

ATP Synthase as a Target to Combat Antibiotic Resistance in *Pseudomonas aeruginosa* †

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Abstract: *Pseudomonas aeruginosa* is a pathogenic gram-negative bacterium resulting in diseases and infections in nosocomial environments. It is an infamous member of ESKAPE pathogens, insinuating its notoriety for escaping the effects of many commercially available antibiotics. Drug efflux pumps confer antibiotic resistance by purging out the antibiotics from the cell. These efflux pumps work by the principle of proton motive force involving the action of two important proteins – porins and ATP synthase. These efflux pumps are encoded by the chromosomal genes *MexAB*, *MexXY* etc, and are ATP dependent. Bacterial ATP synthase consists of subunits quite simpler than its eukaryotic counterparts. Of all the subunits, the subunit epsilon (ϵ) is important since it connects the F_0 with the F_1 site. Also, this ϵ subunit is involved in the inhibition of ATP hydrolysis by restricting the stalk movement, thus making it a potential candidate to counter Proton Motive Force crucial for the function of efflux pumps. Though ATP synthase is ubiquitous among all life, there can be minor changes in the structures between organisms. The crystal structure of ATP synthase of *Pseudomonas aeruginosa* is not available in the databases, and thus it has to be theoretically modeled using bioinformatics tools and software, which is briefly reviewed here.

Keywords: *Pseudomonas aeruginosa*; drug efflux; ATP synthase.

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Conflicts of Interest

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