Farah Yousef, J Clin Exp Pathol 2018, Volume 8
DOI: 10.4172/2161-0681-C3-051

Using Computer Aided Drug Design and docking softwares to determine *In-Silico* Metformin Binding site with its receptor AMP Kinase Enzym

Farah Yousef
Damascus University, Syria

Metformin receptor has been studied for decades as this drug is one of the most popular drugs used in the treatment of Type II diabetes Mellitus (TIIDM) in the globe. Different studies have confirmed that its receptor is AMPKinase enzyme in the liver cells. But, no crystal structure was found yet for its binding to the proposed enzyme. What we tried here is to use our experiences in medicinal Chemistry and Computer Aided Drug Design in a try to study Metformin binding site with AMPKinase in silico using two docking softwares and one internet site. AMPKinase crystal structure was downloaded from Protein Data Bank database, while Metformin structure was got from Pubchem database. After analyzing the structures and the docking results we had, we came to a conclusion that agrees with recent biological studies about this investigation. We hope these results help researchers in drug design field to discover and\or developing new agents for the treatment of TIIDM considering Metformin as a lead compound for that.

Biography

Farah Yousef is a PhD student from Damascus University. She has finished her previous studies at Faculty of Pharmacy at Tishreen University, Syria. She has published 6 articles so far in reputed journals and many Arabic articles in Arabic websites and has been serving as an editorial board member of repute in different journals. She has participated in different Syrian and Global conferences so far.

farahyousef90@yahoo.com

Notes: