

Response to Reviewers comments on the Review Manuscript NO.: 80300

The authors are grateful for the thorough review of the manuscript which is essential for improving the quality of the article. All the issues raised have been addressed and the changes made are highlighted below.

Reviewer #1:

It is recommended to add content related to the research content of the article in the two sections of molecular docking and molecular dynamics, rather than simply introducing this method.

Response: More contents on the molecular docking and molecular dynamics simulation have been added to the respective sections.

Reviewer #2:

For the design of small-molecule drugs for the treatment of inflammatory bowel disease, highly effective and time-saving approaches, such as computational methods, are still a viable choice. By complementing experimental studies with computational approaches, the probability of successful drug discovery is increased while simultaneously reducing associated costs. This article provides a summary of current drug discovery pipeline for IBD, with special emphasis on the part played by computational methods. The use of in silico genomic studies, target identification, and virtual screening to find new drugs and repurpose existing ones for the treatment of inflammatory bowel disease (IBD) are discussed. The article is very interesting, but needs further research.

Response: More research contents have been added to the computational methods in IBD drug discovery, specifically in the sections on molecular docking and molecular dynamics simulation.