

Exploring 1,2,4-Triazine-3(2H)-One Derivatives as Anticancer Agents for Breast Cancer: A QSAR, Molecular Docking, ADMET, and Molecular Dynamics

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Abstract : This study aimed to explore the quantitative structure-activity relationship (QSAR) of 1,2,4-Triazine-3(2H)-one derivative as a potential anticancer agent against breast cancer. The electronic descriptors were obtained using the Density Functional Theory (DFT) method, and a multiple linear regression techniques was employed to construct the QSAR model. The model exhibited favorable statistical parameters, including $R^2=0.849$, $R^2_{adj}=0.656$, $MSE=0.056$, $R^2_{test}=0.710$, and $Q^2_{cv}=0.542$, indicating its reliability. Among the descriptors analyzed, absolute electronegativity (χ), total energy (TE), number of hydrogen bond donors (NHD), water solubility (LogS), and shape coefficient (I) were identified as influential factors. Furthermore, leveraging the validated QSAR model, new derivatives of 1,2,4-Triazine-3(2H)-one were designed, and their activity and pharmacokinetic properties were estimated. Subsequently, molecular docking (MD) and molecular dynamics (MD) simulations were employed to assess the binding affinity of the designed molecules. The Tubulin colchicine binding site, which plays a crucial role in cancer treatment, was chosen as the target protein. Through the simulation trajectory spanning 100 ns, the binding affinity was calculated using the MMPBSA script. As a result, fourteen novel Tubulin-colchicine inhibitors with promising pharmacokinetic characteristics were identified. Overall, this study provides valuable insights into the QSAR of 1,2,4-Triazine-3(2H)-one derivative as potential anticancer agent, along with the design of new compounds and their assessment through molecular docking and dynamics simulations targeting the Tubulin-colchicine binding site.

Keywords : QSAR, molecular docking, ADMET, 1,2,4-triazin-3(2H)-ones, breast cancer, anticancer, molecular dynamic simulations, MMPBSA calculation

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