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Full Paper

Auto QSAR- A Fast Approach for Creation and Application of QSAR Models through Automation

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Graphical Abstract

An Auto-QSAR methodology has been used in this work along with molecular docking strategy on phenoxyquinoline c-Met kinase inhibitors. QSAR models were re-validated and comparison of predicted activity with the literature observed activity showed that compound **18 b** as most potent c-Met kinase inhibitor. Moreover, obtained compounds were subjected to *in silico* ADMET studies to screen the drug-likeness and toxicity properties.

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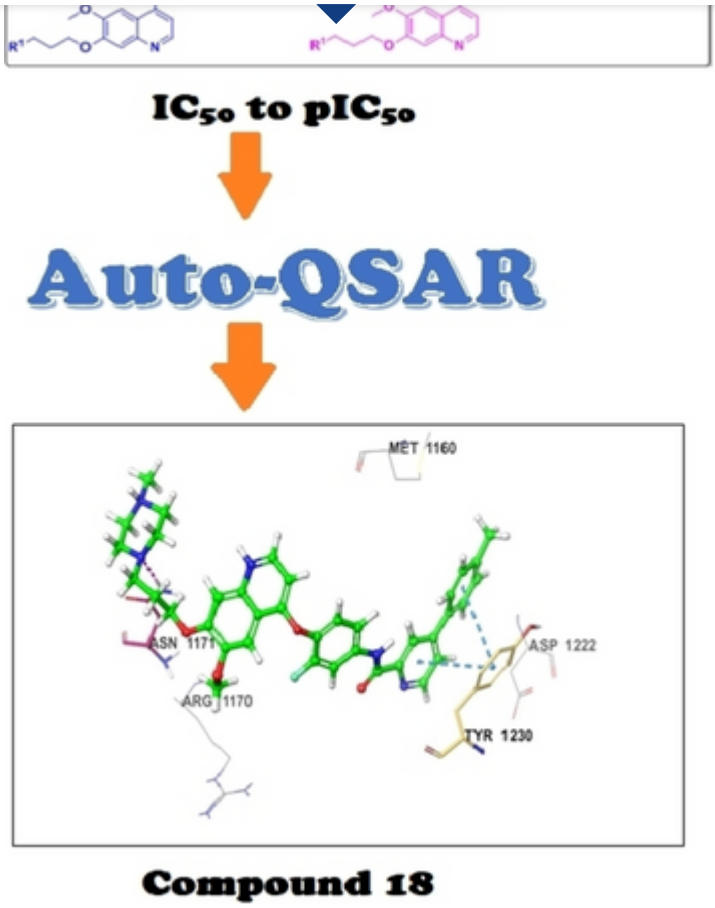

Abstract

A continuous and undefined malignant growth in cancer makes it an extremely heterogeneous complex disease. Different types of enzymes helps in detection of cancerous growth in the human body. In this work, different predictive Quantitative Structure-Activity Relationship (QSAR) models by means of various molecular modeling techniques using 43 novel 6, 7-disubstituted-4-phenoxyquinoline derivatives acting as Tyrosine-protein kinase Met or hepatocyte growth factor receptor (HGFR) (c-Met kinase) inhibitors were designed. Best QSAR models were generated through Auto QSAR. Predicted activity of these models was compared with the observed activity from literature, and it was observed that potent compound **18 b** gave high docking results. Auto-QSAR technique provided the perfect model for the designed derivatives. Binding affinity of compounds for c-Met kinase enzyme was studied by molecular docking and Molecular Mechanics/Generalized Born Surface Area (MM/GBSA dG) binding studies. Optimized compounds were subjected to *in silico* ADMET studies for predicting drug-likeliness and toxicity properties. Reported work will assist to design, refine and construct the novel phenoxyquinoline derivatives as potent c-Met kinase inhibitors in near future.

Conflict of interest

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