

Editor's Comment:

After a careful analysis of the evaluation process, I was able to verify that all evaluators approved the work, and the authors accepted the requested suggestions and corrections. I suggest avoiding the same terms in the title of the work and in the keywords. Regarding the molecular modeling stage, Despite having been removed from the final version (as recommended by one of the reviewers), I leave some valuable recommendations for the authors if they wish to continue this stage in future work:: 1) The images must be improved. For the three-dimensional image of the protein, I suggest that instead of taking a printout from the Swiss-model server, it is done using a molecule editing and visualization program (such as VMD, Pymol, Chimera, Discovery Studio, etc.) 2) It is essential that in the modeling it is clear what the template structure was for building the theoretical model (Access Code and database, resolution, etc.). 3) Model validation was carried out using only the QMEAN Z-score, which is a global quality measure. I also recommend including an analysis of stereochemical quality (Ramachandran graph) and local quality (for example, VERIFY3D). Both tools are freely available and easy to use on the server <https://saves.mbi.ucla.edu/>. 4) The structural analysis is very superficial, I recommend analyzing details of the structure such as binding sites, functional and structural domains, secondary structures and motifs. 5) Modeling of the 540-dihydropteroate synthetase protein suggests that a molecular docking be carried out between this target and Sulfadoxine-Pyrimethamine. I recommend minimizing protein energy before running docking.

My final decision as academic editor is to approve the work for publication.

Editor's Details:

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