World Academy of Science, Engineering and Technology
International Journal of Mathematical and Computational Sciences
Vol:14, No:12, 2020

In silico Analysis of Isoniazid Resistance in Mycobacterium tuberculosis

Authors : A. Nusrath Unissa, Sameer Hassan, Luke Elizabeth Hanna

Abstract : Altered drug binding may be an important factor in isoniazid (INH) resistance, rather than major changes in the enzyme's activity as a catalase or peroxidase (KatG). The identification of structural or functional defects in the mutant KatGs responsible for INH resistance remains as an area to be explored. In this connection, the differences in the binding affinity between wild-type (WT) and mutants of KatG were investigated, through the generation of three mutants of KatG, Ser315Thr [S315T], Ser315Asn [S315N], Ser315Arg [S315R] and a WT [S315]) with the help of software-MODELLER. The mutants were docked with INH using the software-GOLD. The affinity is lower for WT than mutant, suggesting the tight binding of INH with the mutant protein compared to WT type. These models provide the in silico evidence for the binding interaction of KatG with INH and implicate the basis for rationalization of INH resistance in naturally occurring KatG mutant strains of Mycobacterium tuberculosis.

Keywords : Mycobacterium tuberculosis, KatG, INH resistance, mutants, modelling, docking
Conference Title : ICSRD 2020 : International Conference on Scientific Research and Development
Conference Location : Chicago, United States
Conference Dates : December 12-13, 2020