AIM & OBJECTIVE OF THE STUDY

Diseases have been treated with medications for thousands of years. The effects of these drugs were usually discovered over centuries by trial and error. Many drugs used today have been discovered by such observations. However, as the cellular and molecular mechanisms behind many diseases are increasingly understood, new avenues for rational drug development emerge and a systematic search for drugs began. Over time, newly developed techniques and an ever-increasing knowledge led to new, but complementary, strategies for drug discovery. First, animals were used as models for the human organism. However, because many potential drugs could not be adequately tested with animals, in-vitro experiments became more and more important. In in-vitro experiments, the activity of various chemical compounds on cells or on specific proteins is measured in the laboratory. About thirty years ago, computational drug research started to complement experimental techniques.

A decade of world-wide war against tuberculosis with the extensive aid of all the known anti-microbial drugs has shown that the tubercle cannot be beaten so easily as experts thought. Their powers of survival and technique of resistance are great and varied. Like most of the small enemies of mankind, given favourable conditions, they are capable of multiplying in such quick geometrical progression, that a few may grow to millions in a short period of time. Unlike many other micro-organisms, they have the power of living in the absence of moisture and surviving in the dry state for long periods of time. This enables them to reach the lungs of new hosts in the form of dust. They have a fatty coat of arm our that protect them against some forms of attack against them. They have the power of destroying human tissues around them and preparing for themselves dugouts in which they remain comparatively safe from attacks by drugs carried by the blood stream. They are adepts in going “underground” and lying low until fresh opportunities offer for carrying on guerrilla warfare. During the last ten years, the anti-biotics have brought to the forefront, some of the
special powers of defence which tubercle possess. They have the ability to gradually immunise themselves against the drugs; and when attacked, they can go into a kind of hybernation or turn malingerers and simulate death so well, that it becomes a difficult problem for bacteriologists and clinicians to say whether they are really dead or still have the power of revival in them.

The tools of Bioinformatics provide a dynamic platform for structural analysis of the pathogenic proteins which are the key components for occurrence of the disease, it is a well known fact that Mtb is presently posing a big challenge to pharmacists for designing of effective drugs against the Multi Drug Resistant strains, the features of Mtb which have further complicated the task are slow growth of the pathogen and longer period of incubation. Tuberculosis (TB) is a common, deadly infectious disease cause of illness and death worldwide, caused by mycobacteria, mainly *Mycobacterium tuberculosis*. The most recent estimates the incidence of new cases of *Mycobacterium tuberculosis* infection in globally 9.2 millions. India and China were got the First and second Ranks in estimated number of new Tuberculosis cases. India accounts for nearly 20% global tuberculosis burdens even today. The emergence of *M. tuberculosis* strains that are resistant to the drugs represents a serious challenge to tuberculosis control. There is a well documented association between TB and human immunodeficiency virus (HIV). Intense attempts are underway to develop potent analogues of the current antituberculosis, as well as a search for novel drug targets. In *Mycobacterium tuberculosis*, purine metabolic enzyme SAT subunit2 is novel target for designing new inhibitors.

Sulfate adenylyl transferase (SAT) is the first enzyme of the two-step sulfate activation sequence. This enzyme belongs to the family of transferases, specifically those transferring phosphorus-containing nucleotide groups (nucleotidyltransferases). This enzyme participates in 3 metabolic pathways: purine metabolism, selenoamino acid metabolism, and sulfur metabolism and is a druggable target for development of new antitubercular drugs.
• Protein analysis with various bioinformatics tools
• To determine the structural information of Sulfate adenylyltransferase (SAT) subunit2 of *Mycobacterium tuberculosis*.
• To model the enzymes of SAT subunit2 of *Mycobacterium tuberculosis* from the primary structural sequence.
• Refinement of modeled structure through molecular docking and simulation.
• Validation of the structure for the docking with lead molecule.
• Designing of lead molecules and optimization by applications of Cheminformatics.
• Enzyme of SAT subunit2 in *Mycobacterium tuberculosis* and lead molecule docking studies and result analysis.

A detailed understanding of the molecular activity of proteins requires knowledge of their three-dimensional structure. However, experimental methods for determining protein structure, such as crystallography or NMR, are expensive and time consuming. For this reason, experimental structures are only available for approximately 30 thousand of the 30 million protein sequences known today. Computational methods for predicting the three-dimensional structure of proteins from sequence have come a long way in the last ten years. Scientists are seeking answers to a growing number of challenging biological questions and are thus determining the structures of large numbers of proteins and their complexes with substrates, inhibitors, other proteins and nucleic acids. The PDB archive reached a significant milestone in its 37-year history this past spring. The 50,000th molecule structure was released into the archive on April 8, 2008, joining other structures vital to biology, medicine, and education.