



SDI Review Form 1.6

Journal Name:	International Journal of Biochemistry Research & Review
Manuscript Number:	Ms_IJBCRR_23216
Title of the Manuscript:	Optimizing the aggregation propensity of therapeutic monoclonal antibodies against cancer and autoimmune diseases: a computational study
Type of the Article	Original Research Article

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
<u>Compulsory</u> REVISION comments	(1) The data presentation should be re-arranged. Table S₁ and Table S₂ are suggested to be Table 1 and Table 2. The original Table 1 becomes Table 3. (2) Two sets of "References" are cited in the manuscript. One is presented in text and the other is in the "Supplementary Materials". It needs to be rearranged and remains the major literatures. (3) In "Discussion": The limitations and drawbacks of the present study should be discussed in more detail to render the manuscript more completion.	
<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments	This is a computational bio-informatic research by using AMYLPRED2 consensus method to predict the "aggregation-prone" regions on the surface of FDA approved monoclonal IgG₁ antibodies for the treatment of cancer and autoimmune diseases. Then, the author substituted these aggregation-prone groups by specific amino acids with exposed side chains. They successfully reduced or even fully eliminated aggregation of these therapeutic monoclonal antibodies. These datasets may be useful in the clinical application of therapeutic monoclonal antibody technology. However, the present study is no more than a computational bio-information-based knowledge. More investigations are necessary to prove the hypothesis.	

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