Review Form 1.7

Journal Name:	**Annual Research & Review in Biology**
Manuscript Number:	**Ms_ARRB_110470**
Title of the Manuscript:	**In silico analysis and 3-D structure prediction of non-synonymous single nucleotide polymorphisms (nsSNPs) in the human MED12 gene associated with uterine leiomyomas**
Type of the Article	

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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)*
Compulsory REVISION comments 1. **Is the manuscript important for scientific community?** (Please write few sentences on this manuscript) 2. **Is the title of the article suitable?** (If not please suggest an alternative title) 3. **Is the abstract of the article comprehensive?** 4. **Are subsections and structure of the manuscript appropriate?** 5. **Do you think the manuscript is scientifically correct?** 6. **Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form.** **(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)**	1. **Yes. the topic of the manuscript appears to be focused on the analysis and prediction of non-synonymous single nucleotide polymorphisms (nsSNPs) in the human MED12 gene associated with uterine leiomyomas. Understanding the genetic factors and molecular mechanisms underlying uterine leiomyomas is relevant and important in the field of gynecology and reproductive health.** 2. **Yes. The title of the article, "In silico analysis and 3-D structure prediction of non-synonymous single nucleotide polymorphisms (nsSNPs) in the human MED12 gene associated with uterine leiomyomas," appears to be suitable and informative. It accurately reflects the main focus of the study, which is the analysis and prediction of nsSNPs in the MED12 gene and their association with uterine leiomyomas. The title provides a clear indication of the computational approach used (in silico analysis) and the specific aspect of the gene being investigated (non-synonymous SNPs). Additionally, it mentions the relevance of the gene to uterine leiomyomas, which helps to situate the study within the context of gynecologic tumors.** 3. **No. The abstract of the article lacks certain key details that would provide a clearer understanding of the study. It does not provide sufficient information about the sample size or demographics of the patients with uterine leiomyomas, which could impact the generalizability of the findings. Additionally, the abstract does not mention the specific computational tools or algorithms used for the in silico analysis, making it difficult to evaluate the validity and reliability of the predictions made.** **Furthermore, while the abstract mentions the presence of genetic alterations and their predicted deleterious effects, it does not provide specific examples or elaborate on the functional consequences of these mutations. This lack of specific details limits the reader's ability to fully grasp the significance of the findings.** **Overall, the abstract could be improved by including more specific information about the study design, methodology, and results, allowing readers to better assess the scientific rigor and potential implications of the research.** 4. **Yes** 5. **No. it is not possible to evaluate the scientific accuracy or correctness of the manuscript. The truncated content does not provide sufficient details about the experimental methods, data analysis, or results to make an informed judgment on the scientific accuracy of the study.** 6. **Not all of the references recent.**	
Minor REVISION comments 1. **Is language/English quality of the article suitable for scholarly communications?**	Yes. the language and quality of the article appear to be suitable for scholarly communication.	
Optional/General comments	The article addresses an important topic in the field of gynecologic tumors, specifically uterine leiomyomas, which are common benign tumors. The use of molecular dynamics simulations and computational tools for in silico analysis and prediction adds a valuable dimension to the research. The inclusion of a substantial number of uterine leiomyoma samples (50 patients) strengthens the	

	study's findings. The identification of a significant genetic alteration in the MED12 gene, particularly in codon 44 of exon 2, highlights its potential implication in the pathobiology of uterine fibroids. The article provides relevant information on the structure and function of the MED12 gene and its involvement in transcriptional regulation. The utilization of various prediction methods, such as ClinVar, ProtParam, Missense 3D, and MutPred2, enhances the comprehensive analysis of the deleterious impact of non-synonymous variants. However, The article does not provide detailed information about the demographic characteristics of the patient population, such as age range, ethnicity, or other relevant factors. The article lacks information on the specific techniques used for DNA extraction, amplification, and sequencing, which could affect the reproducibility and reliability of the results. The absence of a discussion section limits the opportunity for in-depth interpretation and contextualization of the findings. It would be beneficial to include additional information on the limitations of the study and potential future directions for research in this field. The article does not mention any validation or experimental verification of the in silico predictions, which could impact the reliability of the results.	

PART 2:

	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)*
Are there ethical issues in this manuscript?	*(If yes, Kindly please write down the ethical issues here in details)*	

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