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Silico Docking Studies of Few Antitrypanosomal Inhibitors Obtained from *Eucalyptus Tereticornis* by using Bioinformatics Softwares

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Abstract : Human's trypanosomiasis or sleeping sickness is a protozoan disease which is caused primarily by *Trypanosoma brucei* in India. Trypanosomiasis is re-emerging in India due to the proximity of domesticated animals with the people. Though the human infection through animal vector is unlikely, still there are number of report of a distinctive human infection caused by animal trypanosomes in recent times. As the available medication is either too expensive or possess side effects, there is an urgent need for the discovery of novel natural drugs. In this research, a study was performed to identify an efficient drug molecule possessing antitrypanosomal activity. From the literature study, plant Compounds of *Eucalyptus tereticornis* which is well known for its antiparasitic property have been identified and its structure was retrived and tested for its drug likeness activities. The proteins responsible for causing Trypanosomiasis were identified, their structures were retrieved and their binding sites were predicted. *In Silico* molecular docking was performed and the result demonstrated a particular target revealing exceptional binding affinity with the inhibitors in contrast to other targets. Further, clinical studies will confirm the inhibitors efficiency as a superior contender for development of improved drug against Trypanosomiasis.

Keywords: Human's trypanosomiasis, *Eucalyptus tereticornis, Trypanosoma brucei,* Trypanosomal Inhibitors, Molecular Docking.

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