

**W. Akhtar<sup>1</sup>****G. Verma<sup>1</sup>****M. F. Khan<sup>1</sup>****M. Shaquiquzzaman<sup>1</sup>****M. M. Alam<sup>1</sup>**

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**PHARMACOPHORE MODELING, 3D-QSAR,  
DOCKING AND DRUG LIKELINESS PREDICTION  
OF ANTITUBULIN AGENTS**

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<sup>1</sup>Drug Design & Medicinal Chemistry Lab, Department of Pharmaceutical Chemistry, School of Pharmaceutical Education & Research, Jamia Hamdard, Hamdard Nagar, New Delhi, India

*wasimakhtar123@gmail.com*

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A set of Acyl 1,3,4-thiadiazole amides and sulfonamide derivatives based antitubulin inhibitors [1,2] was subjected to pharmacophore modeling, molecular docking and *in silico* ADME prediction. This study has been performed to identify the binding pattern and drug likeliness nature of these microtubule inhibitors. For these compounds, a four point pharmacophore model (AAHR.11) was generated. This model came out to be statistically significant as it had a correlation coefficient ( $R^2$ ) of 0.89, which was considerably towards higher side, a cross validation coefficient ( $Q^2$ ) of 0.82 and F value of 44.3 at 6 component PLS factor. Results of external validation were also indicative of high predictive power ( $R^2 = 0.83$ ). This model also passed Tropsha's test for predictive ability and Y-randomization test. The Domain of Applicability (APD) of the model was also successfully defined to ascertain whether the given prediction can be considered reliable or not. Further, to determine the effectiveness of docking protocol, co-crystallized ligand was extracted from the ligand binding domain of the protein and was re-docked into the same position. The conformer obtained on re-docking and the cocrystallized ligand were superimposed. Root mean square deviation (RMSD) between the two was found to be 0.853 Å, justifying the efficacy of performed docking. Outcomes of this work provide an insight for the development of novel potential antitubulin agents.

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1. Yang X.H. et al. *Bioorganic & Medicinal Chemistry*, 2012, **20**: 1181-1187.

2. Luo Y. et al. *Bioorganic & Medicinal Chemistry*, 2011, **19**: 4730-4738.

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*The authors would like to acknowledge Jamia Hamdard, New Delhi, India-110062.*

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