- Researcher informations
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- Title of the project: Identification of natural inhibitors of Pseudomonas aeruginosa through virtual screening
- Keywords: virtual screening, docking, inhibitors, pseudomonas
- Introduction: Pseudomonas aeruginosa is an opportunistic, gram-negative human pathogen. It is associated with nosocomial infections and with cystic fibrosis. The occurrence of Pseudomonas aeruginosa multi-drug resistance in clinically isolated cases requires the development of better or new drugs against this pathogen. In this study we prioritized the drug targets using physico-chemical, structural properties and broad-spectrum analysis from 45 identified drug targets from our previous study using subtractive genomics. We will use virtual screening method to find natural inhibitors drug against this pathogen. The outcome of this study will useful in identifying better therapeutic drug targets against this pathogen.
- Objectives: To find putative drug target for Pseudomonas aeruginosa
- To find natural inhibitor drug for Pseudomonas aeruginosa
- Methodology: Previously we have used subtractive genomics to find suitable drug target. We request dockthor server to identify natural inhibitors by using virtual screening method.
- Perspectives: The outcome of the study will help to identify novel natural inhibitor



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