

Answers to Reviewers

(1) The method part is too simple. What is the standard for template search?

There are no standards for finding templates for proteins as different as the ones modeled in this study, there are only criteria. For better understanding, the criteria have been better described in MATERIAL and METHODS in the manuscript.

(2) The template Identity of one protein is only 40%, which is too low.

According to several classical studies on comparative modeling, it is already known that this modeling technique can be employed using templates with sequence identity greater than 30% (Chothia; Lesk, 1986; Xiang, 2006; Chakravarty et al., 2008). Therefore, 40% is above the required value, and even so the pipeline used has been improved for templates with low identity, and a homologous template has been used.

(3) The simulated structure obtained by the authors should be optimized, and molecular dynamics simulation is necessary.

Indeed, molecular dynamics is very important to predict the behavior of the 3D structure, since the protein is not a rigid structure. However, this kind of computational simulation is indispensable for rational drug planning. In this work the intention is to have a vision of the 3D structure to study and understand the antigen recognition aiming a future study for the development of serological test based on spot synthesis; in this case the antigen recognition is done with linear epitopes, the 3D structure of the whole antigen would be a complement for the study of this recognition. Our research group has already been using this kind of approach, as indicated in Soares BA et al. (2021) - DOI: 10.1016/j.molimm.2021.07.021.

(4) The AlphaFold Protein Structure Database also has prediction results for these proteins, whether the author's results are better than them.

The structure models deposited in Alphafold show regions with no defined structure, possibly due to lack of coverage during the molecular modeling process. In the models obtained in this study we got the complete structure.

(5) The language of the manuscript needs to be improved.

This request has been fulfilled.

Best regards,

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