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Structure based drug design to address bacterial antibiotic resistance

The infection of susceptible individuals with pathogens resistant to conventional antimicrobials is becoming worrisome. In addition to per se highly antibiotic resistant spp. such as *Clostridium difficile,* the namely ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumanii*, *Pseudomonas aeruginosa* and *Enterobacter spp*.) family of pathogens are capable to develop resistance not only to common antibiotics in clinical use if not to those consider of the last resort (like as carbapenems). New antimicrobial drugs must replace antibiotics that lose their effectiveness. Development of pharmacological therapies to address antibiotic resistance or any other medical affliction through trial and error is a time-consuming and costly proposition. Structure-based rational drug design accelerates drug discovery by linking together structural information, computational techniques, high-throughput screening and combinatorial chemistry. Common mechanisms of antimicrobial resistance that could be addressed by a structure-based rational design approaches to address this threat will be discussed.

Biography

Mario Antonio Bianchet has completed his PhD from La Plata University, Argentina and Postdoctoral studies from Johns Hopkins University School of Medicine. Presently, he is an Assistant Professor of the Departments of Neurology and Biophysics and Biophysical Chemistry at Johns Hopkins School of Medicine. He has published about 70 papers in structural enzymology with a focus on biomedical interest problems in reputed journals. Structure based drug design of antibacterial and antiviral drugs are among his primary interests.

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