Francisco Javier Alvarez Martinez et al., J Drug Metab Toxicol 2017, 8:2(Suppl)
DOI: 10.4172/2157-7609-C1-009

Molecular screening *in silico* for the discovery of inhibitors of PBP2a

Francisco Javier Alvarez Martinez[1], Barrajón-Catalán E[1], Micol V[1], Galiano V[1], Rodríguez-Díaz J C[2] and **Encinar J A[1]**
[1]Miguel Hernandez University of Elche, Spain
[2]General University Hospital of Alicante, Spain

The PBP2a protein is encoded by the mecA gene and confers resistance to antibiotics such as methicillin, penicillin and derivatives thereof. The main bacterium carrying this gene is methicillin-resistant *Staphylococcus aureus* (MRSA). The main objective of the present work is the identification of natural compounds with inhibitory capacity of the microbial protein PBP2a. Firstly, several files with the three-dimensional structure of crystallized MRSA PBP2a proteins (obtained from RCSB Protein Data Bank) were collected. Secondly, 67,408 natural inhibitor-targeting structures were obtained by entering 14 electronic chem libraries and downloading the desired files. Once the molecules were obtained, they were subjected to a filtration to eliminate those molecules that did not fulfill the common characteristics of a conventional drug. Once ligands and receptors were obtained, a docking study was performed to determine the free binding energy between the natural molecules and the target proteins. A total of 2,820 compounds with suitable pharmacological properties and interaction free energies of -9.5Kcal/mol or less were obtained, indicating a strong binding affinity. Three molecules from this set were selected based on their commercial availability, absence of previous studies and possibility of handling in the laboratory to go to the phase of *in vitro* tests. *In silico* molecular sieving is a powerful tool for the selection of compounds with specific pharmacological properties. In the absence of *in vitro* and *in vivo* assays, *in silico* results predict a marked therapeutic potential of the natural compounds selected for the treatment of MRSA infections and other pathogens possessing the antibiotic resistance protein PBP2a. Soon we will perform bacterial inhibition experiments using the disc-plate method to test the three compounds selected against various strains of MRSA.

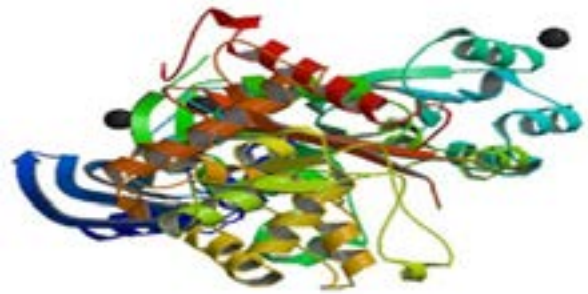

Figure 1: Structure of PBP2a of MRSA strain 27r. PDB code: 1VQQ.

Biography

Francisco Javier Alvarez Martinez is a Molecular Biology PhD student at the Universidad Miguel Hernández of Elche. The main theme of his thesis is the identification of natural compounds with antimicrobial capacity to act as antibiotics or in conjunction with those already existing in the treatment of microbial diseases, especially those resistant to traditional drugs. To reach these objectives, computational approaches and *in vitro* studies using reference microbial strains are used in addition to clinical isolates collected at the General University Hospital of Alicante.

f.alvarez@umh.es

Notes: