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Retraction

Retracted: Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach

Computational and Mathematical Methods in Medicine

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This article has been retracted by Hindawi following an investigation undertaken by the publisher [1]. This investigation has uncovered evidence of one or more of the following indicators of systematic manipulation of the publication process:

(1) Discrepancies in scope

(2) Discrepancies in the description of the research reported

(3) Discrepancies between the availability of data and the research described

(4) Inappropriate citations

(5) Incoherent, meaningless and/or irrelevant content included in the article

(6) Peer-review manipulation

The presence of these indicators undermines our confidence in the integrity of the article's content and we cannot, therefore, vouch for its reliability. Please note that this notice is intended solely to alert readers that the content of this article is unreliable. We have not investigated whether authors were aware of or involved in the systematic manipulation of the publication process.

Wiley and Hindawi regrets that the usual quality checks did not identify these issues before publication and have since put additional measures in place to safeguard research integrity.

We wish to credit our own Research Integrity and Research Publishing teams and anonymous and named external researchers and research integrity experts for contributing to this investigation.

The corresponding author, as the representative of all authors, has been given the opportunity to register their agreement or disagreement to this retraction. We have kept a record of any response received.

References

[1] H. Zulfiqar, M. S. Masoud, H. Yang, S. Han, C. Wu, and H. Lin, "Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach," *Computational and Mathematical Methods in Medicine*, vol. 2021, Article ID 6683407, 9 pages, 2021.

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Research Article

Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach

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Allergens have the ability to enter the body and cause illness. Leukotriene is the widespread allergen which could stimulate mast cells to discharge histamine which causes allergy symptoms. An effective strategy for treating leukotriene-induced allergy is to find the inhibitors of leukotriene or histamine activity from phytochemicals. For this purpose, a library of 8,500 phytochemicals was generated using MOE software. The structures of histamine-1 receptor and cysteinyl leukotriene receptor-1 were predicted by the homology modeling method through the SWISS model. The phytochemicals were docked with predicted structures of histamine-1 and cysteinyl leukotriene receptor-1 in MOE software to determine the binding affinity of the phytochemicals against the targets. Moreover, chemoinformatics properties and ADMET of phytochemicals were assessed to find the drug likeness behavior of compounds. Compound ID 10054216 has the lowest *S*-score value for H-1 receptor that is -18.9186 kcal/mol which is lower than the value of standard -15.167 kcal/mol. The other compounds 393471, 71448939, 10722577, and 442614 also showed good *S*-score values than the standard. Moreover, compound ID 11843082 has the lowest *S*-score value for CL1R that is -15.481 kcal/mol which is lower than the value of standard -12.453 kcal/mol. The other compounds 72284, 5282102, 66559251, and 102506430 also showed good *S*-score values than the standard. In this research article, we performed molecular docking to find the best inhibitors against H1R and CL1R and their antiallergic efficacy. This in silico knowledge will be helpful in near future for the design of novel, safe, and less costing H-1 receptor and CL1R inhibitors with the aim to improve human life quality.

1. Introduction

Allergy is the worldwide chronic disease. Many people around the globe have allergy problems because allergies have no boundary restrictions. It is most common in underdeveloped countries especially in South Asia because billions of people live in this area and majority of this population lives beneath the poverty line. The environment of this region is polluting badly day by day. Air pollution and water pollution are the frontline cause of allergies. There are many types of allergy. Some are more severe and could cause life threat. Pollen allergy, food allergy, sting allergy, and drug allergies are the most common allergy types nowadays. A hot topic in the world is "Global Warming" which is the main cause of allergy and smoke/smog allergy [1]. Smoke and smog allergies are severe and cause life-threatening effects. Asthma is the best example of smoke and smog allergies. In asthma, allergens directly affect the bronchial tubes. An example in Figure 1 shows the normal and asthmatic bronchial tubes. Normal bronchial tubes have wider opening for air transfer

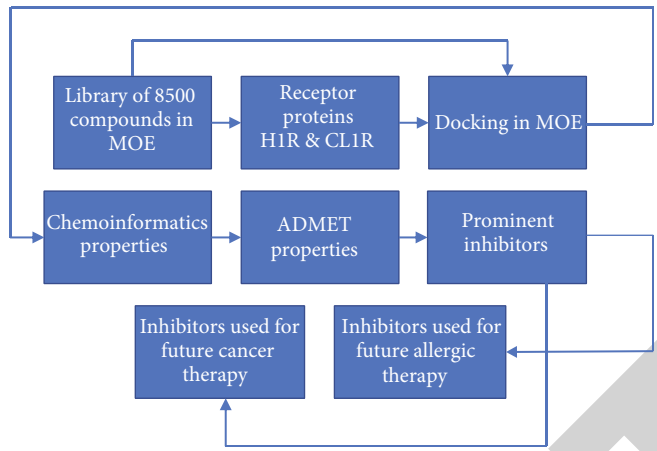

Figure 1: Flowchart of the whole study.

and the other hand. On the contrary, inflamed bronchial tubes have narrower opening for air transfer due to the effects of allergens and cause cough and severe type of lung diseases.

Due to the narrowing of the bronchial tubes, no sufficient air can pass through the tubes, which causes alveoli (which are air sacs) contracts and ultimately damage to the lungs. Allergens are like invaders which have the ability to enter into the body and cause illness. Some of the allergens are stings of insects, pollens and molds, etc. The immune system protects us from the invaders that can cause illness. It is automatically defending our body when invaders attack our body [2]. Our immune system activates and starts producing immunoglobulin antibodies when invaders enter the body [3]. This antibody protects our body from the invaders to reduce or demolish their effect. There are many types of allergy receptors in which two are clinically important: histamine-1 receptor and cysteinyl leukotriene receptor-1. Histamine-1 receptor belongs to a group of family e.g., rhodopsin-like G protein-coupled receptors. Majority of its expressions are in the heart and in the central nervous system (CNS). However, some of its expressions also present in endothelial cells. Actually, histamine-1 receptor is a protein and often combines with histamines to generate unambiguous impact on the living organisms [4]. There are many receptors in this family including H-1 receptor, H-2 receptor, H-3 receptor, and H-4 receptor.

These receptors are found in the uterus of females and the heart of both male and female genders [5]. Histamine-1 to Histamine-4 receptors could bind to histamines that transduce signals to cells through a dissimilar way. The expression of these receptors in odd cells and cell subsets is synchronized. In fact, the assorted effects of histamine on immune regulation are due to differential expression of four histamine receptors and their discrete intracellular signals [6]. The main cause of the histamine is the immune system cell maturation and changing their activation as well as chemotoxicity. The capability of histamine receptor antagonists to inhibit mast cell degranulation implies that they might be developed as a group of mast cell stabilizers [7, 8]. Recently, a series of experiments on dispersed colon mast cells recommended that mast cells in the human body have at least two ways to strengthen their own activation-degranulation signals in automatic or paracrine manners [9–11]. Histamine is an important mediator in allergic diseases; its antagonists may be used as a group of mast cell stabilizers for the treatment of these diseases [12]. The histamine also controls particular antigens like TH-1 and TH-2. It also controls the B-cells, T-cells, and isotype reaction of antibody [13]. H-1 receptor inhibitors have been found to inhibit the TH2-associated responses and are proposed for the treatment of allergy. H-1 receptor antagonists have been shown to inhibit the generation of IL-4 and IL-13. They could also prevent airway inflammation and hyperreactivity which is caused by allergens [14]. The known inhibitors of histamine-1 receptors are levocetirizine [15], desloratadine [16], and fexofenadine [17]. Cysteinyl leukotriene receptor-1 is the receptor of leukotriene. Binding of different types of leukotriene with cysteinyl leukotriene receptor-1 in lesser extent contributes to mediating different types of allergic reactions but causing different types of side effects [18–20].

Cysteinyl leukotrienes are produced by basophils digesting arachidonic acid during the early phase of antigen reaction and produced by eosinophils and macrophages during the late phase [21]. The cysteinyl leukotrienes level in nasal exudations is higher after short-term allergen instillation. These lipid mediators act locally and systemically by interacting with receptors, mainly cysteinyl leukotriene receptor-1, on target cells. Evidence from topical application of cysteinyl leukotrienes in the nose and from the effects of cysteinyl leukotriene receptor antagonists has shown that cysteinyl leukotriene receptor-1 contributes to nasal mucous excretion, cramming, and soreness [22]. Cysteinyl leukotrienes endorse allergic soreness by enhancing immune responses and the construction, grip, passage, and survival of inflammatory cells such as eosinophils. They also increase the generation of an array of other proinflammatory mediators, for example cytokines, which in turn increase the production of cysteinyl leukotriene receptors. Clinical trials have demonstrated that leukotrienes receptor antagonists have substantial but uncertain efficacy as single agents but chemically effective when used with other classes of agents [23, 24]. It also provides a new perspective for many studies of side effect. These two

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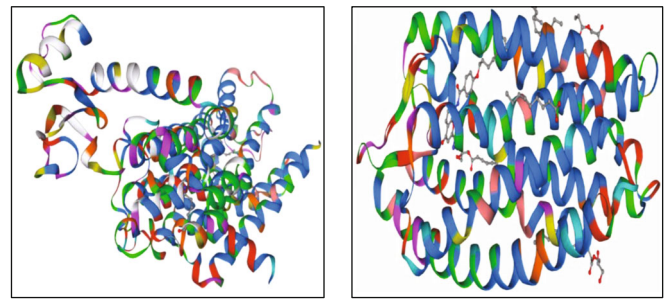
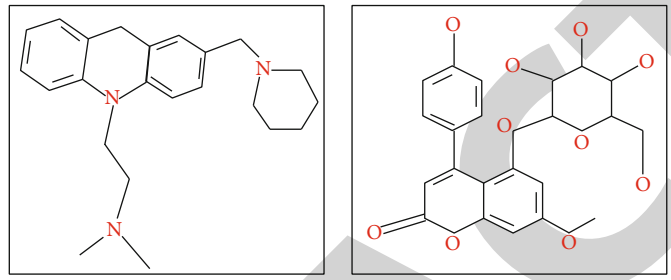


(a) (b)

Figure 2: Predicting structure of (a) histamine-1 receptor and (b) cysteinyl leukotriene receptor-1.



(a) (b)

Figure 3: Chemical structure of (a) compound ID 10054216 and (b) compound ID 11843082.

Table 1: Top 10/10 good scoring compounds against H1R and CL1R.

Compound ID		S-score		RMSD refine		Receptor		Interaction	
H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R
10054216	11843082	-18.918	-15.481	1.965	1.068	Tyr 458, Lys191, Ser111, His450	Ser118, Phe202, Tyr209,Thr290	H-don, H-don, H-Accp, H-donar	H-Accp, H-Pi, H-Don, H-Don
393471	72284	-18.361	-15.451	1.528	1.754	Asn443, Lys191	Tyr209, Phe202	H-don, H-don	H-Don, H-Pi
71448939	5282102	-18.040	-15.444	1.412	2.338	Lys274, Lys 245, Arg377	Phe202,Thr239	H-don, H-don	H-Pi, H-Accp
10722577	66559251	-17.067	-14.364	2.461	1.520	Thr112, Asp107	Asp19, Lys162, His190, Tyr104	H-don, H-Accp	H-Accp, H-Don, H-Don, H-Accp
442614	102506430	-15.518	-14.258	1.370	2.090	Lys245	Arg79, Tyr104, Glu175	H-pi	H-Don, H-Accp, H-Accp
10436583	10365031	-15.333	-13.828	2.399	2.236	Ala343, Trp257, Lys274	His190, Arg79	H-Accp, H-Pi, H-Pi	H-Accp, H-Don
71306915	10742453	-15.045	-13.652	2.305	2.135	Ala343, Lys274	Asp19, Gln274, Arg253	H-Accp, H-Don	H-Accp, H-Don, H-Don
11968893	6476337	-13.677	-13.462	1.522	2.239	Ser378, Lys274, Lys245, Thr382	Phe202,Tyr209	H-Accp, H-Don, H-Accp	H-Pi, H-Accp
44566649	10746683	-13.204	-13.376	1.489	1.806	Lys245, Asn243, Glu345	Ser118	H-Don, H-Don, H-Accp	H-Accp
161538	44479224	-13.028	-12.954	0.8953	1.3401	Lys245, Glu254	Ser118	H-Don, H-Accp	H-Donor

known inhibitors against cysteinyl leukotriene receptor-1 are montelukast and zafirlukast which have been used for the therapy of allergic diseases.

In this study, we report computer-based screening of phytochemicals for the identification of potential inhibitors against allergy. In silico studies and molecular docking procedures are done on compounds to find the binding sites. The chemoinformatics properties and ADMET properties of the compounds are also analyzed to check the adsorption, absorption, and toxicity of the compound inhibitors [25, 26]. The detail structure of H-1 receptor and cysteinyl leukotriene receptor-1 could give us possible binding sites where compounds (inhibitors) possibly bind. This gives us the good prediction of compounds that attach well in the H-1 receptor and cysteinyl leukotriene receptor-1. The molecular docking was performed to study the binding between compounds and

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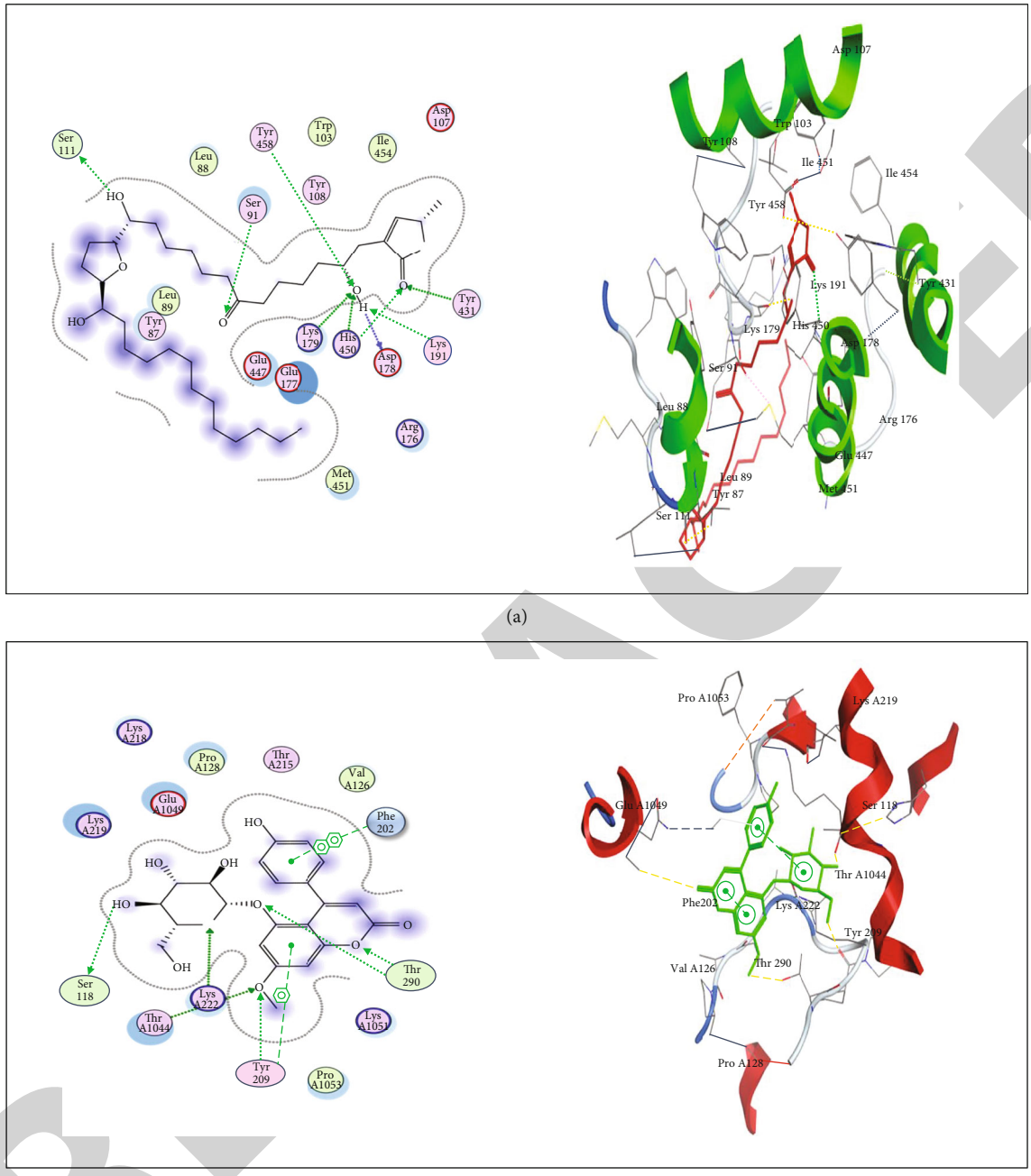

Figure 4: Ligand interaction and 3D picture of (a) compound ID 10054216 for H1R and (b) compound ID 11843082 for CL1R.

H-1 receptor as well as cysteinyl leukotriene receptor-1 by using Molecular Operating Environment (MOE) software [27]. Two reference drugs montelukast for cysteinyl leukotriene receptor-1 and loratadine for histamine-1 receptor were selected as the standard for comparison. The flowchart which makes the paper easily understandable [28, 29] is shown in Figure 1.

2. Materials and Methodologies

2.1. Receptor Proteins and Compound Structures. The structure prediction is extremely important for interaction study between two molecules [30]. The structures of histamine-1 receptor and cysteinyl leukotriene receptor-1 were predicted by the homology modeling method through the SWISS Model [31] showing in Figure 2. The sequence similarity with target proteins, local and global quality estimates, and molecular formulas and names of compound IDs are also available in Supplementary file (available here). The structures of compounds that were drawn by using the ChemDraw software [32] showing in Figure 3 were tested against histamine-1 receptor and cysteinyl leukotriene receptor-1 protein in MOE (Molecular Operating Environment) software http://github.com/Yelp/MOE [27, 33] to identify and predict which

Table 2: Chemoinformatics properties of top 10/10 compounds of H1R and CL1R.

Compound ID		MW		HBD		Log*P*		Mol Vol		PSA (A2)	
H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R
10054216	11843082	494.87	446.41	3	5	8.28	0.95	499.87	373.70	113.29	159.05
393471	72284	496.89	456.69	4	4	8.41	0.40	499.75	433.98	116.45	447.10
71448939	5282102	447.12	448.38	5	5	-0.50	0.12	460.62	364.19	307.37	190.28
10722577	66559251	490.93	456.71	3	2	8.80	6.29	480.50	472.11	105.46	49.69
442614	102506430	344.32	499.63	3	5	1.59	5.59	289.93	492.83	121.13	147.67
10436583	10365031	496.50	424.49	5	4	3.58	5.87	438.78	393.20	167.90	107.22
71306915	10742453	498.96	456.54	5	4	1.02	4.96	500.10	424.98	234.30	116.45
11968893	6476337	469.05	452.65	5	5	2.40	0.39	240.38	477.55	240.38	223.31
44566649	10746683	444.89	438.93	5	4	4.58	8.03	177.13	456.55	177.13	125.69
161538	44479224	468.50	298.29	3	2	-0.64	2.74	148.83	258.38	148.83	79.90

compound structures have good binding interactions with proteins.

MOE was selected for docking among various available resources as it has a user-friendly graphical interface. It provides a good graphical view to show ligand and receptor binding residues with their positions and interactions. In MOE [27], receptor–ligand binding affinities with all possible binding geometries are prioritized on the basis of a numerical value called *S*-score. MOE has also multidisciplinary applications, such as structure-based design, fragment-based design, pharmacophore discovery, medicinal chemistry applications, biologics applications, protein and antibody modeling, molecular modeling and simulations, cheminformatics and QSAR, and method development and deployment. It can identify salt bridges, hydrogen bonds, hydrophobic interactions, sulfur-LP, cation-π, and solvent exposure. Thus, in this work, the interactions between inhibitors and receptor proteins are predicted on the basis of the *S*-score from MOE.

Phytochemicals were collected from online database PubChem [34] and MAPS database [35]. Actually, a library with 8,500 phytol chemical structures was made in MOE software [27] in order to find the best inhibitors against histamine-1 receptor protein and cysteinyl leukotriene receptor-1 protein.

2.2. Chemoinformatics Properties of Compounds. Chemoinformatics characteristics of compounds were checked using computational tools. The phytochemicals were evaluated on the basis of their chemoinformatics properties by using Lipinski's rule of five [36]. The rule defines the permeability of drugs that are orally taken in the body. It is a method to predict compounds which have poor absorption. The Lipinski rules of compounds were checked using the Molinspiration [25] http://www.molinspiration.com/.

2.3. ADMET Properties of Compounds. ADMET denotes absorption, distribution, metabolism, excretion, and toxicity. The compounds were checked for these properties in ADMET analysis. The prediction of ADMET properties plays a crucial role in finding of effective drugs and also helps us to eliminate unwanted compounds in early steps of drug designing. The ADMET properties of compounds were evaluated using the online server pKCSM [26].

3. Results and Discussion

3.1. Docking Analysis of Compound. The molecular docking was performed to investigate the interaction between 8,500 chemicals and histamine-1 receptor protein as well as cysteinyl leukotriene receptor-1 protein. In Table 1, for each protein, compounds with the lowest *S*-score were selected. The *S*-score results in MOE [27] showed that all selected inhibitors were in the pocket of the target protein, exhibiting a possible interaction with protein. The docking results were manipulated using the GBVI/WSA dG scoring function with the generalized Born solvation model (GBVI). The GBVI/WSA dG is a force field-based scoring function, which estimates the free energy of binding of the ligand from a given orientation. Interaction results were evaluated with the *S*-score. Inhibitors with the lowest *S*-score tend to establish a strong interaction with protein on specific active sites. After in silico docking, we identified a compound showing the minimum *S*-score among all the inhibitors. These compounds are regarded as the best compounds because they could bind receptors with high binding energy. For example, compound ID 10054216 has the lowest "*S*-score" value that is -18.919 kcal/mol which is lower than the value of standard compound loratadine -15.167 kcal/mol. Another four compound IDs 393471, 71448939, 10722577, and 42614 also showed lower "*S*-score" values than the standard loratadine, suggesting that these compounds have good interaction with protein histamine-1 receptor and can be regarded as potential inhibitors for the receptor. This can also be demonstrated by their RMSD values which were below 3.

Moreover, the ligand interaction of compounds with protein histamine-1 receptor was also analyzed. The top 10 compounds which have lowest "*S*-score" values were selected for checking of their ligand interaction. The compound ID 10054216 has a good interaction with the protein histamine-1 receptor. The residues His450, Tyr458, Lys191, and Ser111 could interact with the hydroxyl group [4] and (O) group of histamine-1 receptor. Residues of His450, Lys191, and Tyr458 were donating hydrogen, and on the

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Table 3: ADMET properties of top 10/10 compounds against H1R and CL1R.

ADMET properties																			
WS		IS %abs		LogKp		LogBB		CNSP		CYP3A4		AMEST		ORAT		HT		SS	
H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R	H1R	CL1R
-4.72	-2.89	79.15	34.34	-2.71	-2.73	-1.45	-1.98	-3S	-3.44	Yes	No	No	No	1.88	2.48	Yes	No	No	No
-4.99	-2.98	70.51	48.12	-2.72	-2.73	-1.42	-1.50	-3	-3.00	Yes	No	No	No	1.98	2.53	Yes	No	No	No
-2.81	-2.86	2.016	48.05	-2.73	-2.73	-2.04	-1.51	-5.49	-3.00	No	No	No	No	2.75	2.54	No	No	No	No
-5.124	-6.04	77.06	92.96	-2.72	-3.00	-1.47	-0.06	-3	-1.55	Yes	Yes	No	No	2.08	3.13	No	Yes	No	No
-2.952	-3.29	79.83	64.46	-2.83	-2.73	-1.003	-1.42	-3	-3.00	Yes	Yes	Yes	No	1.83	2.69	No	No	No	No
-2.892	-3.60	65.00	83.36	-2.73	-2.73	-1.48	-0.81	-3	-2.78	Yes	Yes	No	No	2.52	2.21	No	No	No	No
-3.716	-4.02	45.62	76.50	-2.73	-2.73	-1.807	-1.14	-3	-3.00	Yes	Yes	No	No	3.316	2.24	No	No	No	No
-3.75	-2.94	48.70	31.05	-2.73	-2.73	-2.209	-1.72	-3	-3.00	Yes	No	No	No	3.532	2.77	No	No	No	No
-3.85	-4.80	53.22	67.47	-2.73	-2.72	-1.601	-1.57	-3.00	-3.00	Yes	Yes	No	No	1.937	2.06	No	No	No	No
-4.358	-3.54	61.73	94.24	-2.90	-2.74	-1.096	-0.31	-3.00	-2.26	No	Yes	No	Yes	2.327	2.11	No	No	No	No

other hand, residue Ser 111 was accepting hydrogen. Compound ID 10054216 which has lowest "*S*-score" value can also interact with residues His450, Tyr458, Lys191, and Ser111 as shown in the ligand interaction of 10054216. Figure 4(a) displayed that compound ID 10054216 binds to the active site of protein histamine-1 receptor. From Figure 4(a), we noticed that many residues are very close and can interact with the ligand demonstrating that this compound has good interaction with protein histamine-1 receptor.

However, compound ID 11843082 has the lowest "*S* -score" value that is -15.481 kcal/mol which is lower than the value of the standard compound montelukast -12.453 kcal/mol values. Another four compounds 72284, 5282102, 66559251, and 102506430 also showed lower "*S* -score" values than the standard montelukast, suggesting that these compounds have good binding interactions with the protein cysteinyl leukotriene receptor-1 and can be regarded as potential inhibitors for the receptor. This can also be demonstrated by RMSD values which were not more than 3. Compound ID 11843082 has a good interaction with the protein cysteinyl leukotriene receptor-1. The residues Ser 118, Phe202, Tyr209, and Thr 290 could interact with the hydroxyl group and (O) group of cysteinyl leukotriene receptor-1. Residues of Ser118 was accepting hydrogen and residues of Tyr 209 and Thr 290 were donating hydrogen, and residue Phe 202 was making a ring with ligand. Figures 4(a) and 4(b) and Table 1 also show the bind interactions of residues and compounds. Compound ID 11843082 which have lowest " *S*-score" was also interacting with residues Phe202 and Tyr209 as shown in the ligand interaction of 11843082. Figure 4(b) displayed that compound ID 11843082 binds to the active site of protein cysteinyl leukotriene receptor-1. From Figure 4(b), we noticed that many residues are very close and can interact with the ligand, demonstrating that this compound have good binding interaction with protein cysteinyl leukotriene-1 receptor. The chemoinformatics properties [37] of compounds were also evaluated using the online server Molinspiration [25] on the basis of the Lipinski rule of 5 [36].

The Lipinski rule of 5 [36] is a rule of thumb to evaluate drug likeness if a chemical compound with a certain pharmacological or biological activity has chemical properties that would make it a likely orally active drug in humans (e.g., a molecule with a molecular mass less than 500 Da, no more than 5 hydrogen bond donors, no more than 10 hydrogen bond acceptors, and an octanol–water partition coefficient Log*P* not greater than 5). It is believed that the compounds which follow the Lipinski rule [36] of five are very good candidates for drug [36, 38, 39]. The chemoinformatics results of test compounds in Table 2 show that they follow the Lipinski rule [36] of five very well except in the case of compound ID 10054216 against histamine-1 receptor, their Log*P* value outpaced the standard value of 5. The values of the test compounds were in between the standard values. This shows that these compounds might be good target for drug designing. The absorption, distribution, metabolism, excretion, and toxicity (ADMET) characteristics of the compounds were also evaluated using the online server pKCSM [26] which is a tool to check the pharmacokinetic properties of compounds. In Table 3, it was found that compounds have good absorption values which showed that the drug likeness behavior of compounds and distribution values are good too; this showed that these compounds penetrate through any barrier and reach the target receptor molecule.

The ADMET properties also show that compounds are very less toxic that makes it a favorable target for drug designing. The computational and in silico study show that these compounds have good potential to inhibit the activity of histamine-1 receptor and cysteinyl leukotriene receptor-1 and also the chemoinformatics properties and Lipinski rule of 5 [36] indicate the less toxicity of compounds and also drug likeness behavior of the compounds. The best common inhibitor compound ID 442614 showed the *S*-score value -15.5180 kcal/mol against histamine-1 receptor protein and *S*-score value -11.7557 kcal/mol against cysteinyl leukotriene receptor-1 protein. The ADMET analysis values of compounds showed that these may be absorbed and distributed in the body very well. This indicates that these compounds can be an excellent candidate and target for drug discovery [40].

4. Conclusion

This study focused on the interaction between small molecules with two allergy receptors. In this study, we report computer-based screening of phytochemicals for the identification of potential inhibitors against allergy. In silico studies and molecular docking procedures are done on compounds to find the binding sites. The chemoinformatics properties and ADMET properties of the compounds are also analyzed to check the adsorption, absorption, and toxicity of the compound inhibitors on the basis of the Lipinski rule of five [36]. The detail structure of H-1 receptor and cysteinyl leukotriene receptor-1 could give us possible binding sites where compounds (inhibitors) possibly bind. This gives us the good prediction of compounds that attach well in the H-1 receptor and cysteinyl leukotriene receptor-1. The molecular docking was performed to study the binding between compounds and H-1 receptor as well as cysteinyl leukotriene receptor-1 by using Molecular Operating Environment (MOE) software [27]. The results provided a potential guide for further drug development. This molecular dynamic strategy can also be applied in other fields including anticancer drug [41–45] and antimalaria drug discovery [46]. We also hope the machine learning [47–53] and computational intelligence [54–61] methods can be applied in the drug discovery.

Data Availability

The data can be downloaded from a public database.

Conflicts of Interest

The authors declare that there is no conflict of interests.

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Supplementary Materials

Compounds' molecular names and molecular formulas. Sequence similarity of H1R. Sequence similarity of CL1R. *(Supplementary Materials)*

References

[1] R. Pawankar, G. W. Canonica, S. T. Holgate, and R. F. Lockey, "Allergic diseases and asthma: a major global health concern," *Current Opinion in Allergy and Clinical Immunology*, vol. 12, no. 1, pp. 39–41, 2012.

[2] J. Kim, P. J. Bentley, U. Aickelin, J. Greensmith, G. Tedesco, and J. Twycross, "Immune system approaches to intrusion detection–a review," *Natural Computing*, vol. 6, no. 4, pp. 413–466, 2007.

[3] L. Cheng, C. Qi, H. Zhuang, T. Fu, and X. Zhang, "gutMDisorder: a comprehensive database for dysbiosis of the gut microbiota in disorders and interventions," *Nucleic Acids Research*, vol. 48, no. D1, pp. D554–D560, 2020.

[4] Y. Ohsawa and N. Hirasawa, "The antagonism of histamine H1 and H4 receptors ameliorates chronic allergic dermatitis via anti-pruritic and anti-inflammatory effects in NC/Nga mice," *Allergy*, vol. 67, no. 8, pp. 1014–1022, 2012.

[5] P. Panula, P. L. Chazot, M. Cowart et al., "International union of basic and clinical pharmacology. XCVIII. Histamine receptors," *Pharmacological Reviews*, vol. 67, no. 3, pp. 601–655, 2015.

[6] C. A. Akdis and K. Blaser, "Histamine in the immune regulation of allergic inflammation," *Journal of Allergy and Clinical Immunology*, vol. 112, no. 1, pp. 15–22, 2003.

[7] E. B. Thangam, E. A. Jemima, H. Singh et al., "The role of histamine and histamine receptors in mast cell-mediated allergy and inflammation: the hunt for new therapeutic targets," *Frontiers in Immunology*, vol. 9, 2018.

[8] H. Dong, Y. Wang, X. Zhang et al., "Stabilization of brain mast cells alleviates LPS-induced neuroinflammation by inhibiting microglia activation," *Frontiers in Cellular Neuroscience*, vol. 13, 2019.

[9] J. Becker, D. Ott, and M. Diener, "Impact of sensitization and inflammation on the interaction of mast cells with the intestinal epithelium in rats," *Frontiers in Physiology*, vol. 10, p. 329, 2019.

[10] S.-H. He and H. Xie, "Inhibition of tryptase release from human colon mast cells by protease inhibitors," *World Journal of Gastroenterology*, vol. 10, no. 3, pp. 332–336, 2004.

[11] S.-H. He, H. Xie, and Y.-L. Fu, "Inhibition of tryptase release from human colon mast cells by histamine receptor antagonists," *Asian Pacific Journal of Allergy and Immunology*, vol. 23, no. 1, pp. 35–39, 2005.

[12] H. Xie and S.-H. He, "Roles of histamine and its receptors in allergic and inflammatory bowel diseases," *World Journal of Gastroenterology*, vol. 11, no. 19, pp. 2851–2857, 2005.

[13] C. A. Akdis and F. E. R. Simons, "Histamine receptors are hot in immunopharmacology," *European Journal of Pharmacology*, vol. 533, no. 1-3, pp. 69–76, 2006.

[14] P. J. Bryce, C. B. Mathias, K. L. Harrison, T. Watanabe, R. S. Geha, and H. C. Oettgen, "The H1 histamine receptor regulates allergic lung responses," *The Journal of clinical investigation*, vol. 116, no. 6, pp. 1624–1632, 2006.

[15] C. Barniol, E. Dehours, J. Mallet, C.-H. Houze-Cerfon, D. Lauque, and S. Charpentier, "Levocetirizine and prednisone are not superior to levocetirizine alone for the treatment of acute urticaria: a randomized double-blind clinical trial," *Annals of emergency medicine*, vol. 71, no. 1, pp. 125–131.e1, 2018.

[16] I. Fritz, P. Wagner, M. Bottai et al., "Desloratadine and loratadine use associated with improved melanoma survival," *Allergy*, vol. 75, no. 8, pp. 2096–2099, 2020.

[17] C.-z. Huang, Z.-h. Jiang, J. Wang, Y. Luo, and H. Peng, "Antihistamine effects and safety of fexofenadine: a systematic review and Meta-analysis of randomized controlled trials," *BMC Pharmacology and Toxicology*, vol. 20, no. 1, p. 72, 2019.

[18] E. A. Mellor, A. Maekawa, K. F. Austen, and J. A. Boyce, "Cysteinyl leukotriene receptor 1 is also a pyrimidinergic receptor and is expressed by human mast cells," *Proceedings of the National Academy of Sciences*, vol. 98, no. 14, pp. 7964–7969, 2001.

[19] Y. Ding, J. Tang, and F. Guo, "Identification of drug-side effect association via multiple information integration with centered kernel alignment," *Neurocomputing*, vol. 325, pp. 211–224, 2019.

[20] H. Liu, L. Luo, Z. Cheng et al., "Group-sparse modeling drug-kinase networks for predicting combinatorial drug sensitivity in cancer cells," *Current Bioinformatics*, vol. 13, no. 5, pp. 437–443, 2018.

[21] A. Abbas, S. Shahid, A. Sabah et al., "The clinical complications of asthma and its pharmacotherapy," *Journal of British Biomelical Bulletin*, vol. 2, no. 1, pp. 2347–5447, 2014.

[22] A. Jo-Watanabe, T. Okuno, and T. Yokomizo, "The role of leukotrienes as potential therapeutic targets in allergic disorders," *International Journal of Molecular Sciences*, vol. 20, no. 14, p. 3580, 2019.

[23] R. M. Naclerio, F. M. Baroody, and A. G. Togias, "The role of leukotrienes in allergic rhinitis: a review," *American Review of Respiratory Disease*, vol. 143, no. 5, Part 2, pp. S91–S95, 1991.

[24] M. Peters-Golden and W. R. Henderson Jr., "The role of leukotrienes in allergic rhinitis," *Annals of Allergy, Asthma & Immunology*, vol. 94, no. 6, pp. 609–618, 2005.

[25] C. Molinspiration, "Calculation of molecular properties and bioactivity score," 2011, http://www.molinspiration.com/cgi-bin/properties.

[26] D. E. V. Pires, T. L. Blundell, and D. B. Ascher, "pkCSM: predicting small-molecule pharmacokinetic and toxicity properties using graph-based signatures," *Journal of Medicinal Chemistry*, vol. 58, no. 9, pp. 4066–4072, 2015.

[27] Chemical Computing Group Inc, *Molecular Operating Environment (MOE)*, Chemical Computing Group Inc 1010, Montreal, Canada, 2016.

[28] Y.-H. Yang, C. Ma, J.-S. Wang et al., "Prediction of N7-methylguanosine sites in human RNA based on optimal sequence features," *Genomics*, vol. 112, no. 6, pp. 4342–4347, 2020.

[29] J. X. Tan, S. H. Li, Z. M. Zhang et al., "Identification of hormone binding proteins based on machine learning methods," *Mathematical Biosciences and Engineering*, vol. 16, no. 4, pp. 2466–2480, 2019.

RETRACTED

[30] D. Liu, G. Li, and Y. Zuo, "Function determinants of TET proteins: the arrangements of sequence motifs with specific codes," *Briefings in Bioinformatics*, vol. 20, no. 5, pp. 1826–1835, 2019.

[31] N. Guex, M. C. Peitsch, and T. Schwede, "Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: a historical perspective," *Electrophoresis*, vol. 30, no. S1, pp. S162–S173, 2009.

[32] N. Mills, "ChemDraw Ultra 10.0 CambridgeSoft, 100 CambridgePark Drive, Cambridge, MA 02140. http://www.cambridgesoft.com. Commercial price: $1910 for download, $2150 for CD-ROM; academic price: $710 for download, $800 for CD-ROM," *Journal of the American Chemical Society*, vol. 128, no. 41, pp. 13649-13650, 2006.

[33] U. Roy and L. A. Luck, "Molecular modeling of estrogen receptor using molecular operating environment," *Biochemistry and Molecular Biology Education*, vol. 35, no. 4, pp. 238–243, 2007.

[34] E. E. Bolton, Y. Wang, P. A. Thiessen, and S. H. Bryant, "PubChem: integrated platform of small molecules and biological activities," in *Annual Reports in Computational Chemistry*, pp. 217–241, Elsevier, 2008.

[35] U. A. Ashfaq, A. Mumtaz, T. Ul Qamar, and T. Fatima, "MAPS database: medicinal plant activities, phytochemical and structural database," *Bioinformation*, vol. 9, no. 19, pp. 993–995, 2013.

[36] C. A. Lipinski, F. Lombardo, B. W. Dominy, and P. J. Feeney, "Experimental and computational approaches to estimate solubility and permeability in drug discovery and development settings," *Advanced Drug Delivery Reviews*, vol. 23, no. 1-3, pp. 3–25, 1997.

[37] R. Goodwin, J. Bunch, and D. McGinnity, "Mass spectrometry imaging in oncology drug discovery," in *Advances in Cancer Research*, pp. 133–171, Elsevier, 2017.

[38] L. Yu, J. Zhao, and L. Gao, "Drug repositioning based on triangularly balanced structure for tissue- specific diseases in incomplete interactome," *Artificial Intelligence in Medicine*, vol. 77, pp. 53–63, 2017.

[39] L. Yu, F. Xu, and L. Gao, "Predict new therapeutic drugs for hepatocellular carcinoma based on gene mutation and expression," *Frontiers in Bioengineering and Biotechnology*, vol. 8, p. 8, 2020.

[40] L. Yu, S. Yao, L. Gao, and Y. Zha, "Conserved disease modules extracted from multilayer heterogeneous disease and gene networks for understanding disease mechanisms and predicting disease treatments," *Frontiers in Genetics*, vol. 9, 2019.

[41] X. Zeng, S. Zhu, X. Liu, Y. Zhou, R. Nussinov, and F. Cheng, "deepDR: a network-based deep learning approach to in silico drug repositioning," *Bioinformatics*, vol. 35, no. 24, pp. 5191–5198, 2019.

[42] H.-Y. Lai, C.-Q. Feng, Z.-Y. Zhang, H. Tang, W. Chen, and H. Lin, "A brief survey of machine learning application in cancerlectin identification," *Current Gene Therapy*, vol. 18, no. 5, pp. 257–267, 2018.

[43] L. Wei, C. Zhou, H. Chen, J. Song, and R. Su, "ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides," *Bioinformatics*, vol. 34, no. 23, pp. 4007–4016, 2018.

[44] L. Yu, J. Zhao, and L. Gao, "Predicting potential drugs for breast cancer based on miRNA and tissue specificity," *International Journal of Biological Sciences*, vol. 14, no. 8, pp. 971–982, 2018.

[45] J. Wang, H. Wang, X. Wang, and H. Chang, "Predicting drug-target interactions via FM-DNN learning," *Current Bioinformatics*, vol. 15, no. 1, pp. 68–76, 2020.

[46] H. Ding and D. Li, "Identification of mitochondrial proteins of malaria parasite using analysis of variance," *Amino Acids*, vol. 47, no. 2, pp. 329–333, 2015.

[47] F.-Y. Dao, H. Lv, H. Zulfiqar et al., "A computational platform to identify origins of replication sites in eukaryotes," *Briefings in Bioinformatics*, 2020.

[48] X. Zhao, Q. Jiao, H. Li et al., "ECFS-DEA: an ensemble classifier-based feature selection for differential expression analysis on expression profiles," *BMC Bioinformatics*, vol. 21, no. 1, article 43, 2020.

[49] G. Wang, Y. Wang, W. Feng et al., "Transcription factor and microRNA regulation in androgen-dependent and -independent prostate cancer cells," *BMC Genomics*, vol. 9, Supplement 2, p. S22, 2008.

[50] L. Wei, P. Xing, J. Zeng, J. X. Chen, R. Su, and F. Guo, "Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier," *Artificial Intelligence in Medicine*, vol. 83, pp. 67–74, 2017.

[51] C. Long, W. Li, P. Liang, S. Liu, and Y. Zuo, "Transcriptome comparisons of multi-species identify differential genome activation of mammals embryogenesis," *Ieee Access*, vol. 7, pp. 7794–7802, 2019.

[52] Z.-M. Zhang, J.-S. Wang, H. Zulfiqar, H. Lv, F.-Y. Dao, and H. Lin, "Early diagnosis of pancreatic ductal adenocarcinoma by combining relative expression orderings with machine-learning method," *Frontiers in Cell and Developmental Biology*, vol. 8, 2020.

[53] F.-Y. Dao, H. Lv, Y.-H. Yang, H. Zulfiqar, H. Gao, and H. Lin, "Computational identification of N6-methyladenosine sites in multiple tissues of mammals," *Computational and Structural Biotechnology Journal*, vol. 18, pp. 1084–1091, 2020.

[54] Q. Jiang, G. Wang, S. Jin, Y. Li, and Y. Wang, "Predicting human microRNA-disease associations based on support vector machine," *International Journal of Data Mining and Bioinformatics*, vol. 8, no. 3, pp. 282–293, 2013.

[55] X.-J. Zhu, C.-Q. Feng, H.-Y. Lai, W. Chen, and L. Hao, "Predicting protein structural classes for low-similarity sequences by evaluating different features," *Knowledge-Based Systems*, vol. 163, pp. 787–793, 2019.

[56] S. Basith, B. Manavalan, T. H. Shin, and G. Lee, "iGHBP: Computational identification of growth hormone binding proteins from sequences using extremely randomised tree," *Computational and Structural Biotechnology Journal*, vol. 16, pp. 412–420, 2018.

[57] Y. Zuo, Y. Li, Y. Chen, G. Li, Z. Yan, and L. Yang, "PseKRAAC: a flexible web server for generating pseudo K-tuple reduced amino acids composition," *Bioinformatics*, vol. 33, no. 1, pp. 122–124, 2016.

[58] B. Manavalan, S. Basith, T. H. Shin, D. Y. Lee, L. Wei, and G. Lee, "4mCpred-EL: an ensemble learning framework for identification of DNA N4-methylcytosine sites in the mouse genome," *Cells*, vol. 8, no. 11, p. 1332, 2019.

[59] K. Qu, L. Wei, and Q. Zou, "A review of DNA-binding proteins prediction methods," *Current Bioinformatics*, vol. 14, no. 3, pp. 246–254, 2019.

[60] N. Noureen, S. Fazal, M. A. Qadir, and M. T. Afzal, "HCVS: pinpointing chromatin states through hierarchical clustering and visualization scheme," *Current Bioinformatics*, vol. 14, no. 2, pp. 148–156, 2019.

[61] X. Chen, W. Shi, and L. Deng, "Prediction of disease comorbidity using HeteSim scores based on multiple heterogeneous networks," *Current Gene Therapy*, vol. 19, no. 4, pp. 232–241, 2019.

RETRACTED