Dear Editor,

**Article ID: 4810**

**Docking Studies Reveal Zerumbone Targets -catenin of the Wnt--catenin Pathway in Breast Cancer**

Thank you for considering our manuscript for your journal. The revised manuscript after the second round of feedback is being submitted along with this letter. We have incorporated the reviewer’s comments to the best of our abilities. The changes have been highlighted in the manuscript. Briefly, the homology modelling section has been removed based on the feedback from reviewers. Since Figure 4 has been removed from the manuscript, the Figures 5-8 have been renumbered as Figures 4-7 and improved based on comments from reviewers.

I hope the journal is satisfied with our efforts. Please let me know if you need any other information.

Thank you

Yours sincerely

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**Reviewer’s Comments**

Reviewer A:

ADDITIONAL COMMENTS
Please indicate the page numbers for suggested corrections.
Please, be as specific as possible if major correction by the author(s) is
recommended! :

1. Although a major effort was made toward increasing the figure quality,
Figures 5, 6, 7, and 8 are still not acceptable for publication. Please take
care that all panel labels are of the same size and aligned (as already
noted in the original review).

The panel labels for Figures 5-8 have resized. The figures have also been renumbered as Figures 4-7 after removal of Figure 4.

2. Authors should take care of many abbreviations in the manuscript. While
most of them were properly introduced, some of them were not explained at
the first appearance, and some are not explained at all. Authors should
therefore either properly introduce all abbreviations, or make an
Abbreviation section in the paper.

The abbreviations have been explained at first appperance.

3. On page 5, authors state that they "determine the exact binding
mechanism". This is a clear overstatement.

The statement has been removed.

4. On page 7, the description of the force field equations takes more than
half a page, and it is not essential at all. This equation is very famous in
the computational chemistry community, and hence, it does not require an
introduction. It is, therefore, my recommendation to remove this whole
paragraph (ending with a reference (MacKerell et al., 1998). ).

The explanation has been removed as recommended.

5. Authors should, instead, explicitly state that the binding energies they
compute are the 'potential' interaction energies, and not the more common
and more informative Gibbs free energies.

The explanation has been included in the Experimental section.

6. It is still not clear why authors use homology modeling at all when the
sequence identity is 98%.

The section has been removed after the feedback.

7. Finally, authors should properly screen their manuscript for numerous
present typos.
We have tried our best to remove the typo errors.