## Review Form 3

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| Journal Name: | Current Journal of Applied Science and Technology |
| Manuscript Number: | **Ms_CJAST_130593** |
| Title of the Manuscript: | **Performing effective calculations of protein - ligand binding free energy with the help of molecular dynamics methods** |
| Type of the Article | |

**PART 1: Comments**

| | **Reviewer's comment** | **Author's Feedback** *(Please correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
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| **Please write a few sentences regarding the importance of this manuscript for the scientific community. A minimum of 3-4 sentences may be required for this part.** | This manuscript provides a practical approach to accurately calculating protein-ligand binding free energy using molecular dynamics methods. These calculations are vital for drug design, helping predict how well a drug binds to its target protein. Accurate methods save time and resources by guiding experimental efforts. The study offers clear guidelines to improve computational efficiency and reliability, benefiting researchers in drug discovery and molecular biology. | |
| **Is the title of the article suitable? (If not please suggest an alternative title)** | **yes** | |
| **Is the abstract of the article comprehensive? Do you suggest the addition (or deletion) of some points in this section? Please write your suggestions here.** | **Required rewrite** | |
| **Is the manuscript scientifically, correct? Please write here.** | yes | |
| **Are the references sufficient and recent? If you have suggestions of additional references, please mention them in the review form.** | yes | |

## Review Form 3

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| **Is the language/English quality of the article suitable for scholarly communications?** | Need revised | |
| **Optional/General** comments | **Comments for Authors**<br><br>This manuscript addresses an important topic in computational chemistry, specifically the calculation of protein-ligand binding free energies using molecular dynamics methods. The calculation of protein-ligand binding free energies is a cornerstone of computational drug discovery. Molecular dynamics (MD) methods have emerged as powerful tools for simulating biomolecular interactions at the atomic level, providing insights into binding mechanisms, thermodynamics, and structural dynamics.<br><br>Prior to publication, the following amendments are required:<br><br>1. The introduction is not well-organized; the motivation and statement of the problem are not clearly explained.<br>2. The terms MM/PBSA and MM/GBSA are repeated. Please remove one. Additionally, ensure the first occurrence of abbreviations such as MM/PBSA, VMD, and XA includes their full names.<br>3. Change "material" to "materials."<br>4. Why 1F0R, 1FJS, 1KSN, 1NFU, and 2J34 proteins selected? Please explain?<br>5. In the Results and Discussion section, the statement “These numbers show that, as expected, more calculations can be made per unit time by decreasing the volume of the systems and the number of atoms they contain” is unclear. Please revise for clarity.<br>6. The phrase "as expected" is not scientifically precise. For example: “As seen in Table 3, it was observed that the simulation speeds decreased as the volumes of the systems and the number of atoms they contain increased, as expected.” Rewrite this sentence using precise, scientific language.<br>7. Ensure uniform formatting for Figure 2 and Fig 3. Also, compare these results with relevant literature. Figure 2 is not visible; please replot it for better clarity.<br>8. The conclusion is not well-written. Rewrite the conclusion, focusing on the key findings and their implications. | |

## Review Form 3

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

**Reviewer Details:**

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|---|---|
| Name: | **Umer Sherefedin Yasin** |
| Department, University & Country | **Adama Science and Technology University, Ethiopia** |