Outlines

- Screening of FDA approved non-TB for the management of TB infections.
- Drug-repurpose approach become the favorite strategy for its low cost and less time to get already approved drugs other than for which it was discovered.

Through several pharmacoinformatics approaches, a set of non-TB drugs was proposed for TB.

Overview

Tuberculosis (TB) is a contagious disease, and, one of the major threats to global public health. It is one of the leading causes of human death and the development of effective antibiotics is an appealing strategy to tackle the global epidemic by fading the resistance to medication, reduction of long-time treatment schedules, and stopping co-infections. Drug repurposing is an opportunistic and serendipitous strategy and become one of the top most choice in the pharma industry for identifying new uses for approved or investigational drugs that are outside the scope of the original medical indication. This approach lowers the risk during the development of the drugs as already the pharmacokinetics, toxicity, and clinical trials completed. Drug-repurpose already become a pivotal strategy for the development of repurposable compounds.

Challenges

Screening non-TB FDA approved drug molecules against rare TB targets using advanced pharmacoinformatics approaches.

Approach

We screened non-TB FDA drugs against the selected TB targets using multiple validated and well approved molecular docking engines. High affinity and strong binder drugs were taken into consideration for all atoms MD simulations. The potentiality of the molecules was assessed using the statistical parameters and binding free energy obtained from MD simulation trajectories.

Results

We have taken into consideration two rare TB targets for the virtually screening of FDA approved non-TB drugs. Based on high negative binding energy from multiple molecular docking energies, about 30 molecules were considered for all atoms MD simulation. We have analysed the MD simulation trajectories to explore the stability between the molecules and the protein targets. The strong affinity was confirmed by the calculation of binding free energy from the MD simulation trajectories. Finally, we have proposed a set of potential non-TB drugs for the management of TB infections.