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Correction: The biological activity and molecular docking studies of three multiple myeloma drugs

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This is correction to the paper entitled "The biological activity and molecular docking studies of three multiple mylemoa drugs" by A. K. Srivastava et al. J. Sci. Res. Adv. 2 (2015) 51-53. Below is the addition of a subsection in Results and discussion part of the paper [1].

Molecular Docking

The results of molecular docking of thalidomide, lenalidomide and pomalidomide are displayed in Fig. 2. The docking region is encircled by white in order to locate the position of ligand. One can note that thalidomide binds to middle segment of C-protein. On the contrary, lenalidomide and pomalidomide binds to upper segment and left segment of the same receptor, respectively. The binding of a ligand to the receptor provides the mechanism of biological actions.

The docking results in an E-value which is equivalent to the interaction energy between ligand and receptor. During the process, it is E-value which we seek to minimize. The more negative is the E-value, more efficient will be docking. Table 2 list the docking scores (E-values) for three multiple myeloma drugs. In the view of these values, one can conclude that pomalidomide can be expected to be more active than lenalidomide. This result is consistent with the calculated Log P and Log S values of lenalidomide and pomalidomide.

Notes and References

Journal of Scientific Research and Advances apologizes for any inconvenience with the readers as well as authors.

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1. A. K. Srivastava, A. Dwivedi, R. Das, A. K. Pandey, N. Misra, Journal of Scientific Research and Advances Vol. 2, No. 1, 2015, 51-53.