RESEARCHERID
THOMSON REUTERS

[K S * *et al.*, 6(8): August, 2017]
IC™ Value: 3.00

ISSN: 2277-9655
Impact Factor: 4.116
CODEN: IJESS7

IJESRT

INTERNATIONAL JOURNAL OF ENGINEERING SCIENCES & RESEARCH TECHNOLOGY

INSILICO DOCKING BASE ANALYSIS OF DRUG CANDIDATES AGAINST MYCOBACTERIUM TUBERCULOSIS

Praveen kumar K S*, Sandra Joshy*, B. Aarthi Rashmi* & J. Vasanth Nirmal Bosco
*Department of Bioinformatics ,Sri Krishna Arts and Science College,Coimbatore-08.

DOI: 10.5281/zenodo.848628

ABSTRACT

Mycobacterium tuberculosis is an obligate pathogenic bacterial species in the family Mycobacteriaceae and the causative agent of tuberculosis. Mycobacterium tuberculosis has an unusual, waxy coating on its cell surface. Tuberculosis is caused by bacteria that spread from person to person through microscopic droplets released into the air. This can happen when someone with the untreated, active form of tuberculosis coughs, speaks, sneezes, spits, laughs or sings. Isoniazid ,Rifampicin,Pyrazinamide,Ethambutol,Streptomycin are the drugs of mycobacterium tuberculosis.The tools used for retrieve the structure and sequence of ESAT-6 associated with M.Tuberculosis,are Protein Data Bank,PUBCHEM, CHEMSKETCH, OPEN BABEL, UCSF CHIMERA,CYGWIN.

KEYWORDS: Mycobacterium tuberculosis,ESAT-6,PUBCHEM,Isoniazid.

I. INTRODUCTION

Mycobacterium tuberculosis is an obligate pathogenic bacterial species in the family Mycobacteriaceae and the causative agent of tuberculosis. First discovered in 1882 by Robert Koch, M. tuberculosis has an unusual, waxy coating on its cell surface primarily due to the presence of mycolic acid. This coating makes the cells impervious to Gram staining, and as a result, M. tuberculosis can appear either Gram-negative or Gram-positive.Acid-fast stains such as Ziehl-Neelsen, or fluorescent stains such as auramine are used instead to identify M. tuberculosis with a microscope. The physiology of M. tuberculosis is highly aerobic and requires high levels of oxygen. Primarily a pathogen of the mammalian respiratory system, it infects the lungs,Tuberculosis is defined as an infectious disease caused by a bacterium; that most commonly affects the lungs. Currently, it kills “three million people a year and could claim up to 30 million lives if not controlledThe primary stage of the disease may be symptom-free, this is called the “inactive stage.” Within the active stage ofthe disease, there might be a slight fever, night sweats, weight loss, fatigue.The symptoms may vary depending on what type of tuberculosis you contract.

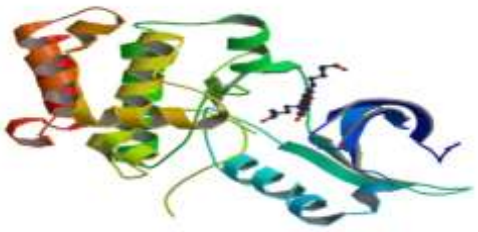
II. REVIEW OF LITERATURE

- Rubin EJ *etal*Despite over a century of research, tuberculosis remains a leading cause of infectious death worldwide. Faced with increasing rates of drug resistance, the identification of genes that are required for the growth of this organism should provide new targets for the design of antimycobacterial agents.
- Brown JR *etal* Mycobacterium tuberculosis, the causative agent of tuberculosis (TB), infects approximately 2 billion people worldwide and is the leading cause of mortality due to infectious disease. Current TB therapy involves a regimen of four antibiotics taken over a six month period

III. DISEASE CAUSING PROTEIN

Catalytic domain of protein kinase PknB from Mycobacterium tuberculosis in complex with mitoxantrone

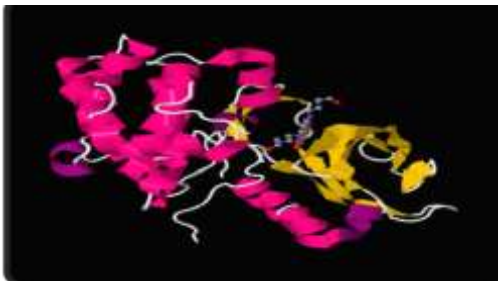
ISSN: 2277-9655
Impact Factor: 4.116
CODEN: IJESS7



PDB ID: 2fum
2fum STRUCTURE PROPERTIES

Resolution : 2.89Å
R -value free : 0.278
R-value work: 0.128

Receptor



Active Compounds Against Mycobaterium Tuberculosis

- Coumarin
- Morpholine
- 5 – amino – 1,3,4 – thiadiazole-2-thiol
- Butyl benzoate
- 1 H- pyrrole

Role Of Bioinformatics In Drug Discovery

- Bioinformatics has made it possible to sequence the genome of various organisms
- The understanding of molecular biology has made it possible to design and develop the drugs
- In the recent years , bioinformatics has made it easy for the researchers that they can now easily target the molecules in the in vitro environment
- Now the screening of newly developed compounds can be done against the molecules of the proteins, it gives very efficient results
- This way of drug development has eased the identification of the disease in an organism

Aim And Objectives

- To retrieve the antigen structure using suitable databases
- To search and retrieve PDB coordinate files of the homologous templates using RCSB-PDB
- To retrieve the suitable ligand from pubchem database
- To perform docking using AUTODOCK tool
- To perform running docking algorithm using Cygwin software
- To visualize the result using UCSF CHIMERA software

IV. MATERIALS AND METHODS

- PDB
- PUBCHEM
- NCBI
- CHEMSKETCH
- SWISS PDB VIEWER
- AUTO DOCK
- OPEN BABEL

ISSN: 2277-9655
Impact Factor: 4.116
CODEN: IJESS7

Docking Result

SL NO	ACTIVE COMPOUNDS	MINIMUM BINDING ENERGY	RUN
1	Coumarin	-5.28	8
2	Morpholine	-7.01	3
3	5-amino-1,3,4-thiadiazole-2-thiol	-4.74	9
4	Butyl benzoate	-5.87	6
5	1-H Pyrrole	-2.88	6

V. RESULT

Active compound (morpholine) is correctly bind with the active site(val 95) of the target protein(2fum) USING AUTODOCK TOOL

VI. CONCLUSION

The docking score using autodock for the ligand protein interaction was found to be there exist a good interaction between them ,The interaction between protein ligand complexes are visualized using various tools, it shows clear atomic interaction between ligand and receptor ,Based on 5 compounds Morpholine is the suitable fit for the receptor to prevent the mycobacterium tuberculosis disease. Thus binding between ligand and receptor prevents the disease. Hence further studies can be taken up to evaluate the use of 5 compunds for preventing mycobacterium tuberculosis

VII. REFERENCES

[1] Madsen U, Krogsgaard-Larsen P, Liljefors T (2002). Textbook of Drug Design and Discovery. Washington, DC: Taylor & Francis. Reynolds CH, Merz KM, Ringe D, eds. (2010) ,Drug Design: Structure- and Ligand-Based Approaches (1 ed.). Cambridge, UK: Cambridge University Press, Murray PR, Rosenthal KS, Pfaller MA (2005). Medical Microbiology. Elsevier Mosby.

CITE AN ARTICLE

KS, P. K., Joshy, S., Rashmi, B. A., & Bosco, J. N. (2017). INSILICO DOCKING BASE ANALYSIS OF DRUG CANDIDATES AGAINST MYCOBACTERIUM TUBERCULOSIS. *INTERNATIONAL JOURNAL OF ENGINEERING SCIENCES & RESEARCH TECHNOLOGY, 6*(8), 408-410. Retrieved August 25, 2017.