \pm 0.01 \mu\text{g/ml}$), **7** ($IC_{50} = 0.69 \pm 0.01 \mu\text{g/ml}$) and **9** ($IC_{50} = 0.74 \pm 0.04 \mu\text{g/ml}$) exhibited
7 moderate activities. Compounds **1, 2, 5, 10** and **11** showed weak activities with IC_{50} values between 0.78
8 and $0.89 \mu\text{g/ml}$.

9 Active site of PTR1 is an elongated and rigid cleft. Arg17, Asn109, Ser111, Phe113, Asp181, Met183,
10 Gln186, Leu188, Tyr194, Lys198, His241 are catalytically important residues (**Figure 1A-C**). Docking
11 analysis of compound **8** with $IC_{50} = 0.63 \pm 0.02 \mu\text{g/ml}$ was performed and our analysis identified unoccupied
12 space, which may be available to attract further modifications. Superimposed model of compound **8** with
13 MTX into the binding site of PTR1 (as viewed in Chimera 1.8.1) [22] is shown in **Figure 1A, B**. It is
14 revealed from **Figure 1C** that pteridine head group of MTX is embedded between Met183, Gln186 and
15 Leu188 and formed interactions with Gln186 at the distance of 1.4 \AA (**Figure 1B**). While the glutamate tail
16 accepted proton from Arg17 and Lys198. Phe113 forms π -stacking interactions with phenyl ring of *para*-
17 aminobenzoate (*pABA*)-glutamate tail (**Figure 1C**). The structure of compound **8** bound to PTR1 binding
18 site showed that carbonyl oxygen of the cyclic urea act as a strong hydrogen bond acceptor and formed
19 hydrogen bond with Lys198. Similarly, carbonyl oxygen of the C-5 acetyl group accepts hydrogen bond
20 from Arg17 (**Figure 1D**). The observed negative fitness value of binding interaction (-8.9001 Kcal/mol)
21 revealed that compound **8** was not tightly fitted into the active site. The orientation of MTX and its
22 hydrogen bonding and π -stacking interactions provide a framework for the novel scaffold design. On the
23 basis of these initial results, further molecular modeling, synthesis and *in vitro* PTR1 inhibition studies of
24 compound **8** and **12** were carried out.

25 We realized that compound **8** can be chose as a benchmark compound for structural modification and both
26 lipophilic and polar groups can be incorporated to probe extra binding interactions with the drug target. For
27 this purpose, we turned our attention to further decorate DHPM scaffold by varying substituents around
28 DHPM **8** to generate additional interactions with the drug target (**Series 1**). More specifically, we focused
29 on a well-established chain extension strategy of medicinal chemistry which involves the incorporation of
30 another functional group in the lead compound to enhance extra binding interactions with the PTR1. Based
31 on the input from docking studies (**See below**), we designed analogues by varying substituent at C-5 and C-
32 6 positions. Starting from C-5 acetyl group modification, a set of 5-cinnamoyl derivatives was synthesized
33 in an effort to increase the potency (**Table 2**, Compounds **8a-c**). Additionally, substitution at C-6 position
34 with 4-aminochalcone derivatives (**8d-i**) and the effect of placing 4-aminochalcone group at C-5 position of
35 thioxo-analogues (Compound **12a-d**, $IC_{50} = 0.63 \pm 0.01$) were also explored.

1 2.2. Chemistry

2 Dihydropyrimidines (**1-13**) were synthesized by using three component Biginelli reaction. Aldehydes, 1,3-
3 dicarbonyl compounds and urea/thiourea were reacted in a test tube under ultrasonic irradiation by using
4 SnCl₂ as catalyst and acetonitrile (ACN) as solvent (Scheme 1) [14]. DHPM **3** and **8**, having acetyl group at
5 C-5 position, can undergo Claisen-Schmidt condensation with appropriate aldehydes to form chalcones.
6 Furthermore, these may serve as versatile synthons capable of undergoing facile allylic bromination at C-6,
7 which may undergo nucleophilic displacement with 4-amino chalcones or with any other nucleophile.
8 Kolsov et al. studied effect of tautomerism in these two reactions and concluded that by inserting an alkyl
9 substituent at N-1 position not only increased the solubility but also eliminated the possibility of amide-
10 imidol tautomerism [23-24]. Based on these results, we initially started our investigation at C-5 position of
11 N-methyl DHPM **8** and a set of three 5-cinnamoyl-6-methyl-4-aryl-3,4-dihydropyrimidin-2(1H)-one (**8a-c**)
12 derivatives were synthesized by using Claisen-Schmidt condensation conditions (Scheme 2). The structures
13 of synthesized compounds were confirmed on the basis of their physical constants and spectral data. ¹H
14 NMR data of 5-cinnamoyl derivatives revealed the absence of C-5 acetyl protons and showed two
15 deshielded doublets, one proton integration each, appeared at 7.79-7.89 ppm and 7.56-7.59 ppm which
16 could be assigned to olefinic protons of α , β -unsaturated ketone. Their coupling constant ($J= 15.6-15.9$ Hz)
17 indicated the trans-relationship of H- α and H- β and hence confirming *E*-configuration of the compounds.

18 During one-pot Biginelli reaction, methyl group is generally introduced at C-6 position of the pyrimidine
19 ring by using a 1,3-dicarbonyl compound essentially having an acyl group. This methyl group can undergo
20 a facile bromination, described as allylic bromination, which may undergo nucleophilic substitution
21 reaction leading to C-6 modified DHPMs. Allylic bromination was carried out at low temperature (0°C) in
22 chloroform. The composition of crude reaction mixtures was monitored by LC/MS. In the chromatograms
23 of the initial reaction mixture, peaks of 6-methyl brominated product (**19A**), 5-bromo acetyl product (**19B**)
24 along with some di-brominated products was observed. The main peak (83%) corresponds to **19A**. These
25 results were consistent with results reported in the literature [24]. The mixture of compounds was separated
26 through standard silica gel column chromatography using n-hexane/ethyl acetate mixture as eluent. A
27 mixture of 6-bromomethyl derivative of DHPM and 4'-aminochalcones (**14-18**, Scheme 3a) in THF were
28 stirred in ultrasonic bath at the 40-45°C to yield products (**8d-h**, Scheme 3b).

29 Rigidification has been an important medicinal chemistry tactic used to increase the activity of drug.
30 Number of rotatable bonds measures molecular flexibility. Considering this medicinal chemistry approach,
31 we decided to rigidify the Compound **8e** by converting chalcone (rotatable bonds=8) moiety to a five-
32 membered pyrazoline ring (**8i**, rotatable bonds=7) (Scheme 4). Synthesis of pyrazoline **8i** involved [3+2]
33 annulation of enone functionality of chalcone **8e** by reaction with hydrazine and NaOH [25]. A pale yellow
34 colored solid was obtained by ultrasonic assisted reaction of chalcone with hydrazine and NaOH in 51%
35 yield. In ¹H NMR spectrum, an AMX pattern was observed. H_A, H_M and H_X protons of pyrazoline ring

1 appeared as doublets of a doublet at 4.81 ppm ($J=12.3$ Hz, 7.8 Hz) 3.93 ($J=17.1$ Hz, 12.3 Hz) and 3.44
2 ($J=7.8$ Hz, 17.1 Hz) ppm. The appearance of a downfield broad signal at 9.10 ppm was noticed for the
3 phenolic-OH. In ^{13}C -NMR spectra, C-4 and C-5 of pyrazoline ring appeared at 45.6 ppm and 56 ppm
4 respectively.

5 We also synthesized a new series of thioxo-analogues by substituting C-5 ethyl ester group with 4-amino
6 chalcone. This nucleophilic displacement reaction was carried out with 4-amino chalcones (**14-18**, Scheme
7 **3a**) in THF in ultrasonic bath at 40-45°C to yield products (**12a-d**). The synthesized compounds were
8 characterized on the basis of their physical constants and spectral data. ^1H NMR data of new thioxo-
9 analogues were recorded, and a few generalizations could be made. Absence of signals of C-5 ethyl ester (a
10 triplet at 1.09-1.14 ppm and a quartet at 4.01-4.10 ppm) and observation of a broad singlet, appeared at
11 9.23-9.27 ppm, was attributed to C-5 amide proton (NH-C=O) and was a clear indication of substitution
12 reaction. Similarly, two deshielded doublets, one proton integration each, appeared at 7.99-8.04 ppm and
13 7.61-7.63 ppm which could be assigned to olefinic protons of α , β -unsaturated ketone.

14 **2.3. *In vitro* antileishmanial assay**

15 Substitution at C-5 gave a comparable potency to lead compound **DHPM 8**. The presence of a nitro group
16 at 3-position of phenyl ring (**8a**) exhibited lower *in vitro* inhibition. However, compounds with hydroxyl
17 and chlorine group at 4-position of phenyl ring (**8b** & **c** respectively) have shown similar potency to **DHPM**
18 **8**. The results are summarized in Table 2. Furthermore, substitution at C-6 position with 4-aminochalcone
19 derivatives resulted in significant influence on antileishmanial activity with an IC_{50} values ranging from
20 0.51 to 0.71 $\mu\text{g/ml}$. As shown in Table 2, chalcone derivative **8f** with nitro group at 3-position of phenyl
21 ring has shown reduced potency. Similarly, derivative **8h** with 4-dimethylamino group also exhibited
22 reduced potency with IC_{50} value $0.71\pm 0.01\mu\text{g/mL}$. Compound **8e** ($\text{IC}_{50}= 0.51 \mu\text{g/ml}$) having 4-hydroxy
23 substituent at ring B of the chalcone moiety has emerged as the most promising compound of this series.
24 Compound **8g** with chloro substituent at 4-position showed IC_{50} value of 0.53 $\mu\text{g/ml}$. This could suggest
25 that certain aromatic substituents at 4-position on ring B of the chalcone moiety are important for
26 antileishmanial activity. The significance of the 4-hydroxyl group was investigated further and compound
27 **8e** ($\text{IC}_{50}= 0.51 \mu\text{g/ml}$) was selected as a representative derivative to explore the effect of cyclization. As can
28 be seen, our pyrazoline derivative **8i**, with $\text{IC}_{50}= 0.47 \mu\text{g/ml}$, is more potent than corresponding chalcone
29 analogue **8e**.

30 To determine whether the SAR study around thioxo-analogues has improved effect on the biological
31 activity, *in vitro* antileishmanial activity was evaluated. SAR data in Table 3 shows that the most potent
32 compound of this series **12c** ($\text{IC}_{50}= 0.51\pm 0.04$) has hydroxyl group at *meta* position of the C-4 phenyl ring
33 on DHPM and at *para* position of chalcone ring B. Addition of nitro group at position R^1 results in
34 decrease in activity compared to hydroxyl group.

1 The synthesized compounds were also tested against the promastigotes of *L. donovani*. Most of compounds
2 have shown no inhibition. However, lead compound **8i** have shown excellent activity with $IC_{50}= 1.5 \mu\text{g/ml}$.
3 Compound **12c** have shown good activity with $IC_{50}= 5.58\mu\text{g/ml}$. It is concluded that our lead compound **8i**
4 is efficient enough to eradicate both visceral and topical leishmaniasis.

5 **2.4. Molecular docking analysis of designed compounds**

6 In an attempt to gain insights and to explore the probable binding modes of synthesized compounds,
7 molecular docking of these compounds was performed into the active site of LmajPTR1 (*Lm*PTR1, PDB
8 1e7w) via MOE docking program. We focused on the properties of pteridine reductase 1 (PTR1) as drug
9 target for antileishmanial drug discovery. From Protein Data Bank, the available solved X-ray structures for
10 LmajPTR1 are: 1E7W, 1W0C, 2BF7, 1E92 and 3H4V. These crystal structures are in ternary complexes
11 with methotrexate (MTX), 7,8-dihydrobiopterin and 2,4,6-triaminoquinazoline. Selection of MTX, a folate
12 antagonist, resistant Leshmania, has provided much information about drug resistance. Two step folate
13 reduction mechanisms is the similar approach followed in both leishmania as well as in resistant
14 trypanosome. Therefore, we opted 1E7W as a useful target against resistant strains of the *L. major*. Another
15 intracellular protozoan species, *L. donovani*, is responsible for the most severe form of leishmaniasis i.e.
16 visceral leishmaniasis. *L. major* and *L. donovani* enzymes share 91% sequence identity and the catalytic
17 residues Asp181, Tyr191, Tyr194, and Lys198 are conserved; therefore, the details of the catalytic
18 mechanism are expected to be identical between them [26-28].

19 Present study encompasses the synthesis and *in vitro* evaluation of racemic DHPMs derivatives as
20 antileishmanial agents by exploiting the *in silico* predictive power. Hence, we were interested in exploring
21 the probable binding modes of enantiomerically pure (R) and (S) DHPMs into the active site of PTR1.
22 Molecular docking studies were carried out on both enantiomers of the synthesized DHPMs analogues.
23 Analysis of the 2D interactions of the compounds with better IC_{50} values showed a fair correlation between
24 the docking scores and their inhibitory activity against PTR1 (**Figure 2**). Docking analysis of the
25 compound **8a** ($IC_{50}= 0.59 \mu\text{g/mL}$, binding score -11.7909 Kcal/mol) is shown in **Figure 2A**. Phenyl ring at
26 C-4 nucleus of DHPM ring formed strong π - π interactions with Phe113. Carbonyl oxygen of α,β -
27 unsaturated ketone pointed towards Arg17. Similarly, carbonyl oxygen of the cyclic urea moiety formed a
28 hydrogen bond with Lys198.

29 In order to explore the potent inhibitory activity of chalcone (**8e**) and its pyrazoline analogue (**8i**), we
30 docked these compounds into the active site of PTR1. The binding model of compounds **8e** and **8i** is shown
31 in **Figure 2B-C**. Key interactions stabilized both compounds, and the important contact residues for the
32 docked ligands were Arg17, Ser111, Phe113, Met183, Gln186 and Leu188. The phenolic ring of compound
33 **8i**, similarly to **8e**, stabilized through H-bond with Met183, Gln186 and Leu188. The distance between the
34 hydroxyl group and these residues is shown in **Figure 2B** and **C**. In addition, these compounds are also
35 involved in the π - π stacking interactions between the aromatic ring A of chalcone/pyrazoline and Phe113.

1 The docking score, binding affinity and binding energy of ligand-protein complex were also compared.
2 Compound **8i** has the docking score -14.0053, strong binding affinity -10.463 Kcal/mol and lower binding
3 energy -42.899 Kcal/mol. On the other hand, fitness values of interactions for compound **8e** were -12.9871,
4 -9.236 Kcal/mol and -40.973 Kcal/mol respectively. Therefore, it is concluded that the difference of almost
5 2.0 Kcal/mol in the binding energy confirmed the stabilization of ligand-protein complex of **8i** as compared
6 to **8e**. This showed a fair correlation between the predicted binding free energy values of the compounds
7 and their inhibitory activity against PTR1 (1E7W). Superimposition of top-ranked docking conformations
8 revealed that phenolic ring of pyrazoline moiety of **8i** undergoes a rotation of 180 degrees relative to **8e**,
9 which alter the position of the hydroxyl group (**Figure 3**). Despite this difference in docking orientation,
10 phenolic group of both compounds share the same binding region and a trivial (from $IC_{50} = 0.51$ to 0.47
11 $\mu\text{g/mL}$) increase in the potency may be anticipated due to this conformational motion.

12 Parallel studies on weakly active compounds, for example compound **8a** and **8h**, were also conducted. It
13 can be noticed from Table 2 that compounds with 5-cinnamoyl core (**8a-c**) has showed decreased activity
14 due to missing interactions. Visual inspection of docked binding pose of compound **8a** indicates that it does
15 not share the complete space in the binding site of PTR1 and showed very few binding interactions with
16 target (**Figure 4A**). Similarly, compound **8h** oriented in such a way that it shows only one hydrogen bond
17 with Lys198 (**Figure 4B**). This may be explained by its improper fitting into the active site due to bulky
18 dimethyl amino group. The observed negative fitness values of binding interactions (-8.763 and -9.106
19 Kcal/mol respectively) for these compounds revealed that these compounds were not tightly fitted into the
20 active sites. This clearly demonstrates the weak activity of these compounds.

21 To explore how compounds of **Series 2** interacts with the active site residues, molecular docking studies of
22 the most active compound **12c** was carried out. The hydroxyl group (R), pointed towards Met 183 and
23 Gln186 and acts as a hydrogen bond donor. Carbonyl oxygen of chalcone pointed towards the guanidinium
24 group of Arg17 as hydrogen bond acceptor. Docking poses of **12c** are shown in **Figure 5**. In view of the
25 above, we were successful in occupying the empty space in the binding site of PTR1 and the observed
26 negative fitness values of interactions (i.e. docking score, binding affinity and binding energy) has shown a
27 rational correlation between the docking scores and their inhibitory activity toward PTR1.

28 **2.5. *In silico* ADMET predictions**

29 It is well recognized that employing computational absorption, distribution, metabolism and excretion
30 (ADME) predictions in combination with *in vitro* prediction (Docking studies) as early as possible in the
31 drug discovery process helps to reduce the number of safety issues and help to improve prediction success.
32 This early *in silico* ADME profiling, has in fact, decreased the proportion of drug candidates that fail in
33 clinical trials for ADME reasons. Owing to the excellent *in vitro* activity, we initiated *in silico* calculations
34 for drug-like characteristics and ADME prediction of compounds. An inspection of the data given in **Table**
35 **4** revealed that almost all compounds of **Series 1** have octanol-water partition coefficient (i.e. LogP) values
36 ranging from 3.49 to 5.42. However, molecular hydrophobicity, calculated as LogP, is not the only

1 indicator of drug absorption. Aqueous solubility of a compound is also an important factor and is the direct
2 measure of hydrophobicity of a compound [29]. **Table 4** shows the predicted values of solubility of
3 compounds (S_w in mg/ml) and it is clear that due to the low predicted values of solubility, these compounds
4 have shown less LogPermeability. On the other hand, amphotericin B has shown the lowest
5 LogPermeability (-11.516) and decreased logD values (less than -2.3, **Table 4**) and these decreased values
6 of amphotericin B are key factors responsible for its availability as IV-infusions clinically. Lead compound
7 **8i** is also predicted to be administered *via* IV-infusion to attain 100% bioavailability due to its reduced
8 LogPermeability (-10.5468) values. However, compound **8b** can be administered orally due to its improved
9 native solubility (0.0143 mg/mL), logP (3.49) and LogPermeability (-9.1511). Furthermore, compound **8h**
10 and **8i** are predicted to possess enhanced solubility in the gastric environment due to their reduced logD
11 values (-0.30 and -0.52) irrespective of curtailed native solubility of 0.0014 and 0.0038 mg/ml respectively
12 (**Table 4**). **12a-d** (Series 2) can be utilized to be administered *via* oral administration due to improved logD
13 to molecular weight band distributions (>50% orally bioavailable) irrespective of their low solubilities.
14 Total polar surface area (TPSA), another biological membrane penetration indicator, was calculated for
15 different pH values. In the blood stream (pH=7.4), a trivial increase TPSA of our lead compound **8i** (114.85
16 A^2 to 116.46 A^2) and amphotericin B (319.61 A^2 to 324.06 A^2) has been observed (**Figure 6**).
17 It was seen that some compounds like **8f**, **8h**, **12b** and **12c** violate some of the Lipinski's rule of 5 (Ro5) as
18 obvious from **Table 4**. But this Ro5 is not the only parameter to scrutinize the fate of the drug candidate to
19 enter the market. As referenced drug (amphotericin B) utilized in the present research also violate the MW
20 parameter with 924.09 Da. The allowed MW for amphotericin is <300 Da according to its log logD -2.31.
21 It is therefore, due its high molecular weight to logD distribution (less than 50% orally bioavailable), it is
22 administered as intravenous route to overcome the oral permeability barrier which is also obvious from its
23 low logPermeability (-11.516). Therefore, all the compounds were screened against their allowed molecular
24 weights to logD distributions at physiological pH 7.4.
25 It was found that allowed molecular weight range for these compounds depicts the accurate correlations
26 between the oral bioavailable >50% to that of calculated logPermeability of compounds. Where, compound
27 with no Ro5 violation (**8i**) but still pertain less logPermeability of -10.5468, as its allowed molecular
28 weight is between 350-400 Da. Henceforth, it pertains less oral bioavailability irrespective of obeying the
29 Ro5 and is suited to be administered intravenously.
30 With respect to tissue distribution, logD value of compounds was correlated with the plasma protein
31 binding (PPB). The logD values of all the compounds at various physiological pH of the alimentary canal is
32 tabulated and shown in **Figure 7a-b**. From the data presented in **Figure 7**, it is significant that almost all
33 the compounds pertaining logD values greater than 3 have more than 90% PPB, which is consistent with
34 results described in literature [30]. However, high protein binding of amphotericin B is eccentric to its high
35 molecular weight (i.e. greater than 500 Da) rather than logD [31]. Owing to the increased PPB capacity,
36 lead compounds **8i**, **12a-12d** pertain long duration of action and can be used to eradicate the visceral and
37 topical leishmaniasis (**Table 4**). Furthermore, increase in logD values of compound is responsible for

1 increased metabolic clearance over renal clearance as renal clearance decreases with lipophilicity [32]. In
2 addition, renal clearance is also related with the molecular weight distribution and hydrogen bond donor
3 (HBD) capacity of compounds. Hence, small molecules with MW below 350 Da will eliminate *via* renal
4 and higher molecular weight compounds *via* partially fecal route [33]. Similarly, compounds with HBD >4
5 will have greater tendency to eliminate *via* phase-II metabolism (glucoronidation) [34]. The renal clearance
6 of the compounds were predicted by their unbound percentage in the blood and tabulated in ml/min/kg
7 (**Table 4**). These predicted renal clearances may vary due to molecular weight distribution, active secretion
8 (*via* ATP driven efflux transporter P-glycoprotein). Therefore active eliminations are prone at the distal
9 parts of nephron (**Figure 8a-c**). The literature cut off values for propensity of molecules to be the substrate
10 at P-glycoprotein is: > 400 Da for MW and > 90 Å² for TPSA [35]. These predictions are promising and
11 hence deserve to be investigated further to assess the complete drug-likeness.

12 **3. Conclusion**

13 In summary, we have carried out medicinal chemistry-driven structure based modifications of 3,4-
14 dihydropyrimidine core. It is clear from the SAR exploration around DHPM **8** analogues that certain
15 aromatic substituents at 4-position on ring B of the chalcone moiety are important for antileishmanial
16 activity. Attempt to decrease the number of rotatable bonds resulted in increased potency presumably due
17 to hydrogen bond donor pattern of 4-OH group. In terms of potency, SAR exploration in Series 2
18 compounds offered generally lower potency over Series 1 compounds. In addition, *in silico* ADME data
19 revealed that the results of both series encourage further investigation on structural optimization and on *in*
20 *vivo* models.

21 **4. Experimental**

22 **4.1 General**

23 All the reagents and solvents were purchased from standard commercial vendors and were used without
24 any further purification. Sonication was performed in Elma E 30 H (Germany) ultrasonic cleaner with a
25 frequency of 37 KHz and a nominal power of 250 W. ¹H and ¹³C-NMR spectra were recorded in deuterated
26 solvents on a Bruker spectrometer at 300 and 75 MHz respectively using tetramethylsilane (TMS) as
27 internal reference. Chemical shifts are given in δ scale (ppm). Melting points were determined in open
28 capillaries using Gallenkamp melting point apparatus (MP-D). The progress of all the reactions was
29 monitored by TLC on 2.0 x 5.0 cm aluminum sheets pre-coated with silica gel 60F254 with a layer
30 thickness of 0.25 mm (Merck). LC-MS spectra were obtained using Agilent technologies 1200 series high
31 performance liquid chromatography comprising of G1315 DAD (diode array detector) and ion trap LCMS
32 G2445D SL.

33
34

1 **4.2. General method for the synthesis of 3,4-dihydropyrimidine-2-ones and 3,4-dihydropyrimidine-2-**
 2 **thiones (1-13)**

3 Dihydropyrimidines were synthesized according to our previous report procedure using ultrasonication
 4 [14].

5 A mixture of an aldehyde (10 mmol), a diamino compound (12 mmol), a dicarbonyl compound (10 mmol,
 6 mL), SnCl₂.2H₂O (10 mol %) and acetonitrile (10 mL) was mixed in a pyrex tube. The mixture was then
 7 irradiated in ultrasonic bath at 70-75°C. The reaction was monitored by TLC. After the completion of the
 8 reaction, the resulting precipitate was filtered and crude product was recrystallized from an appropriate
 9 solvent or purified through column chromatography. Spectroscopic data was consistent with the previously
 10 reported for these compounds.

11 **4.3. Synthesis of chalcones from dihydropyrimidines (Scheme 2, 8a-8c)**

12 In a pyrex tube 25 mL ethanol and 30 mL of NaOH (4M) solution was added. The flask was cooled in an
 13 ice-bath and then 2 mmol DHPM (0.488 gm) and substituted aldehydes (2 mmol) was finally added and
 14 placed in ultrasonic bath at 40-50 °C. After completion of the reaction (TLC), quenched in ice-cold water
 15 and then acidified with aq. HCl (1N). The precipitate obtained was re-crystallized from mixture of
 16 ethanol/water (1:0.5).

17 **4.3.1. 5-cinnamoyl-1,6-dimethyl-4-(3-nitrophenyl)-3,4-dihydropyrimidin-2(1H)-one (8a)**

18 Yield 610 mg (81%). Brown solid; Mp. 219-221 °C. R_f=0.45 (n-hexane/ethyl acetate 3:1). ¹H NMR (300
 19 MHz, DMSO-d₆): 8.81 (br s, 1H, NH), 8.19 (m, 2H, Ar-H), 7.92 (d, 1H, *J* = 15.6 Hz, H-C_β), 7.68 (m, 2H,
 20 Ar-H), 7.41 (d, 1H, *J* = 15.6 Hz, H-C_α), 7.10 (m, 5H, Ar-H), 5.11 (d, 1H, *J* = 3.0 Hz, CH), 3.19 (s, 3H, N-
 21 CH₃), 2.15 (s, 3H, CH₃). ¹³C-NMR (75 MHz, DMSO-): 190.1, 152.7, 151.0, 150.20, 149.0, 147.1, 144.3,
 22 136.4, 134.9, 132.6, 130.3, 129.9, 129.1, 126.2, 125.3, 120.0, 54.1, 30.7, 18.1. MS (EI) m/z 377.0 [M]⁺.

23 **4.3.2. (E)-5-cinnamoyl-4-(4-hydroxyphenyl)-1,6-dimethyl-3,4-dihydropyrimidin-2(1H)-one (8b)**

24 Yield 536 mg (77%). Yellow solid. Mp. 199-200°C. R_f=0.41 (n-hexane/ethyl acetate 5:1); ¹H NMR (300
 25 MHz, DMSO-d₆): δ 9.3 (s, 1H, OH), 8.87 (br s, 1H, NH), 7.81 (d, *J* = 15.9 Hz, 1H, H-C_β), 7.67 (d, *J* = 15.9
 26 Hz, 1H, H-C_α), 7.14 (m, 7H, Ar-H), 6.83 (d, 2H, *J* = 6.6 Hz, Ar-H), 5.07 (d, 1H, *J* = 3.3 Hz, CH), 3.17 (s,
 27 3H, N-CH₃), 2.18 (s, 3H, CH₃); ¹³C-NMR (75 MHz, DMSO-): δ 190.0, 162.2, 157.9, 153.1, 152.0, 149.4,
 28 145.1, 129.8, 128.4, 128.2, 122.0, 120.7, 118.0, 115.0, 54.9, 30.6, 18.0. MS (EI) m/z 348.0 [M]⁺.

29 **4.3.3. (E)-4-(4-chlorophenyl)-5-cinnamoyl-1,6-dimethyl-3,4-dihydropyrimidin-2(1H)-one (8c)**

30 Yield 651 mg (89%). Yellow solid. Mp. 211-212 °C. R_f: 0.47 (n-hexane/ethyl acetate 2:1). ¹H NMR (300
 31 MHz, DMSO-d₆): δ 8.93 (br s, 1H, NH), 7.79 (d, 1H, *J* = 15.9 Hz, H-C_β), 7.59 (d, 1H, *J* = 15.9 Hz, H-C_α),
 32 7.43 (d, 1H, *J* = 8.4 Hz, Ar-H), 7.32 (d, 1H, *J* = 8.4 Hz, Ar-H), 7.14 (m, 5H, Ar-H), 5.13 (d, 1H, *J* = 3.3
 33 Hz, CH), 3.21 (s, 3H, N-CH₃), 2.23 (s, 3H, CH₃); ¹³C-NMR (75 MHz, DMSO-): δ 192.6, 152.4, 150.9,
 34 145.7, 135.3, 130.2, 128.32, 127.1, 125.2, 122.9, 121.1, 119.8, 55.1, 30.3, 17.8. MS (EI) m/z 366.0 [M]⁺.

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36

4.4. Synthesis of 4'-aminochalcones (Scheme 3a, 14-18)

4'-aminochalcones were synthesized according to literature procedure [36].

To a stirred ice-cold solution of 4'-aminoacetophenone (1.352 gm, 10 mmol) and potassium hydroxide (1-2 pellets) in 20 mL ethanol was added drop-wise substituted aromatic benzaldehydes (10 mmol). Temperature of the reaction mixture was kept at room temperature. After completion of reaction mixture was poured into ice-water with continuous stirring and kept at 0-4 °C overnight. The precipitate obtained was filtered, washed and re-crystallized from mixture of ethanol/water (1:0.5).

4.4.1. (E)-1-(4'-aminophenyl)-3-phenylprop-2-en-1-one (14)

14 was synthesized by using 4'-aminoacetophenone (1.352 gm, 10 mmol) and benzaldehyde (1.06 gm, 10 mmol). Yellow solid; Yield 1.54 gm (69%). Mp = 146 °C; R_f = 0.51 (n-hexane:ethyl acetate 3:1); $^1\text{H NMR}$ (300 MHz, CDCl_3): δ (ppm) = 7.97 (d, J = 15.9 Hz, 1H, H-C $_{\beta}$), 7.69 (m, 3H, H-C $_{\alpha}$, 2 \times Ar-H), 7.18-7.30 (m, 5H, Ar-H), 6.81 (m, 2H, Ar-H), 5.82 (bs, 2H, NH $_2$); EIMS: $\text{C}_{15}\text{H}_{13}\text{NO}$, 223.0.

4.4.2. (E)-1-(4'-aminophenyl)-3-(4-hydroxyphenyl)prop-2-en-1-one (15)

15 was synthesized by using 4'-aminoacetophenone (1.352 gm, 10 mM) and 4-hydroxyphenyl benzaldehyde (1.22 gm, 10 mM). Yellow solid. Yield. 1.67 gm (71%). R_f = 0.55 (n-hexane:ethyl acetate 3:1). $^1\text{H NMR}$ (300 MHz, CDCl_3): δ 9.71 (s, 1H, OH), 7.93 (d, J = 15.6 Hz, 1H, H-C $_{\beta}$), 7.65 (m, 3H, H-C $_{\alpha}$, 2 \times Ar-H), 7.27-7.29 (m, 2H, Ar-H), 6.79-6.83 (m, 4H, Ar-H), 5.87 (bs, 2H, NH $_2$); MS (EI) m/z 239.0 [M] $^+$.

4.4.3. (E)-1-(4'-aminophenyl)-3-(4-nitrophenyl)prop-2-en-1-one (16)

16 was synthesized by using 4'-aminoacetophenone (1.352 gm, 10 mM) and 4-nitrophenyl benzaldehyde (1.51 gm, 10 mM). Dark yellow solid, Yield. 1.53 gm (57%). R_f = 0.40 (n-hexane/ethyl acetate 3:1). Mp: 185 °C.; $^1\text{H NMR}$ (300 MHz, CDCl_3) δ 8.21 (m, 2H, Ar-H), 7.98 (d, J = 15.6 Hz, 1H, H-C $_{\beta}$), 7.71 (d, J = 15.6 Hz, 1H, H-C $_{\alpha}$), 7.61 (m, 4H, Ar-H), 6.81 (m, 2H, Ar-H), 5.81 (bs, 2H, NH $_2$); LC-MS m/z 269 [M+H].

4.4.4. (E)-1-(4'-aminophenyl)-3-(4-chlorophenyl)prop-2-en-1-one (17)

17 was synthesized by using 4'-aminoacetophenone (1.352 gm, 10 mM) and 4-chlorophenyl benzaldehyde (1.40 gm, 10 mM). Yellow solid, Yield 1.31 gm (51%). R_f = 0.53 (n-hexane/ethyl acetate 2:1). Mp: 171 °C.; $^1\text{H NMR}$ (300 MHz, CDCl_3) δ 7.93 (d, J = 15.9 Hz, 1H, H-C $_{\beta}$), 7.69 (m, 3H, H-C $_{\alpha}$, 2 \times Ar-H), 7.23-7.25 (m, 4H, Ar-H), 6.86-6.88 (m, 2H, Ar-H), 5.83 (bs, 2H, NH $_2$); LC-MS m/z 258 [M+H].

4.4.5. (E)-1-(4'-aminophenyl)-3-(4-(dimethylamino)phenyl)prop-2-en-1-one (18)

18 was synthesized by using 4'-aminoacetophenone (1.352 gm, 10 mM) and 4-(dimethylamino)phenyl benzaldehyde (1.492 gm, 10 mM). Light yellow solid, Yield. 81%. R_f = 0.47 (n-hexane/ethyl acetate 3:1). m.p = 157 °C; $^1\text{H NMR}$ (300 MHz, CDCl_3) δ 7.93 (d, J = 15.6 Hz, 1H, H-C $_{\beta}$), 7.61 (m, 3H, H-C $_{\alpha}$, 2 \times Ar-H), 7.23-7.27 (m, 2H, Ar-H), 6.73-6.77 (m, 4H, Ar-H), 5.86 (bs, 2H, NH $_2$), 2.97 (s, 6H, N(CH $_3$) $_2$); LC-MS m/z 267 [M+H].

1 **4.5. Synthesis of 6-bromo DHPM (Scheme 3b)**

2 Dihydropyrimidine (**8**) (2.44 gm, 10 mmol) was suspended in 30 mL CHCl₃ and then bromine (0.52 ml, 10
3 mmol) was added drop-wise through dropping funnel and stirred at 4 °C for 18 hrs. After completion of
4 reaction, the solvent was removed under reduced pressure and residue was purified by silica gel column
5 chromatography to afford the product.

6 **4.5.1. 5-acetyl-6-(bromomethyl)-1-methyl-4-phenyl-3,4-dihydropyrimidin-2(1H)-one (19A)**

7 Yield. 2.51 gm (78%). White solid. Mp: 135-137 °C. R_f: 0.38 (n-hexane:ethyl acetate 3:1). UV absorption
8 at 297.00 nm, ¹H NMR (300 MHz, DMSO-d₆): δ 9.49 (s, 1H, NH), 7.24 (m, 5H, Ar-H), 5.16 (d, 1H, J=3.0
9 Hz, CH), 4.64 (s, 2H, CH₂Br), 3.16 (s, 3H, N-CH₃), 2.50 (s, 3H, COCH₃). ¹³C-NMR (75 MHz, DMSO-d₆):
10 δ 194.7, 152.9, 145.9, 120.2-127.0, 101.18, 53.3, 39.78, 30.5, 29.4; LC-MS m/z 323 (M+H).

11 **4.5.2. 5-(2-bromoacetyl)-1,6-dimethyl-4-phenyl-3,4-dihydropyrimidin-2(1H)-one (19B)**

12 Yield. 0.58 gm (18%). White solid. LC-MS m/z 323 (M+H)

13 **4.6. C-6 substitution reaction of brominated DHPM (Scheme 3b, 8d-h)**

14 In a pyrex tube, a mixture of 4'-aminochalcones (**14-18**, 2 mmol) and 6-bromo DHPM (0.646 gm, 2 mmol)
15 in THF (5 mL) was heated in ultrasonic bath at 40 °C. The reaction was monitored by TLC. The precipitate
16 obtained was filtered, washed with sodium bicarbonate (2 × 10 mL, 0.1M). The crude solid was
17 recrystallized from a mixture of petroleum ether/ethanol (1:1).

18 **4.6.1. (E)-5-acetyl-6-((4-cinnamoylphenylamino)methyl)-1-methyl-4-phenyl-3,4-dihydropyrimidin-2(1H)-**
19 **one (8d)**

20 Yellow crystals. Yield 716 mg (77%). LC-MS purity 99.98%, t_R= 5.3min. Mp.=211-213 °C. R_f=0.53 (n-
21 hexane/ethyl acetate 3:1). ¹H NMR (300 MHz, DMSO-d₆) δ 9.53 (s, 1H, NH pyrimidine), 7.83 (d, J = 15.9
22 Hz, 1H, H-β (Vinyl)), 7.71 (m, 3H, H-C_α 2 × Ar-H), 7.11 (m, 10H, Ar-H), 6.71 (d, 2H, Ar-H), 6.07 (t, 1H,
23 J=5.7Hz, 1H, CH₂-NH), 5.17 (d, 1H, J=3.0 Hz, CH), 3.23 (s, 3H, N-CH₃), 3.13 (d, 2H, J=7.2 Hz, CH₂N),
24 2.31 (s, 3H, COCH₃); ¹³C-NMR (75 MHz, DMSO-d₆): δ 195.0, 190.0, 151.1, 147.3, 142.5, 133, 120.0-
25 129.0, 103.6, 59.33, 53.3, 30.1, 28.7. LC-MS m/z 466.2 [M+H].

26 **4.6.2. (E)-5-acetyl-6-((4-(3-(4-hydroxyphenyl)acryloyl)phenylamino)methyl)-1-methyl-4-phenyl-3,4-**
27 **dihydro-pyrimidin-2(1H)-one (8e)**

28 Yellow crystals. Yield. 548 mg (57%). Yield 716 mg (77%). LC-MS purity 100.00%, t_R= 4.9 min. Mp:
29 223-224 °C. R_f: 0.42 (n-hexane/ethyl acetate 5:1). ¹H NMR (300 MHz, DMSO-d₆) δ 9.71 (s, 1H, OH), 9.57
30 (br s, 1H, NH pyrimidine), 7.79 (d, 1H, J = 15.9 Hz, H_β (Vinyl)), 7.63 (m, 3H, 1H-C_α, 2 × Ar-H), 7.13 (m,
31 7H, Ar-H), 6.79 (m, 4H, Ar-H), 6.13 (t, 1H, J=5.7 Hz, CH₂-NH), 5.21 (d, 1H, J=3.0 Hz, CH), 3.25 (s, 3H,
32 N-CH₃), 3.11 (d, 2H, J=7.2 Hz, CH₂N), 2.37 (s, 3H, COCH₃). ¹³C-NMR (75 MHz, DMSO-d₆): δ 195.0,
33 190.5, 159.1, 150.2, 147.6, 142.7, 133.9, 131.0, 130.5, 129.5, 129.2, 128.1, 127.5, 118.9, 113.5, 103.3,
34 58.9, 52.1, 30.4, 28.1. LC-MS m/z 482.2 [M+H].

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1 **4.6.3. (E)-5-acetyl-1-methyl-6-((4-(3-(3-nitrophenyl)acryloyl)phenylamino)methyl)-4-phenyl-3,4-**
 2 **dihydropyrimidin-2(1H)-one (8f)**

3 Brown crystals. Yield 643mg (63%). LC-MS purity 100.00%, $t_R=6.0$ min. Mp: 229-231 °C. R_f : 0.42 (n-
 4 hexane/ethyl acetate 3:1). ^1H NMR (300 MHz, DMSO- d_6) δ 9.61 (br s, 1H, NH pyrimidine), 8.37 (s, 1H,
 5 Ar-H), 8.17 (m, 1H, Ar-H), 7.98 (d, 1H, $J = 15.9$ Hz, H_β (Vinyl)), 7.71 (d, 1H, $J = 15.9$ Hz, $H-\text{C}_\alpha$), 7.51 (m,
 6 4H, Ar-H), 7.14 (m, 5H, Ar-H), 6.73 (d, 2H, Ar-H), 6.19 (t, 1H, $J=5.7$ Hz, $\text{CH}_2\text{-NH}$), 5.17 (d, 1H, $J=3.0$ Hz,
 7 CH), 3.29 (s, 3H, N- CH_3), 3.13 (d, 2H, $J=7.2$ Hz, CH_2N), 2.33 (s, 3H, COCH_3). ^{13}C -NMR (75 MHz,
 8 DMSO- d_6): δ 195.5, 189.1, 150.5, 149.0, 147.6, 142.3, 121.9, 113.8-132.0, 103.2, 58.7, 53.6, 30.9, 27.9.
 9 LC-MS m/z 511.2 [M+H].

10 **4.6.4. (E)-5-acetyl-6-((4-(3-(4-chlorophenyl)acryloyl)phenylamino)methyl)-1-methyl-4-phenyl-3,4-**
 11 **dihydro-pyrimidin-2(1H)-one (8g)**

12 Yellow crystals. Yield. 509 mg (51%). LC-MS purity 99.53%, $t_R=8.9$ min. Mp: 193-194 °C. R_f : 0.50 (n-
 13 hexane/ethyl acetate 2:1). ^1H NMR (300 MHz, DMSO- d_6) δ 9.58 (bs, 1H, NH pyrimidine), 7.91 (d, 1H, $J =$
 14 15.9 Hz, H_β (Vinyl)), 7.67 (m, 3H, $H-\text{C}_\alpha$, 2 \times Ar-H), 7.10 (m, 9H, Ar-H), 6.79 (m, 2H, Ar-H), 6.27 (t, 1H,
 15 $J=5.7\text{Hz}$, 1NH, $\text{CH}_2\text{-NH}$), 5.29 (d, 1H, $J=3.0$ Hz, CH), 3.37 (d, 2H, $J=7.2$ Hz, CH_2N), 3.21 (s, 3H, N- CH_3),
 16 2.37 (s, 3H, COCH_3); ^{13}C -NMR (75 MHz, DMSO- d_6): δ 195.5, 189.3, 159.6, 152.6, 151.1, 146.9, 144.3,
 17 142.4, 135.2, 134.1, 130.0, 127.9, 126.6, 125.6, 123.0, 120.3, 119.9, 102.9, 58.3, 53.8, 30.3, 27.3. LC-MS
 18 m/z 500.2 [M+H].

19 **4.6.5. (E)-5-acetyl-6-((4-(3-(4-(dimethylamino)phenyl)acryloyl)phenylamino)methyl)-1-methyl-4-**
 20 **phenyl-3,4-dihydropyrimidin-2(1H)-one (8h)**

21 Brown solid. Yield 742 mg (73%). LC-MS purity 100.00%, $t_R=10.2$ min. Mp: 237-239 °C. $R_f=0.45$ (n-
 22 hexane/ethyl acetate 3:1). ^1H NMR (300 MHz, DMSO- d_6) δ 9.60 (br s, 1H, NH pyrimidine), 7.99 (d, 1H, J
 23 = 15.9 Hz, H_β), 7.65 (m, 3H, $H-\text{C}_\alpha$, 2 \times Ar-H), 7.06 (m, 7H, Ar-H), 6.68 (m, 4H, Ar-H), 6.26 (t, 1H,
 24 $J=5.7\text{Hz}$, $\text{CH}_2\text{-NH}$), 5.28 (d, 1H, $J=3.0$ Hz, CH), 3.37 (d, 2H, $J=7.2$ Hz, CH_2N), 3.20 (s, 3H, N- CH_3), 2.91
 25 (s, 6H, N(CH_3) $_2$), 2.33 (s, 3H, COCH_3). ^{13}C -NMR (75 MHz, DMSO- d_6): δ 195.0, 189.6, 151.4, 154.9,
 26 151.4, 149.4, 146.5, 142.3, 132.0, 130.6, 129.6, 128.8, 128.5, 127.2, 126.5, 124.5, 122.2, 121.3, 120.2,
 27 102.4, 58.0, 53.2, 41.4, 30.8, 27.0; LC-MS m/z 509.2 [M+H].

28 **4.7. Synthesis of pyrazolines (Scheme 4, 8i)**

29 In a pyrex tube containing 2.5 mmol of solid NaOH in ethanol (15 mL) was added chalcone (2 mmol) and
 30 hydrazine (2 mmol). The reaction mixture was heated in ultrasonic bath at 40 °C. Upon completion of the
 31 reaction (TLC), the reaction mixture was cooled to room temperature and quenched with 5 mL of a solution
 32 of dil. HCl. The reaction mixture concentrated to dryness in vacuum to afford the product as a solid. The
 33 crude solid was recrystallized from a mixture of n-hexane and methanol.

34 **4.7.1. 5-acetyl-6-((4-(5-(4-hydroxyphenyl)-4,5-dihydro-1H-pyrazol-3-yl)phenylamino)methyl)-1-methyl-**
 35 **4-phenyl-3,4-dihydropyrimidin-2(1H)-one (8i)**

36 Pale yellow solid. Yield 502 mg (51%). LC-MS purity 100.00%, $t_R=3.3$ min. Mp: 198-200 °C. $R_f=0.47$ (n-
 37 hexane/ethyl acetate 3:1). ^1H NMR (300 MHz, DMSO- d_6) δ 9.87 (s, 1H, pyrimidine-NH), 9.10 (s, 1H, Ar-

1 OH), 8.80 (s, 1H, pyrazoline-NH), 7.79 (d, 2H, $J=7.5$ Hz, Ar-H), 6.98 (m, 7H, Ar-H), 6.64 (d, 2H, $J=8.4$
 2 Hz, Ar-H), 6.42 (d, 2H, $J=8.4$ Hz, Ar-H), 5.99 (t, 1H, $J=5.7$ Hz, $\text{CH}_2\text{-NH}$), 5.15 (d, 1H, $J=3.0$ Hz,
 3 pyrimidine-CH), 4.81 (dd, $J=12.3$ Hz, 7.8 Hz, 1H, pyrazoline-CH), 3.93 (dd, $J=17.1$ Hz, 12.3 Hz, 1H,
 4 pyrazoline-CH), 3.44 (dd, $J=7.8$ Hz, 17.1 Hz, 1H, pyrazoline-CH), 3.23 (s, 3H, N- CH_3), 3.16 (d, 2H, $J=7.2$
 5 Hz, CH_2N), 2.39 (s, 3H, COCH_3); $^{13}\text{C-NMR}$ (75 MHz, DMSO- d_6): δ 195.0, 159.95, 153.50, 151.1, 149.9,
 6 148.9, 142.5, 139.0, 128.9, 128.8, 127.9, 126.6, 124.9, 123.5, 121.1, 121.0, 120.0, 103.0, 76.0, 59.33, 56.0,
 7 51.0, 30.5, 28.1; LC-MS m/z 493.2 [M+H].

8 **4.8. Series 2: SAR exploration around thioxo-analogues 12 and 13 (12a-d).**

9 In a pyrex tube, a mixture of 4'-aminochalcones (2 mmol) and thioxo DHPM **12** (0.58 gm, 2 mmol) and **13**
 10 (0.585 gm, 2 mmol) in THF (5 mL) was heated in ultrasonic bath at 40 °C. The reaction was monitored by
 11 TLC. The precipitate obtained was filtered, washed with sodium bicarbonate (2×10 mL, 0.1M). The crude
 12 solid was recrystallized from a mixture of petroleum ether/ethanol (1:1).

13 **4.8.1. (E)-N-(4-(3-(4-hydroxyphenyl)acryloyl)phenyl)-6-methyl-2-thioxo-4-p-tolyl-,3,4-dihydropyrimidine** 14 **-5-carboxamide (12a)**

15 Yellow crystals. Yield 589 mg (61%). LC-MS purity 99.98%, $t_R=17.6$ min. Mp: 219-221 °C. $R_f=0.38$ (n-
 16 hexane/ethyl acetate 5:1). $^1\text{H NMR}$ (300 MHz, DMSO- d_6) δ 9.88 (s, 1H, OH), 9.57 (br s, 1H, NH
 17 pyrimidine), 9.23 (br s, 1H, NH-CO), 8.24 (br s, 1H, NH), 8.04 (d, 1H, $J = 15.6$ Hz, H_β (Vinyl)), 7.71 (m,
 18 4H, Ar-H), 7.59 (d, 1H, $J = 15.6$ Hz, $H-C_\alpha$), 7.21 (m, 2H, Ar-H), 7.01 (m, 4H, Ar-H), 6.79 (m, 2H, Ar-H),
 19 5.14 (d, 1H, $J=3.3$ Hz, CH), 2.21 (s, 6H, $2 \times \text{CH}_3$); $^{13}\text{C-NMR}$ (75 MHz, DMSO- d_6): δ 190.5, 182.8, 167.2,
 20 159.6, 148.5, 144.7, 142.3, 139.9, 135.3, 133.5, 131.6, 129.8, 129.2, 129.0, 128.9, 128.8, 127.0, 125.6,
 21 124.9, 113.0, 100.72, 54.6, 26.3, 18.2. LC-MS m/z 484.2 [M+H].

22 **4.8.2. (E)-6-methyl-N-(4-(3-(3-nitrophenyl)acryloyl)phenyl)-2-thioxo-4-p-tolyl-3,4-dihydropyrimidine-5-** 23 **carboxamide (12b)**

24 Dark yellow crystals. Yield 584 mg (57%). LC-MS purity 100.00%, $t_R=11.2$ min. Mp =242-243 °C. R_f
 25 =0.38 (n-hexane/ethyl acetate 5:1). $^1\text{H NMR}$ (300 MHz, DMSO- d_6) δ 9.59 (bs, 1H, NH pyrimidine), 9.27
 26 (br s, 1H, NH-CO), 8.50 (s, 1H, Ar-H), 8.37 (br s, 1H, NH), 8.29 (m, 1H, Ar-H), 8.17 (d, 1H, $J = 15.9$ Hz,
 27 H_β), 7.99 (d, 1H, $J = 15.9$ Hz, H_α), 7.82 (d, 4H, Ar-H), 7.67 (d, 1H, Ar-H), 7.65 (d, 1H, Ar-H), 7.14 (s, 4H,
 28 Ar-H), 5.17 (d, 1H, $J=3.3$ Hz, CH), 2.23 (s, 6H, $2 \times \text{CH}_3$); $^{13}\text{C-NMR}$ (75 MHz, DMSO- d_6): δ 190.5, 182.8,
 29 167.2, 151.0, 148.5, 144.7, 124.9, 113.0-132.0, 54.6, 26.3, 18.2. LC-MS m/z 513.2 [M+H].

30 **4.8.3. (E)-4-(3-hydroxyphenyl)-N-(4-(3-(4-hydroxyphenyl)acryloyl)phenyl)-6-methyl-2-thioxo-3,4-** 31 **dihydro-pyrimidine-5-carboxamide (12c)**

32 Yellow crystals. Yield 650 mg (67%). LC-MS purity 100.00%, $t_R=10.3$ min. Mp: 219-221 °C. $R_f=0.51$
 33 (Chloroform/Methanol 5:1). $^1\text{H NMR}$ (300 MHz, DMSO- d_6) δ 9.96 (br s, 1H, OH-pyrimidine) 9.68 (s, 1H,
 34 OH-chalcone), 9.47 (bs, 1H, NH-pyrimidine), 9.21 (br s, 1H, NH-CO), 8.14 (br s, 1H, NH-pyrimidine), 7.99
 35 (d, 1H, $J = 15.9$ Hz, H_β), 7.61 (m, 5H, $H-C_\alpha$, $4 \times \text{Ar-H}$), 7.23 (d, 2H, $J = 6.3$ Hz, Ar-H), 6.96 (t, 1H, $J = 8.1$
 36 Hz, Ar-H), 6.74 (m, 3H, $J = 5.1$ Hz, Ar-H), 6.71 (d, 2H, $J = 5.1$ Hz, Ar-H), 5.27 (d, 1H, $J=3.3$ Hz, CH),
 37 2.26 (s, 3H, CH_3); $^{13}\text{C-NMR}$ (75 MHz, DMSO- d_6): δ 191.8, 182.1, 167.6, 160.4, 155.9, 148.7, 145.1,

1 144.9, 142.3, 131.1, 130.2, 129.6, 129.4, 128.7, 125.5, 124.1, 123.2, 120.1, 115.2, 112.0, 100.2, 54.9, 18.6.
2 LC-MS 486.1 [M+H].

3 **4.8.4. (E)-4-(3-hydroxyphenyl)-6-methyl-N-(4-(3-(3-nitrophenyl)acryloyl)phenyl)-2-thioxo-3,4-dihydro**
4 **pyrimidine-5-carboxamide (12d)**

5 Yellow crystals. Yield 648 mg (63%). LC-MS purity 100.00%, t_R =11.9 min. Mp: 229-230 °C. R_f =0.57
6 (Chloroform/Methanol 3:1). ^1H NMR (300 MHz, DMSO- d_6) δ 9.83 (br s, 1H, OH-pyrimidine), 9.51 (bs,
7 1H, NH-pyrimidine), 9.23 (br s, 1H, NH-CO), 8.59 (s, 1H, Ar-H), 8.43 (br s, 1H, NH-pyrimidine), 8.29 (m,
8 1H, Ar-H), 8.18 (d, 1H, J = 15.9 Hz, H_β), 7.94 (d, 1H, J = 15.9 Hz, $H-C_\alpha$), 7.85 (d, 4H, J = 6.6 Hz, Ar-H),
9 7.63 (d, 1H, J = 6.3 Hz, Ar-H), 7.49 (m, 1H, Ar-H), 7.011 (m, 1H, Ar-H), 6.67 (m, 3H, Ar-H), 5.27 (d,
10 1H, J =3.3 Hz, CH), 2.26 (s, 3H, CH_3); ^{13}C -NMR (75 MHz, DMSO- d_6): δ 191.2 (C=O), 181.3 (C=S), 167.1
11 (NHC=O), 161.9 (C-OH-pyrimidine), 151.8 (C- NO_2), 148.3 (C_β), 145.0 ($\text{CH}_3\text{C}=\text{C}$), 124.1 (C_α), 113.3-
12 129.2 (C-aromatic), 54.7 (CH-Ar), 26.2 (C-aromatic- CH_3), 18.5 (CH_3); LC-MS m/z 515.1 [M+H].

13 **4.8. Computational studies**

14 **3.8.1. Docking studies**

15 Docking studies were performed, using the Molecular Operating Environment (MOE) version 2011.12. The
16 program operated under 'Windows XP' operating system. To initialize the *in silico* studies, high resolution
17 crystal structures of proteins were retrieved from the PDB (PDB ID 1E7W, from *L. major*). The 3D
18 protonation of the 1E7W was done and energy minimization of the retrieved protein molecule was carried
19 out by using default parameters of MOE energy minimization algorithm [gradient: 0.05, Force Field:
20 MMFF94X]. Root mean square deviation (RMSD) was used to compare the ligand between the predicted
21 and its corresponding crystal structure. The resulting docked poses with RMSD less than 1.5Å were
22 clustered together. The lowest energy minimized pose was used for further analysis.

23 **4.8.2. ADMET predictions**

24 Various descriptors like logP, solubility (S_w) calculated as logS by MOE software and converted to mg/ml
25 units. Hydrogen bond acceptor (HBA), hydrogen bond donor (HBD), number of rotatable bonds (NOR)
26 and molecular weight (MW) were calculated by MOE software. While, logD7.4 and total polar surface area
27 (TPSA) was calculated via Marvin 6.0.0 software of Chemaxon [37]. Whereas, renal clearance (Cl), plasma
28 protein binding (PPB) and LogPermeability were calculated theoretically [38].

29 **4.9. In vitro antileishmanial activity**

30 Antileishmanial activity of the compounds was assayed using a pre-established culture of clinical isolate of
31 *L. major* and *L. donovani* obtained from National Institute of Health (NIH), Islamabad, Pakistan [10, 18].
32 Promastigotes were cultured in medium 199 (Cassion Laboratories, Inc. USA) containing 10 % fetal bovine
33 serum (ICN Flow, UK), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), sodium bicarbonate
34 (Sigma), penicillin (ICN Biochemicals, Inc. Germany), and streptomycin (Sigma). Incubation and growth
35 of the parasite were carried out at 24 °C. Briefly after 6–7 days of the culture, the promastigotes were

1 centrifuged at 3,000 rpm for 3 min, the supernatant was discarded and the pellet was washed three times
2 with phosphate buffer saline (MP-Biomedicals, Inc. France) and re-suspended in medium 199 at 2.9 × 10⁶
3 cell/mL. Promastigotes were seeded in 96-well round bottom microtiter plates (TPP, Switzerland)
4 containing serial dilution of the compound and media 199. Amphotericin B (BioChemica, Germany) and
5 DMSO were used as positive and negative controls, respectively. The plates were incubated for 72 h at 24
6 °C in shaker incubator. All the compounds were assayed in triplicate and the number of alive parasites was
7 determined by counting in Neubauer chamber. The inhibitory concentrations for the 50 % of the inhibition
8 IC were calculated by GraphPad Prism (GraphPad Prism Software, Inc. USA) software and data reported as
9 the mean ± SD.

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Figure Legends

Figure 1: Computer generated molecular models of Compound **8** (gold) superimposed on MTX (purple) docked into the binding site of PTR1 (A) Overall structure (B) Close-up view with important interactions (C) & (D) 2D ligand interaction maps of MTX and compound **8** respectively.

Figure 2: (A-C) 2D ligand interaction maps of compounds of Series 1 docked into the binding site of PTR1.

Figure 3: a) Superposition of the best conformations of Compound **8e** (Reddish brown) and **8i** (magenta) into the binding site of PTR1.

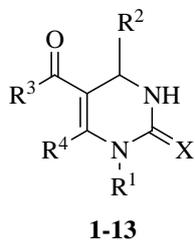
Figure 4: 2D ligand interaction maps of weakly active compounds (A) compound **8a** (B) compound **8h**.

Figure 5: Docking of **12c** in the active site of PTR1 a) 3D view b) 2D ligand interactions

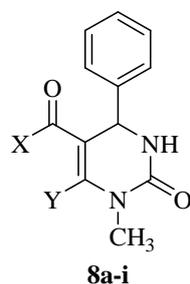
Figure 6: Total polar surface area depicted as TPSA of the compounds calculated by Marvin 6.0.0 of Chemaxon Software.

Figure 7: LogD values at various physiological pH. a) compounds of SAR series 1; 2) Compounds of SAR series 2

Figure 8: (a) and (b) depicts the relation between logD and renal clearances Cl in mg/ml/min. (c) Renal clearance in increasing trend of logD. (d) Increasing trend in renal clearance due to pharmacokinetic factors as MW, TPSA, HBD count (outer ring) as percentile. Highest clearance (24%) shown by lead compound **8i** (inner ring).

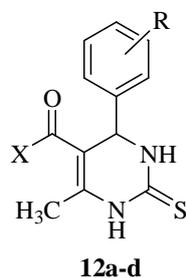
Table 1.*In vitro* antileishmanial activity of dihydropyrimidines (**1-13**)

Compound	R ¹	R ²	R ³	R ⁴	X	IC ₅₀ (μg/mL) ±SEM
1	H	C ₆ H ₅	OEt	Me	O	0.99±0.03
2	CH ₂ .C ₆ H ₅	C ₆ H ₅	OEt	Me	O	0.99±0.02
3	H	C ₆ H ₅	Me	Me	O	0.61±0.01
4	H	3-NO ₂ .C ₆ H ₄	Me	Me	O	0.67±0.04
5	H	3-Me.C ₆ H ₄	Me	Me	O	0.89±0.01
6	H	3-OMe,4-OH.C ₆ H ₃	Me	Me	O	0.71±0.01
7	H	4-OMe.C ₆ H ₄	Me	Me	O	0.69±0.01
8	Me	C ₆ H ₅	Me	Me	O	0.63±0.02
9	H	3-NO ₂ .C ₆ H ₄	OCHMe ₂	Me	O	0.74±0.04
10	H	3-NO ₂ .C ₆ H ₄	OMe	CH ₂ OMe	O	0.95±0.02
11	H	C ₆ H ₅	Me	Me	S	0.78±0.02
12	H	4-Me.C ₆ H ₄	OEt	Me	S	0.63±0.01
13	H	3-OH.C ₆ H ₄	OEt	Me	S	0.65±0.04
Amphoterecin B (Standard drug)						0.56±0.01

Table 2. SAR exploration around DHPM analogues (**8a-8i**)

Compound	X	Y	IC ₅₀ (µg/mL) ±SEM	
			<i>L. major</i>	<i>L. donovani</i>
8a		CH ₃	0.73±0.04	NI
8b		CH ₃	0.59±0.05	NI
8c		CH ₃	0.63±0.04	NI
8d	CH ₃		0.54±0.01	>100
8e	CH ₃		0.51±0.06	7.5
8f	CH ₃		0.67±0.05	>100
8g	CH ₃		0.53±0.04	4.40±0.98
8h	CH ₃		0.71±0.01	NI
8i	-		0.47±0.02	1.5±0.17
Amphoterecin B			0.56±0.01	
SSG (sodium stibogluconate)			-	2.98

SEM=Standard error of the mean; NI=No inhibition

Table 3. SAR exploration around thioxo-analogues (**12a-d**)

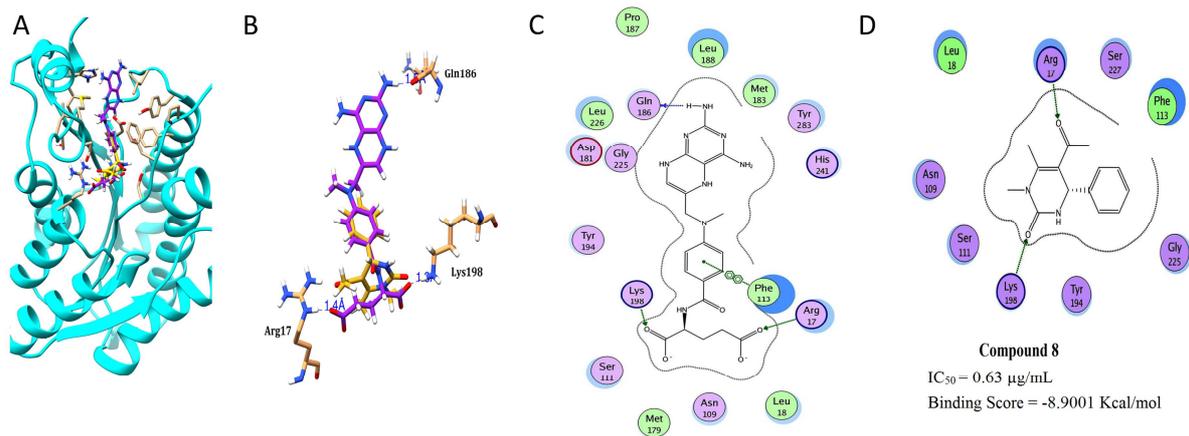
Compound	X	R	IC ₅₀ (μg/mL) ±SEM	
			<i>L. major</i>	<i>L. donovani</i>
12a		4-CH ₃	0.53±0.03	NI
12b		4-CH ₃	0.65±0.01	NI
12c		3-OH	0.51±0.04	5.58±1.1
12d		3-OH	0.58±0.01	NI
	Amphoterecin B		0.56±0.01	-
	SSG (sodium stibogluconate)		-	2.98

SEM=Standard error of the mean; NI=No inhibition

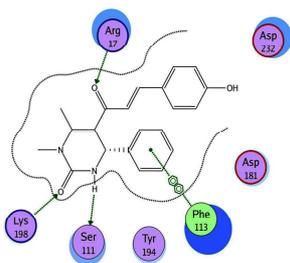
Table 4:

Descriptors of synthesized compounds

Comp.	logP	logD7.4	Sw mg/ml	LogPer	TPSA	HBA	HBD	NOR	CI	MW Da	logK	Allowed MW range	Oral Bioavailability
	MOE				A ²				ml/min/kg				
8a	3.77	3.36	0.0045	-10.2294	187.879	7	1	5	0.10485	377.4	-1.124	400-450	less 50%
8b	3.49	3.1	0.0143	-9.1511	157.403	5	2	4	0.1848	348.4	-0.852	350-400	S. less
8c	4.39	4.02	0.0048	-6.8452	107.21	4	1	4	0.0939	366.85	-1.175	450-500	>50%
8d	4.78	3.89	0.0015	-8.4391	162.639	6	2	8	0.1052	465.55	-1.123	450-500	>50%
8e	4.48	3.58	0.0022	-10.408	211.401	7	3	8	0.1309	481.55	-1.019	450-500	>50%
8f	4.76	3.83	0.0007	-11.675	246.272	9	2	9	0.0957	510.55	-1.166	450-500	less 50%
8g	5.38	4.5	0.0007	-8.2351	164.301	6	2	8	0.0725	499.99	-1.294	450-500	>50%
8h	4.7	4	0.0016	-9.8329	203.068	7	2	9	0.0897	508.62	-1.196	450-500	S. less
8i	4.12	2.53	0.0043	-10.5468	217.243	8	4	7	0.4266	495.58	-0.401	350-400	less 50%
12a	5.14	4.95	0.0003	-6.5709	122.55	4	4	7	0.103	483.59	-1.134	>500	>50%
12b	5.42	5.2	0.0001	-7.4393	148.14	3	3	8	0.081	512.59	-1.245	>500	>50%
12c	4.86	4.14	0.0002	-7.1931	142.78	4	4	8	0.098	514.56	-1.153	450-500	>50%
12d	4.58	4.38	0.0008	-8.52543	168.37	5	5	7	0.089	485.56	-1.195	450-500	>50%
Ampho	0.71	-2.31	0.0149	-11.516	319.61	17	13	3	0.091	924.09	-1.279	<300	less 50%

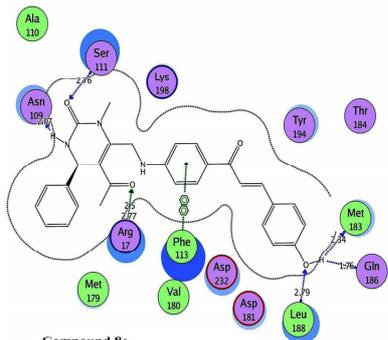


A



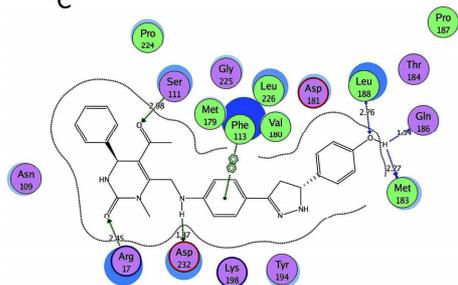
Compound 8a
IC₅₀= 0.59 µg/ml
Binding Score= -11.8301 Kcal/mol

B



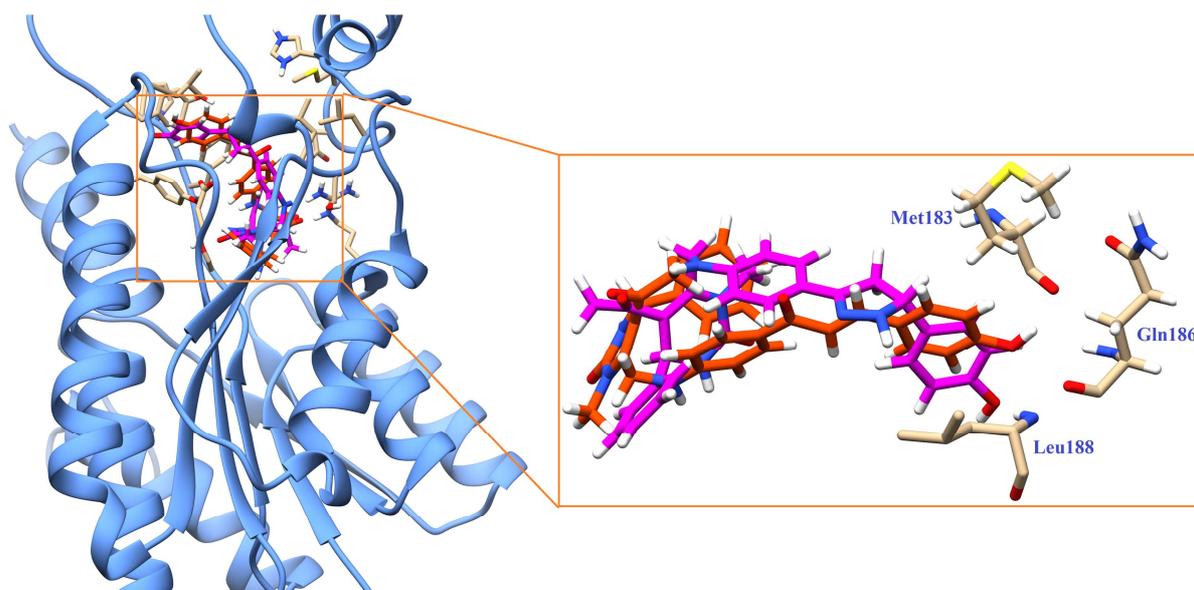
Compound 8c
IC₅₀= 0.51 µg/ml
Binding Score= -12.9871 Kcal/mol

C

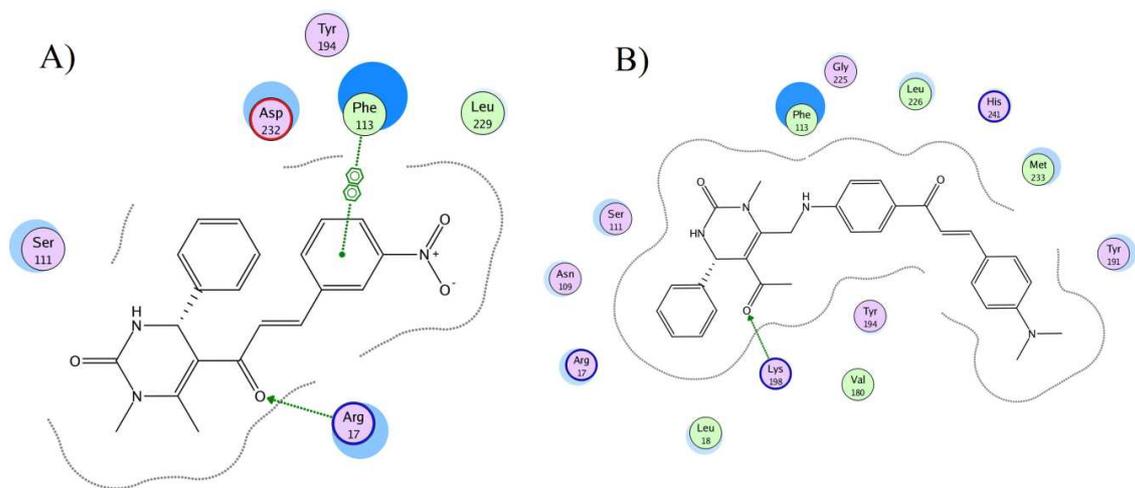


Compound 8i
IC₅₀= 0.47 µg/ml
Binding Score= -14.0053 Kcal/mol

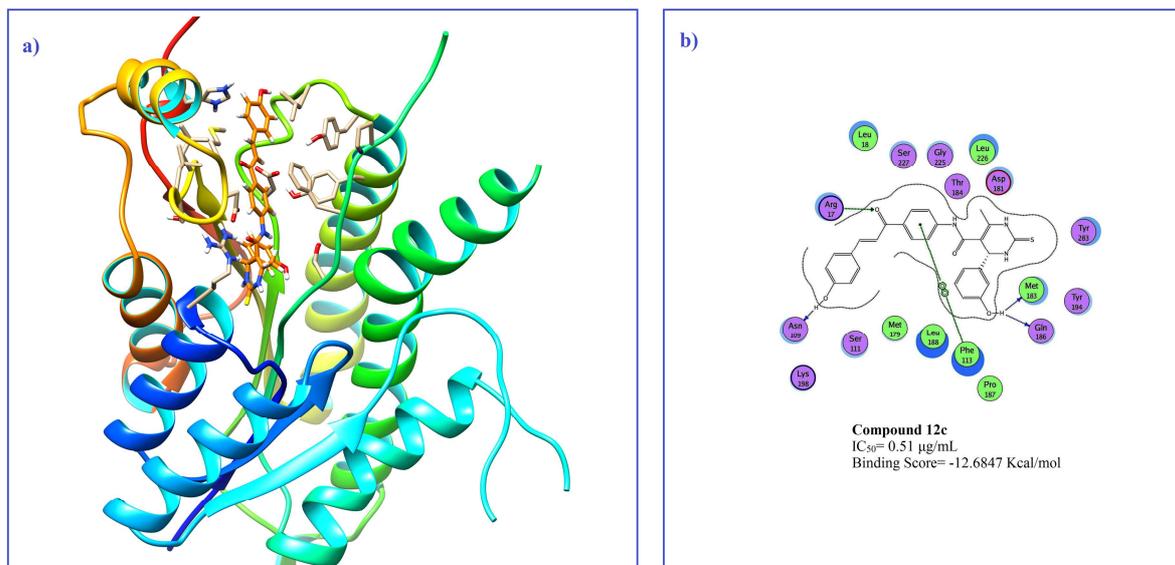
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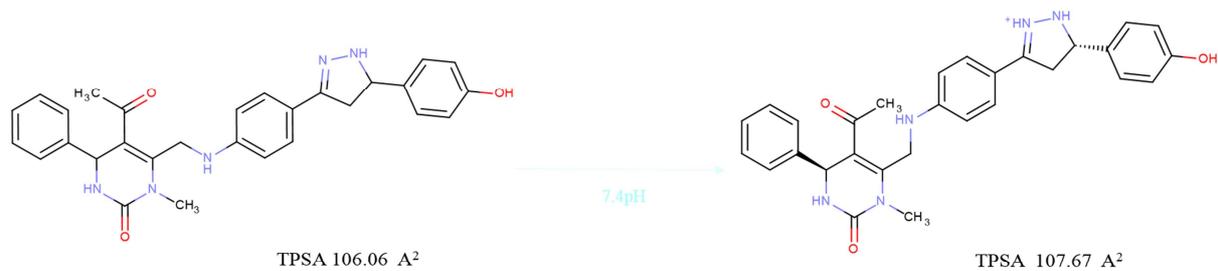
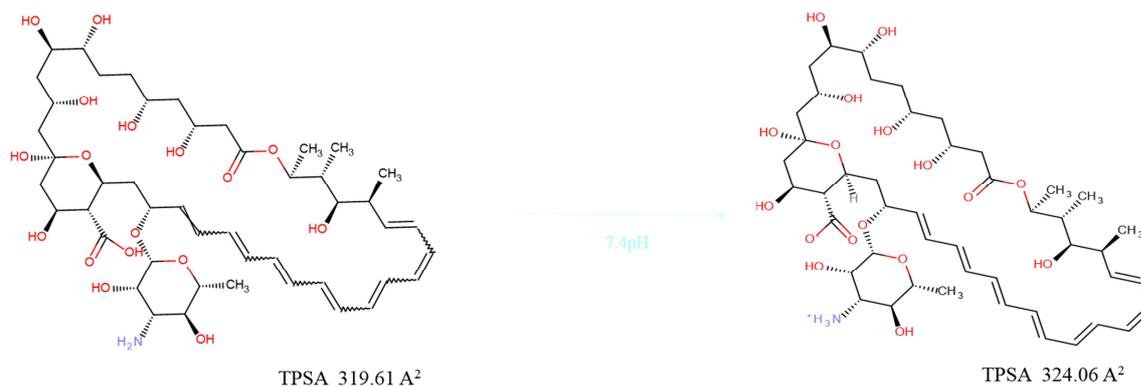
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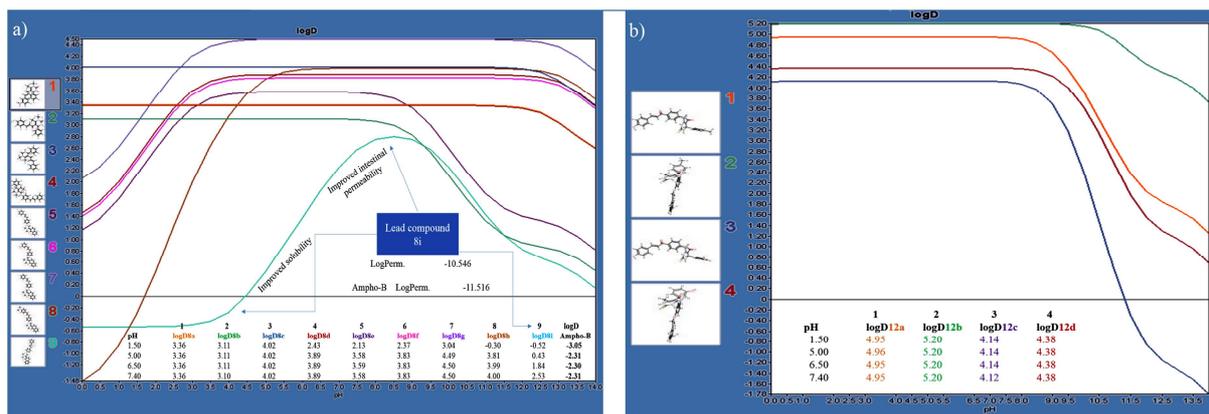


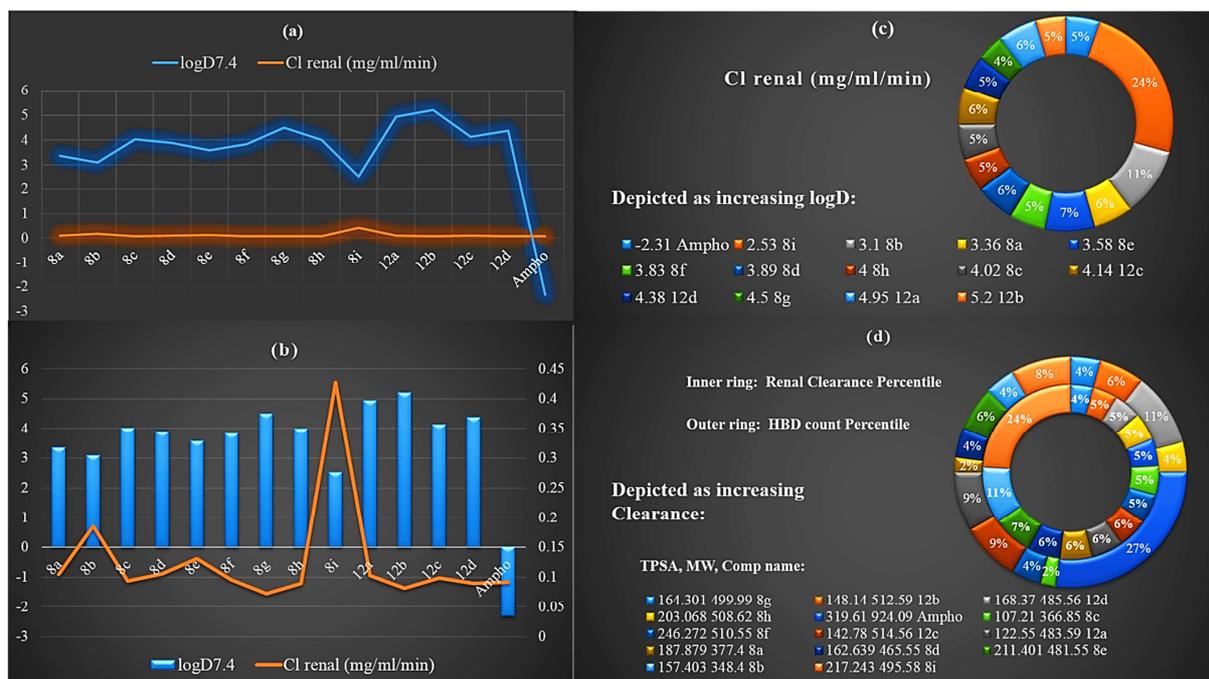
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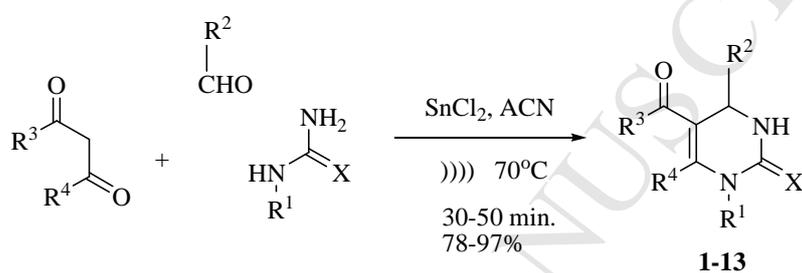
ACCEPTED MANUSCRIPT

**Lead compound 8i****Amphotericin B**

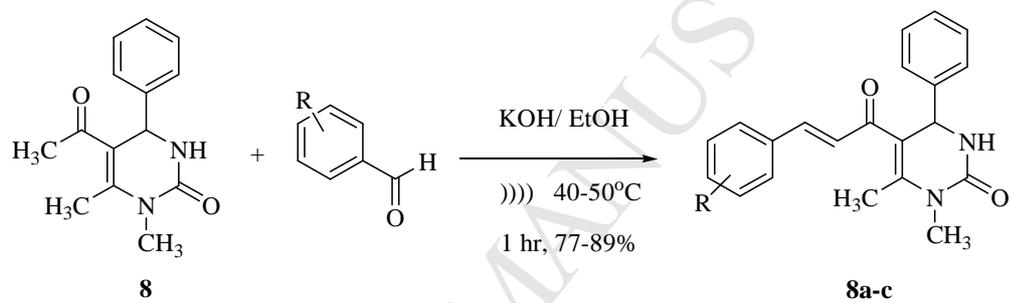




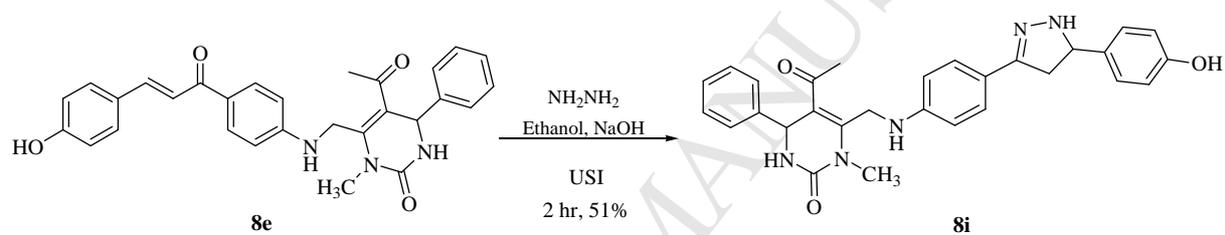
Schemes



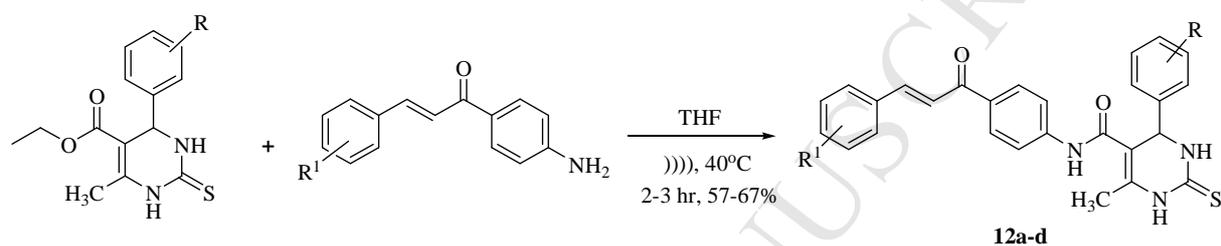
Scheme 1. Synthesis of dihydropyrimidines **1-13**



Scheme 2. Synthesis of chalcones from dihydropyrimidines



Scheme 4. Synthesis of pyrazoline (**8i**) from chalcone **8e**



Scheme 5. SAR exploration around thioxo-analogues **12** and **13** at C-5 position

Highlights

- Structure based C-5 and C-6 modifications of 3,4-dihydropyrimidine core.
- Modifications were found to have enhanced *in vitro* inhibition potential
- Compound **8i** showed potent *in vitro* antileishmanial activity.
- Molecular docking analysis was carried out
- Drug-like properties was evaluated through *in silico* ADMET predictions

ACCEPTED MANUSCRIPT