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Title: Computational studies of potential inhibitors to the protein aurora b kinase

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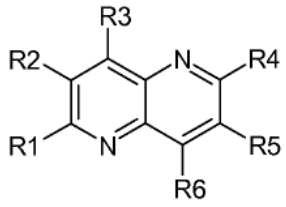
Abstract:

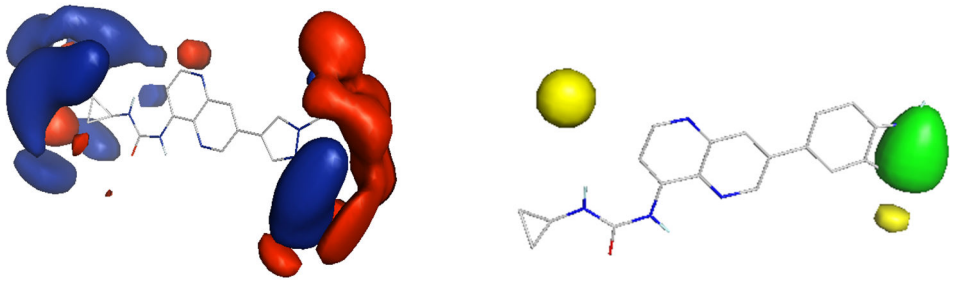
Cancer is a neoplastic disease caused by the uncontrolled growth of malignant cells affecting vital organs. An important target for the treatment of this disease is the aurora B kinase protein. The drugs used in the strives against cancer have high toxicity, resistance and low bioavailability, so it is necessary to study the discovery of new compounds against cancer [1-3]. For this, a molecular docking study (*docking*) was performed between potential inhibitors [4](Figure 1) and the protein active site, aiming to obtain the best conformation of each compound [5]. These conformations were used in the QSAR (Quantitative structure-activity relationships) study relating the structures of potential inhibitors with biological activity [6]. The molecular interaction field (MIFs) steric is based on the parameter AMBER FF99 of Van Der Waals And calculated according to the potential 6-12 de Lennard-Jones between the molecules and a carbon probe sp^3. The MIFs steric is based in the punctual charge model and calculated by the Coulomb interaction between positively charged probes and the atoms of the molecules [7]. Partial Least Squares (PLS) method was used to obtain the best QSAR models. It correlates to experimental binding affinities with the contribution of molecular fields [8].

Figure 1. General formulas of potential inhibitors



The results show through molecular anchorage studies was evaluated the mode of interaction of potential inhibitors On the active site of the aurora B kinase protein, in which it can be observed that there is a tendency between the biological activity and the interactions performed. The analysis of MIF results (Figure 2) showed that compounds with functional groups with high electron density such as pyrazole and with volumes close to cyclopopil are present in favorable regions.

Figure 2. Electrostatic and steric fields



The theoretical results reinforce the experimental, noting that these compounds can be used as a starting point for the development of novel anticancer compounds.

Key-words: Cancer. Aurora B kinase. Molecular docking. QSAR-3D
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