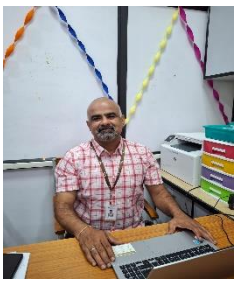
In-silico approaches to understand the mechanisms of antibiotic resistance in ESKAPE pathogens



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In recent decades, antimicrobial resistance has been augmented as a global concern to public health owing to the global spread of multidrug-resistant strains from different ESKAPE pathogens. This alarming trend and the lack of new antibiotics with novel modes of action in the pipeline necessitate the development of non-antibiotic ways to treat illnesses caused by these isolates. In molecular biology, computational approaches have become crucial tools, particularly in one of the most challenging areas of multidrug resistance. The rapid advancements in bioinformatics have led to a plethora of computational approaches involving genomics, systems biology, and structural biology currently gaining momentum among molecular biologists since they can be useful and provide valuable information on the complex mechanisms of AMR research in ESKAPE pathogens. *In-silico* approaches would be helpful in elucidating the AMR mechanisms, identifying important hub genes/proteins, and their promising targets together with their interactions with important drug targets, which is a crucial step in drug discovery. Therefore, we aim to provide holistic information on currently employed bioinformatic tools and their application in the discovery of multifunctional novel therapeutic drugs to combat the current problem of AMR in ESKAPE pathogens. We also summarize the recent advancement in the AMR research in ESKAPE pathogens utilizing the *in- silico* approaches.

Key words:

Computational Biology; Drug Discovery; Drug Resistance; Gene Prediction; Therapeutic target

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