**MOLECULAR DOCKING STUDY ON THE INTERACTION BETWEEN 2-SUBSTITUTED-4,5-DIFURYL IMIDAZOLES WITH DIFFERENT PROTEIN TARGET FOR ANTILEISHMANIAL ACTIVITY.**

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**Abstract:**

Leishmaniasis is a disease which is caused by the protozoa Leishmania and is considered the second-highest cause of death worldwide by parasitic infection. Looking for the right chemotherapy against leishmaniases has been difficult because of the high toxicity of the most effective drugs. Computational Chemistry plays an important role in the research of new possible medicines. In this work, docking analysis was carried out to study the effects of nine 4,5-di (furan-2-yl-1 H-imiazole) on *Leishmania arginase*, *Leishmania trypanothione synthetase amidase* and *Leishmania trypanothione reductase* and results were compared with four known drugs, and with targets’ potential inhibitors. .∆G, Ki and binding interactions in the targets active sites were reported. Results show that 4, 5-di (furan-2-yl)-2-(5-(4-nitrophenyl) furan-2-yl)-1H imidazole and 4-(5-(4, 5-di (furan-2-yl)-1H-imidazol-2-yl) furan-2-yl) benzoic acid are promising leads, so the study of these compounds is recommended.

**Keyword:**

Antileishmanial activity,Molecular docking, 2-substituted-4,5-difuryl imidazoles, *Leishmania*