

## PEER-REVIEW REPORT

**Name of journal:** *World Journal of Gastroenterology*

**Manuscript NO:** 80300

**Title:** Modern drug discovery for Inflammatory Bowel Disease: the role of computational methods

**Provenance and peer review:** Invited Manuscript; Externally peer reviewed

**Peer-review model:** Single blind

**Reviewer's code:** 06333001

**Position:** Peer Reviewer

**Academic degree:** MD

**Professional title:** Doctor

**Reviewer's Country/Territory:** China

**Author's Country/Territory:** Nigeria

**Manuscript submission date:** 2022-09-22

**Reviewer chosen by:** AI Technique

**Reviewer accepted review:** 2022-09-27 13:15

**Reviewer performed review:** 2022-09-28 01:19

**Review time:** 12 Hours

Scientific quality	<input type="checkbox"/> Grade A: Excellent <input type="checkbox"/> Grade B: Very good <input checked="" type="checkbox"/> Grade C: Good <input type="checkbox"/> Grade D: Fair <input type="checkbox"/> Grade E: Do not publish
Language quality	<input type="checkbox"/> Grade A: Priority publishing <input type="checkbox"/> Grade B: Minor language polishing <input checked="" type="checkbox"/> Grade C: A great deal of language polishing <input type="checkbox"/> Grade D: Rejection
Conclusion	<input type="checkbox"/> Accept (High priority) <input type="checkbox"/> Accept (General priority) <input type="checkbox"/> Minor revision <input checked="" type="checkbox"/> Major revision <input type="checkbox"/> Rejection
Re-review	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No



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<b>Peer-reviewer statements</b>	Peer-Review: [ <input checked="" type="radio"/> ] Anonymous [ <input type="radio"/> ] Onymous Conflicts-of-Interest: [ <input type="radio"/> ] Yes [ <input checked="" type="radio"/> ] No
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#### **SPECIFIC COMMENTS TO AUTHORS**

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.

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**Reviewer's Country/Territory:** China

**Author's Country/Territory:** Nigeria

**Manuscript submission date:** 2022-09-22

**Reviewer chosen by:** AI Technique

**Reviewer accepted review:** 2022-09-22 14:50

**Reviewer performed review:** 2022-10-01 02:16

**Review time:** 8 Days and 11 Hours

Scientific quality	<input type="checkbox"/> Grade A: Excellent <input type="checkbox"/> Grade B: Very good <input checked="" type="checkbox"/> Grade C: Good <input type="checkbox"/> Grade D: Fair <input type="checkbox"/> Grade E: Do not publish
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**Peer-reviewer  
statements**

Peer-Review: [ ☒ ] Anonymous [ ☐ ] Onymous

Conflicts-of-Interest: [ ☐ ] Yes [ ☒ ] No

#### **SPECIFIC COMMENTS TO AUTHORS**

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.