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# In silico screening and QSAR based on machine learning to design novel inhibitors againstenoyl acyl carrier protein reductase of *Mycobacterium tuberculosis*

**Naidu Subbarao[4*], Madhulata Kumari[1], NeerajTiwari[2]** and **Subhash Chandra[3]**
[1]Department of Information Technology, Kumaun University, India
[2]Department of Statistics, Kumaun University, India
[3]Department of Botany, Kumaun University, India
[4]School of Computational and Integrative Sciences, Jawaharlal Nehru University, India

Machine learning techniques are advanced computational techniques which can be used to build a predictive model of compounds dataset to find out important features to predict a specific biologicalactivity from unknown compounds and design better drugs. In present study, several QSAR models were constructed by using machine learning approaches on three different datasets ChEMBL3132000, ChEMBL907779, and AID 43299of InhA, the enoyl-acyl carrier protein reductase (ENR) from *Mycobacterium tuberculosis (Mtb)* is one of the key enzymes involved in the mycobacterial fatty acid elongation cycle and has been validated as an effective antimicrobial target. The best QSAR models were built with excellent values of statistical matrices from each dataset and deployed on a data set of 1450 approved drug from drug bank. Amoxicillin found to be highest predicted activity 6.54 pIC50, and Itraconazole is second highest predicted activity 6.4 pIC50 calculated based on the RF model using CFS-GS-FW descriptor set in the dataset of ChEMBL997779 of InhA Mtb. The RF QSAR model predicted several potential drugs which could be novel InhA*Mtb* inhibitors. Additionally, Molecular docking identified top-ranked 10 approved drugs as antitubercular hits showing G-scores-8.23 to -6.95(in kcal/mol). Further, high throughput virtual screening identified top 10 compounds as antitubercular leads showing G-scores -9.26 to -8.24 (in kcal/mol), compared with control compoundsG-scores -7.86 to -6.68 (in kcal/mol) which are known antitubercularInhA*Mtb* inhibitors (ChEMBL907779:DS2 dataset).This result indicates these novel compounds have the best binding affinity for InhA*Mtb*. Among this studies, we conclude that machine learning based QSAR models can be useful for the development of novel target specific antitubercular compounds.