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Lichen Planus drugs re-purposing as potential anti COVID-19 therapeutics through molecular docking and molecular dynamics simulation approach

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Ref.: Ms. No. JCTRes-D-21-00153
Lichen Planus Drugs Re-purposing as Potential Anti COVID-19 Therapeutics through Molecular Docking and Molecular Dynamics Simulation Approach
Journal of Clinical and Translational Research

Dear Dr Gupta,

Reviewers have now commented on your paper. You will see that they are advising that you revise your manuscript. If you are prepared to undertake the work required, I would be pleased to reconsider my decision.

For your guidance, reviewers' comments are appended below.

If you decide to revise the work, please submit a list of changes or a rebuttal against each point which is being raised when you submit the revised manuscript. Also, please ensure that the track changes function is switched on when implementing the revisions. This enables the reviewers to rapidly verify all changes made.

Your revision is due by Nov 02, 2021.

To submit a revision, go to https://www.editorialmanager.com/jctres/ and log in as an Author. You will see a menu item call Submission Needing Revision. You will find your submission record there.

Yours sincerely

Michal Heger
Editor-in-Chief
Journal of Clinical and Translational Research

Reviewers' comments:

Reviewer #1: Dear editor,
Have a nice day. The authors carried out virtual screening for some immunomodulatory drugs against different SARSCOV-2 proteins and ACE 2 using docking studies. MD simulation was carried out.
The manuscript need major revision as follows.
1-The sentence: ((The genetic sequencing of SARS-CoV-2 encodes several proteins such as the main protease (Mpro or 3CLpro), Spike Protein S1 subunit, and Human Angiotensin-converting enzyme 2 (ACE 2) which plays an important role in its pathophysiology)) is incorrect since ACE 2 is a human protein and is not expressed by virus.
2-Docking of reference molecules for each protein should be carried out. you can use the co-crystallized ligand as reference compounds.
3-The authors depended only on the binding energy to distinguish between the different compounds. This case in incomplete. You should depend on the binding mode of the tested compound to select the most promising compounds.
4-Validation of docking studies should be carried out for each protein.
5-Figures of docking studies are not clear.
6-Transfer fig. 1, 2, 3 into sup data.
Best regards

Reviewer #2: The author opted the drug repurposing approach to address gobal pandemic of COVID-19. The study identifies the oral lichens planus (OLP) drugs as possible treatment for COVID-19 via in silico approach. The drugs used for the treatment of OLP were used to dock against the key enzyme of SARS-CoV-2 i.e., Mpro, Spike protein, and Human ACE II. The study identifies Epigallocatechin-3-gallate as potential inhibitor of SARS-CoV-2 key enzymes on the basis of docking scores and MD simulation studies.

However, in order to fulfill the merit of publication in Journal of Clinical and Translational Research, the manuscript needs some major revisions which are as follows:

Graphical Abstract: The graphical abstract can be made more precise. It seems that figure 3, and 4 in graphical abstract has been swapped.

Introduction: This part is unnecessarily long which makes the rational of using OLP drugs for repurposing weak. There is a really long and indirect of correlation OLP and COVID-19 has been described through various cellular and immunological processes which fails to establish

the correlation of OLP with SARS-CoV-2 infection.

It is suggested to include either a figurative illustration of whole process or to define it in a short and concise manner.

Methodology: The methodology is appropriate in terms of selecting the target molecules form SARS-CoV-2.

The full name of software (version, company etc.) should be included.

Correct the notion of writing "SARS-CoV-2" instead of SARS-COV-2.
The resolution of structure of spike protein S1 subunit is quite low i.e., 3.20 Å. It could have been a crystal structure solved by X-ray Diffraction technique of high resolution.

Difference in binding site amino acid residues can be seen from the refence cited for Spike protein and Human ACE-II. The refence used to identify the binding site residues of 6LU7 are the actually the residues which were found to be interacting with the compounds used in respective study. Author may define the rationale behind making the grid using these residues.

The docking studies of OLP Drugs should also be compared with clinically approved antivirals being used for COVID-19 management.

The predicted binding pose of OLP drugs with target protein could also been rescored to determine the predictive binding energies via MMGBSA.

Results:
Section 3.3 Molecular Docking: The results obtained through the Glide module for the docking of protein structure for 6LU7, ACE-2 and Mpro with the selected…….. should be corrected for PDB ID or the name of the protein molecule (one pattern of naming the protein should be used at a time; either PDB ID or the enzyme name)

The resolution of figures should be increased up to 600 dpi.

Discussion: The discussion lost connection various times. The correlation of OLP with COVID-19 is repeated and confusing

The manuscript requires a careful correction of various typographical errors.

References: Reference number 11 is not written correctly.

No references were observed for the various modules of Maestro, Schrodinger used (ligprep, Glide, prime), and Gromac (for MD simulation). kindly incorporate them (for the version of software which was sued in study)

Reference style and format is not consistent throughout.

Reviewer #3: 1.Authors should explain the reason they selected this kind of drugs

2. Authors should explain the reason they selected these specific proteins
3.Authors should explain the reason they did the MD against Mpro only
4.Authors should send the manuscript for language revision by a native speaker, I found plenty mistakes and corrected some of them in the attached file.

Reviewer #4: 1-I recommend, the authors should add some promising compounds with similar structure and uses and testing them on the three proteins.
2- Graphical abstract part should be more advanced.
3- The introduction part must be updated and contain recently statistics about the number of infected persons.
4- The introduction part gave brief review about the Epigallocatechin-3-gallate and neglect the other selected compounds so the authors should give brief review about the other promising compounds even on one target.
5- draw the structure of the selected compounds.
6- what is the structure similarity between the selected compounds that drove the authors to select them.
7- The authors should discuss the co-crystalized ligand's reported binding mode of the selected proteins (give a figure for each one) and the ability of the docking algorithm to retrieve the co-crystallized ligand's reported binding mode to validate the selected docking algorithm.
8- Mutations of pocket residues are also needed to support the docking results
9- the resolutions of figures 4, 5 and 6 should be increase to out line amino acid resides and the binding mode.
10- Scoring energy of the Curcumin and Fenretinide are -4.746 and 4.417 against Spike Glycoprotein which are close to Epigallocatechin-3-gallate so the authors should discuss the binding mode and add two figures about them.
11- Scoring energy of Prednisone is -4.439 against Main-Protease which is close to Epigallocatechin-3-gallate so the authors should discuss the binding mode and add figure about it.

There is additional documentation related to this decision letter. To access the file(s), please click the link below. You may also login to the system and click the 'View Attachments' link in the Action column.

Authors' response

We would like to thank you for considering our manuscript for peer review. We would also like to extend our thanks to the reviewers for spending their valuable time to review the manuscript and provide us with valuable comments on the manuscript.

Here, we are submitting the revised version of the manuscript along with the reply to each comment.

Reviewer #1 comments:

Comment 1 – The sentence: ((The genetic sequencing of SARS-CoV-2 encodes several proteins such as the main protease (Mpro or 3CLpro), Spike Protein S1 subunit, and Human Angiotensin-converting enzyme 2 (ACE 2) which plays an important role in its pathophysiology)) is incorrect since ACE 2 is a human protein and is not expressed by virus.

Answer 1 – Yes, we have incorporated the change in the manuscript. Page 1 line 26-27.

Comment 2 – Docking of reference molecules for each protein should be carried out. you can use the co-crystallized ligand as reference compounds.

Answer 2- In the selected protein structures, there were absence of co-crystallized ligands for 6VYB (Spike protein) and 1R42 (ACE-2), so we compared docking results of the ligands docked with these proteins with reference compounds (Ivermectin and Remdesivir). The table of docking results is given in manuscript in table 5 (Page 14-15).

We found inhibitor in structure 6LU7 (main protease), docking result of this ligand with the enzyme and interaction diagram has been included in supplementary data (Page 6-7).

Comment 3 – The authors depended only on the binding energy to distinguish between the different compounds. This case in incomplete. You should depend on the binding mode of the tested compound to select the most promising compounds.

Answer 3- We have compared docking results of predicted drug with co-crystallized ligands and remdesivir and ivermectin as reference compounds (results are given in supplementary data; Page 6-7 and in the manuscript; Page 14-15). The screened compounds have been analyzed on the basis of their relative docking scores and the binding mode of predicted potential drug with all target proteins has been compared in both processes i.e. after molecular docking & after molecular dynamic simulation and found to be interacting well in generated pocket (fig 4,5,6 and 9,10,11 in the manuscript; Page 17-18).

Comment 4 – Validation of docking studies should be carried out for each protein.

Answer 4- The docking studies have been validated through molecular dynamic simulation (MDS) studies (Page 15-18) and MMGBSA (Page 18-20) for each target proteins and enzyme given in the manuscript.

Comment 5 – Figures of docking studies are not clear.
Answer 5- All the figures of docking studies have been re-uploaded with better visualization (Page 11-14).

Comment 6 – Transfer fig. 1, 2, 3 into sup data.
Answers 6- According to the suggestion, the structures of proteins and enzyme have been transferred to the supplementary data (Page 1-2).

Reviewer #2 comments:

Graphical Abstract:

Comment 1 – The graphical abstract can be made more precise. It seems that figure 3, and 4 in graphical abstract has been swapped.
Answer 1 – Graphical abstract has been corrected.

Introduction:

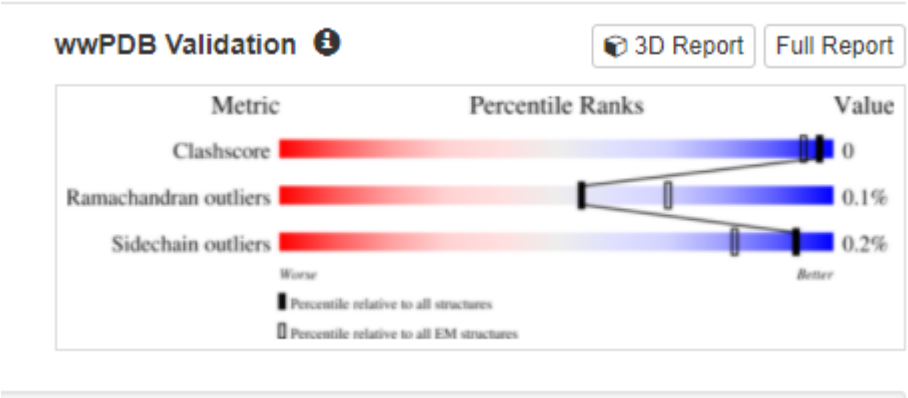
Comment 2 – This part is unnecessarily long which makes the rational of using OLP drugs for repurposing weak. There is a really long and indirect of correlation OLP and COVID-19 has been described through various cellular and immunological processes which fail to establish the correlation of OLP with SARS-CoV-2 infection.
It is suggested to include either a figurative illustration of whole process or to define it in a short and concise manner.
Answer 2 – Thank you for the suggestion. We have revised and shorten the introduction in concise manner.

Methodology:

Comment 3 – The full name of software (version, company etc.) should be included.
Answer 3 – The full name of software is Maestro 12.4 (Schrodinger 2020–2), this has been included in manuscript (Page 5 under the section of molecular docking).

Comment 4 – Correct the notion of writing "SARS-CoV-2" instead of SARS-COV-2. The resolution of structure of spike protein S1 subunit is quite low i.e., 3.20 Å. It could have been a crystal structure solved by X-ray Diffraction technique of high resolution.

Answer 4– The notion has been corrected in the manuscript. We were looking for protein structure of S1 subunit of spike protein as S1 unit of the receptor binding domain (RBD) of this protein interacts first with the host receptor. Also, In the S1 subunit, the loop structure may change structurally in size between CoV species of the betacoronavirus genus. There are two functional domains in the S1 subunit: NTD (N-terminal domain) and C-domain. C-domain acts as RBD (receptor-binding domain). Both of these domains are accountable for the interaction between the virion and the receptor part of the host. This part contains several epitopes that might serve as a potent target for designing the vaccines and developing the antibodies. We have selected PDB ID: 6VYB for S1 subunit of spike protein, the information (interacting amino acid residues) for receptor grid generation was given in the reference paper and it has covered the wide range of amino acids of S1 subunit. Its Ramachandran outlier is also found to be oriented towards wide coverage in the blue region.



Comment 5 – Difference in binding site amino acid residues can be seen from the refence cited for Spike protein and Human ACE-II. The refence used to identify the binding site residues of 6LU7 are the actually the residues which were found to be interacting with the compounds used in respective study. Author may define the rationale behind making the grid using these residues.

Answer 5- The spike protein active site consists of amino acid residues LYS417, GLY446, TYR449, ASN487, GLN493, GLY496, THR500, and GLY502 interacting with active site of Human ACE2 protein which includes ASP30, GLN42, ASP38, GLN24, TYR83, GLU35, LYS353, TYR41, and LYS353for the compound selected for the study of reference paper, The resultant binding site amino acids taken from reference paper were used for receptor grid generation, by doing so, we have found interacting residues for our predicted compound (EGCG) as SER 494, GLY 496 and TYR 505 all forming H-bonds with spike protein and ASP 38, , LYS 353, ALA 386, GLU 37 forming H-Bonds and salt bridge respectively with ACE-2. The similar approach has been adopted for main protease as well for the generation of receptor grid, the residues which were found to be interacting with the compound used in reference paper were found to be covering wide range of active site residues of the enzyme, details are given in Selection and Preparation of Target Protein section of Materials and Method (Page 4).

Comment 6 – The docking studies of OLP Drugs should also be compared with clinically approved antivirals being used for COVID-19 management.
Answer 6 – As per the suggestion, we have compared are docking results of predicted drug with co-crystallized ligand and remdesivir and ivermectin as reference compounds. Results have been included in the manuscript (Page 14-15) and supplementary data (Page 6-7).

Comment 7 – The predicted binding pose of OLP drugs with target protein could also been rescored to determine the predictive binding energies via MMGBSA.
Answer 7 – According to the suggestion, results of predictive binding energies via Prime-MMGBSA have been included in the manuscript (Page 18-20).

Results:

Comment 8 – Section 3.3 Molecular Docking: The results obtained through the Glide module for the docking of protein structure for 6LU7, ACE-2 and Mpro with the selected…….. should be corrected for PDB ID or the name of the protein molecule (one pattern of naming the protein should be used at a time; either PDB ID or the enzyme name)
Answer 8 – The correction has been made as the results obtained through the Glide module for the docking of protein structure for Spike, ACE-2 and Mpro with the selected…….

Comment 9 – The resolution of figures should be increased up to 600 dpi.
Answer 9 – All the figures of docking and simulation studies have been re-uploaded with better resolution.

Discussion:

Comment 10 – The discussion lost connection various times. The correlation of OLP with COVID-19 is repeated and confusing
Answer 10 – We have revised the discussion and included a flowchart (Fig.12) to make it more

clear.

Comment 11 – The manuscript requires a careful correction of various typographical errors.
Answer 11 – All the typographical errors have been corrected.

References:

Comment 12 – Reference number 11 is not written correctly.
Answer 12 –By, mistake it was wrongly formulated. Now correction had been made. Page 25 Line 26-28

Comment 13 – No references were observed for the various modules of Maestro, Schrodinger used (ligprep, Glide, prime), and Gromac (for MD simulation). kindly incorporate them (for the version of software which was sued in study)
Answer 13 – The references for software used for MD and MDS have already been given and few more have been added (Page 26).

Comment 14 – Reference style and format is not consistent throughout.
Answer 14 – Reference style and format has been corrected.

Reviewer #3 comments:

Comment 1 – Authors should explain the reason they selected this kind of drugs
Answer 1– Drugs like Hydroxy-chloroquine and many others are used in clinical trial studies to treat COVID-19. These few drugs are also frequently used to treat OLP, therefore we hypothesized that there must be few similar proteins that are targeted by these drugs found in OLP and COVID-19. So we identified the 17 potential compounds from the database that have been investigated in recent years because of their various pharmacological properties and immunomodulatory activities used in the treatment of OLP disease.
Page 3 Line 21-23

Comment 2 – Authors should explain the reason they selected these specific proteins
Answer 2 – The authors were seeking to see the interaction of drugs which are currently used for oral lichen planus with the enzyme and protein of SARS-CoV-2. Main protease (M^{pro} or $3CL^{pro}$) and Spike glycoprotein plays an important role in pathophysiology of SARS-CoV-2 and Human Angiotensin-converting enzyme-2 (ACE-2) receptor in human body which acts as an entry point for virus. **Spike Glycoprotein** present in the virus contains receptor-binding region, which attaches with **ACE-2 receptors** present on the cell surfaces in host cell. **Main protease (M^{pro} or $3CL^{pro}$)** breaks down spike protein into subunits and helps virus to maturate

and replicate in host cell. That is why; due to its importance we have selected these specific proteins.
Page 2 line 18-22

Comment 3 – Authors should explain the reason they did the MD against Mpro only
Answer 3– The both molecular docking (MD) and molecular dynamic simulation (MDS) has been performed against all above mentioned (comment 2) targets i.e. spike, Mpro and their receptor ACE-2. (Kindly refer sections Molecular Docking and Molecular dynamics Simulation of Materials and method or Fig 4-8).

Comment 4 – Authors should send the manuscript for language revision by a native speaker, I found plenty mistakes and corrected some of them in the attached file.
Answer 4– All the possible corrections and language revision have been included.

Reviewer #4 Comments:

Comment 1 – I recommend, the authors should add some promising compounds with similar structure and uses and testing them on the three proteins.
Answer 1 – we thank you for your recommendation. We are already doing testing for other drugs having similar properties against different target proteins of SARS-CoV-2.

Comment 2 – Graphical abstract part should be more advanced.
Answer 2 – We had made some changes so as to make it more comprehensible**.**

Comment 3 – The introduction part must be updated and contain recently statistics about the number of infected persons.
Answer 3 – Introduction part is updated and recent statistics about the number of infected persons have been added. Page 1 Line 2

Comment 4 – The introduction part gave brief review about the Epigallocatechin-3-gallate and neglect the other selected compounds so the authors should give brief review about the other promising compounds even on one target.
Answer 4– We have added a flowchart (Fig. 12) in which we have explained about other selected compounds targeting other proteins in discussion section.
Page 23.

Comment 5 – draw the structure of the selected compounds.
Answer 5 – The structures of the selected compounds have been drawn and added to the supplementary data (Page 2-6).

Comment 6 – what is the structure similarity between the selected compounds that drove the authors to select them.
Answer 6 – The compounds that have been selected are because of their different pharmacological properties and immunomodulatory activities used in the treatment of OLP disease. All of them are not structurally similar but because of having hydroxy groups and other electron donating-accepting functional groups, they are supposed to make H-bonds and Vander Waal bonds with target proteins and enzyme and able to show considerable binding with them.

Comment 7 – The authors should discuss the co-crystalized ligand's reported binding mode of the selected proteins (give a figure for each one) and the ability of the docking algorithm to retrieve the co-crystallized ligand's reported binding mode to validate the selected docking algorithm.
Answer 7 – The binding mode of co-crystallized ligand of main-protease has been compared with the binding mode of selected ligands, their structure has been included in the supplementary data (Page 6-7). But as there was absence of co-crystallized ligands in the proteins structures of spike protein (6VYB) and ACE-2 (1R42), we could not perform same for these proteins.

Comment 8 – Mutations of pocket residues are also needed to support the docking results
Answer 8– According to the reference paper given below, the amino acids substitutions Alpha (UK) – N501Y; A570D; P681H; T716I; S982A and D1118H, Beta (South Africa) - D80A; D215G; K417 N; E484K; N501Y; A701V; Gamma (Brazil) - L18F; T20 N; P26S; D138Y; R190S; K417T; E484K; N501Y; H655Y; T1027I and Delta (India) – T19R; L452R; T478K; P681R; D950 N showed that virus mutants presented different regions of mutations compared with SARS-CoV-2 from Wuhan (The pdb used in this paper is have similar sequence as the spike pdb we have selected for this study). The interacting amino acids for EGCG are TYR 505, SER 494 and GLY 496, here TYR (Y) is found to be present in Alpha, beta and Gamma variant of SARS-CoV-2 also the predicted drug has ability to form H-bond with amino acids present in pocket residues of different variants which supports the binding of predicted drug with viral protein of COVID-19. Their in silico validation (molecular docking) has also been performed where the predicted drug have shown significant docking with Alpha, Beta and Gamma variants of spike glycoprotein. The result of this analysis can be provided on request.
Reference:
Sanches PRS, Charlie-silva I.,Braz HLB, Bittar C.,Calmon MF, Rahal P.,Cilli EM, Recent advances in SARS-CoV-2 Spike protein and RBD mutations comparison between new variants Alpha (B.1.1.7, United Kingdom), Beta (B.1.351, South Africa), Gamma (P.1, Brazil) and Delta (B.1.617.2, India), *Journal of Virus Eradication*, 2021, 7,3, 100054.

Comment 9 – the resolutions of figures 4, 5 and 6 should be increase to outline amino acid resides and the binding mode.
Answer 9 – The figures 4, 5 and 6 have been revised as per the suggestions provided (page 11-14 in the manuscript).

Comment 10 – Scoring energy of the Curcumin and Fenretinide are -4.746 and 4.417 against Spike Glycoprotein which are close to Epigallocatechin-3-gallate so the authors should discuss the binding mode and add two figures about them.
Answer 10 – As per the suggestion, discussion of binding mode of Curcumin and Fenretinide has been included in the manuscript (Page 8 and 10) and their interaction diagrams in the supplementary data (Fig.1 & 2 on Page 8).

Comment 11 – Scoring energy of Prednisone is -4.439 against Main-Protease which is close to Epigallocatechin-3-gallate so the authors should discuss the binding mode and add figure about
it.
Answer 11– As per the suggestion, discussion of binding mode of Prednisone has been included in the manuscript (Page 10) and along with its interaction diagrams in the supplementary data (Fig 3,4 & 5 on Page 9-11).

2nd Editorial decision
05-Dec-2021

Ref.: Ms. No. JCTRes-D-21-00153R1
Lichen Planus Drugs Re-purposing as Potential Anti COVID-19 Therapeutics through Molecular Docking and Molecular Dynamics Simulation Approach
Journal of Clinical and Translational Research

Dear author(s),

Reviewers have submitted their critical appraisal of your paper. The reviewers' comments are appended below. Based on their comments and evaluation by the editorial board, your work was FOUND SUITABLE FOR PUBLICATION AFTER MINOR REVISION.

If you decide to revise the work, please itemize the reviewers' comments and provide a point-by-point response to every comment. An exemplary rebuttal letter can be found on at http://www.jctres.com/en/author-guidelines/ under "Manuscript preparation." Also, please use the track changes function in the original document so that the reviewers can easily verify your responses.

Your revision is due by Jan 04, 2022.

To submit a revision, go to https://www.editorialmanager.com/jctres/ and log in as an Author. You will see a menu item call Submission Needing Revision. You will find your submission record there.

Yours sincerely,

Michal Heger
Editor-in-Chief
Journal of Clinical and Translational Research

Reviewers' comments:

Reviewer #1: The authors carried out all the requested modifications.
Accordingly, I recommend the publication of the
manuscript.

Reviewer #4: 1- The author must highlight the modified part in the manuscript.
2- Resolution of original graphical abstract is clearer than modified one.
3- The author answered on comment number 6 (the compound containing OH , electron donating and electron with drawing group). this answer is unsatisfactory and he should clarify in introduction part in some details what is the relationship between these compounds.
4- For comment number 7, the authors can change protein code to another one that contain co-crystallized ligand and compare binding mode of the tested compounds.
5- For comment number 8, the authors misunderstand what I mean; manual mutations of pocket residues for the same selected proteins and compare the ability of the tested compound to bind with the mutant one by the same manner.

Authors' response

Reviewer #4

Comment-1 The author must highlight the modified part in the manuscript.

Answer- According to the suggestion, the modified parts have been highlighted in the revised manuscript.

Comment-2 Resolution of original graphical abstract is clearer than modified one.

Answer- The resolution of graphical abstract has been improvised.

Comment-3 The author answered on comment number 6 (the compound containing OH , electron donating and electron with drawing group). this answer is unsatisfactory and he should clarify in introduction part in some details what is the relationship between these compounds.

Answer- We have not based our selection on basis of structure similarity of these compounds but for their action against Lichen Planus. These compounds show their various pharmacological properties and immunomodulatory activities used in the treatment of OLP disease. Drugs such as Prednisone, Dapsone, Flucinonide, Curcumin, Epigallocatechin Gallate (EGCG), Fenretinide, Phenytoin, Hydroxy-chloroquine etc which act as anti-inflammatory, antineoplastic, antifungal, antioxidant and immunosuppressive are used in the treatment of OLP disease. We have included some changes in the introduction part regarding this and also highlighted the same(**Page 4).**

Comment-4 For comment number 7, the authors can change protein code to another one that contain co-crystallized ligand and compare binding mode of the tested compounds.

Answer- We have performed docking with co-crystallized ligand present in structure of main-protease (PDB ID: 6LU7). But, the protein code we selected earlier for Spike Protein (PDB ID: 6VYB) and human ACE-2 (PDB ID: 1R42) do not contain co-crystallized ligand that's why to validate their binding with tested compounds, we performed their docking with standard drugs (Remdesivir and Ivermectin). Since, the proteins code selected for spike protein and human ACE-2 on the basis of interaction residues of spike protein with ACE-2 (having considerable molecular interaction in virus S group and ACE-2) to generate the receptor grid around the receptor binding domain of proteins as mentioned in the reference 14, we politely can request that we cannot change protein code of spike and hACE-2.

Comment-5 For comment number 8, the authors misunderstand what I mean; manual mutations of pocket residues for the same selected proteins and compare the ability of the tested compound to bind with the mutant one by the same manner.

Answer- The correction has been made. We have performed manual mutations of pocket residues of spike protein (PDB ID: 6VYB) for Alpha, Beta, Gamma and Delta variants and performed their docking with the tested compounds. We have observed satisfactory results with all above mentioned mutations of spike protein; their results have been added in Supplementary Data 2.

3rd Editorial decision
08-Jan-2022

Ref.: Ms. No. JCTRes-D-21-00153R2
Lichen Planus Drugs Re-purposing as Potential Anti COVID-19 Therapeutics through Molecular Docking and Molecular Dynamics Simulation Approach
Journal of Clinical and Translational Research

Dear authors,

I am pleased to inform you that your manuscript has been accepted for publication in the Journal of Clinical and Translational Research.

You will receive the proofs of your article shortly, which we kindly ask you to thoroughly review for any errors.

Thank you for submitting your work to JCTR.

Kindest regards,

Michal Heger
Editor-in-Chief
Journal of Clinical and Translational Research

Comments from the editors and reviewers: