## **RETRACTION NOTE**







## Retraction Note: Molecular docking simulation, drug-likeness assessment, and pharmacokinetic study of some cephalosporin analogues against a penicillin-binding protein of *Salmonella typhimurium*

Philip John Ameji · Adamu Uzairu · Gideon Adamu Shallangwa fo · Sani Uba

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The Editor-in-chief has retracted this article because after the publication of the article, a reader noted that erroneous configurations were used for molecular docking calculations. Additionally, the publisher found that the structures presented in Table 1 are incorrect due to errors made during the publication of the article. However, PubChem CIDs displayed in Table 1 remain the same. Further investigation by the Journal found discrepancies in the structures of compounds in Table 1 (derived from PubChem) and the articles cited in PubChem [1–3]. Therefore, the molecular docking calculations presented in this manuscript do not correspond to the antibacterial activity reported in cited articles [1–3]. Additionally, these discrepancies and errors substantially affect the findings and conclusions of the article. Therefore, the Editor-in-Chief has lost confidence in the data of the article.

- The oxime structures of compounds 1–11 are *syn* in [1] and *anti* in PubChem.
- The oxime structures of compounds 12, 13, 15–21, and 23–30 are *syn* in PubChem and in Refs. [2, 3]. However,

absolute configurations of the  $\beta$ -lactam of compounds 12, 13, 15–21, and 23–30 retrieved from 3D structures (PubChem) were found to be wrong. The correct configurations should be 6R,7R because they are cephalosporin derivatives.

None of the authors have responded to any correspondence from the publisher or Editor in Chief regarding the final version of this retraction.

## References

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