Molecular Docking Study of the Ebolavirus Surface Glycoprotein to Develop Anti-Ebola Drug

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Ebola virus disease (EVD) causes hemorrhagic fever infection with a mortality rate of up to 90%. Current treatments, mostly experimental, require medical equipment and facilities often not available to patients during an outbreak. Therefore, there exists a compelling need for an orally bioavailable treatment for the ebolavirus. The purpose of this project is to use computational drug design techniques to predict an orally administrable antiviral drug that will bind tightly to the ebolavirus's surface glycoprotein, which is responsible for facilitating the entrance of the virus into human cells. In this study, first all molecules approved for or being investigated for drug use were downloaded from the ZINC15 small molecule database. Then, these molecules were screened through Lipinski's Rule of 5 to filter for drug-like properties. The resulting molecules were docked against a binding site on the Ebola glycoprotein chosen through use of FTMap and FTSite. The top molecules are run through AdmetSAR2.0 to test for certain ADMET properties and the molecules that best satisfied these properties were put through a more comprehensive docking test with AutoDock Vina. The molecule with the highest binding affinity to the ebolavirus glycoprotein is 2-[3-[4-(5-Fluoro-1H-indol-3-yl)-3,6-dihydro-2H-pyridin-1-yl]propyl]isoindole-1,3-dione with an average best conformation binding energy of -8.76 kcal/mol. The molecule is also predicted to be safe and orally bioavailable. Therefore, with more experimental research to confirm the molecule's predicated qualities and to test its ability to not only bind to, but also to impede the glycoprotein, it could become a promising drug candidate for treat Ebola virus disease.