Abstract

Diabetes mellitus is one of the major disease currently affecting an estimated 143 million people worldwide and the number is growing rapidly. Now a day, as there is a renewed interest in the traditionally used herbal drugs, the present study was aimed to screen the identified constituents of Helicteres isora for determining the potent constituent with antidiabetic activity using insilico approach. Docking studies of the constituents were carried out using autodock 4.0 and the receptors used were aldose reductase and insulin receptor protein. Analysis of the results showed that, with both the receptors, yohimbine had the best binding energy and so most potent antidiabetic constituent among the identified constituents of Helicteres isora.

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Index Terms

Computer Science Applied Sciences

Keywords

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