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Zidovudine – as a potential coronovirus M protease inhibitor 2019-nCoV

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In 2019, a novel Coronavirus 2019-nCoV was found to cause Severe Acute Respiratory symptoms and rapid pandemic in China, France, United States of America, Belgium, Germany, Italy, Japan, India, Russia. In order to find candidate drugs for 2019-nCoV, we have carried out a computational study to screen for effective available drug Zidovudine which may work as inhibitor for the Mpro of 2019-nCoV.

The interaction of the Zidovudine with the Coronavirus 2019-nCoV was performed by molecular docking studies.

In the present work, the molecular docking studies of the Zidovudine molecule were performed against Coronavirus 2019-nCoV using HyperChem Professional 08, PyMOL and Molegro Molecular Viewer software programs.

The molecular docking analysis is an important tool for drug design and molecular structural biology [4]. The aim of molecular docking analysis is to predict the preferred binding location, affinity and activity of drug molecules and their protein targets.

The MEP Map of the optimized molecule Zidovudine was calculated at B3LYP/MidiX level of theory. The electrophilic and nucleophilic reactive sites of the molecular structure are also identified with the MEP map. In MEP map of Zidovudine, the oxygen atom (O13) of hydroxyl group is found to be electron rich site, which is due to the lone pairs of oxygen atoms. Also, the O16 and O19 atom in the carbonyl groups is shown partially negative charge site. Therefore, the O13, O16 and O19 are nucleophilic regions. The H31 atom in the hydroxyl group and the H32 atom in the amide group are shown electron poor and electrophilic sites. The electrophilic and nucleophilic regions of the Zidovudine illustrate the interaction with other molecules in chemical reactions.

Molecular basis of interactions between Coronavirus 2019-nCoV molecule and the Zidovudine can be understood with the help of docking analysis and interactions. We found 5 positions in which there is a strong interaction between the drug molecule and the virus that leads to the destruction of the protein structure. The binding energy for Coronavirus 2019-nCoV and Zi-

dovudine is -47.206 kcal/mol in which shows good binding affinity between the Zidovudine and 2019-nCoV. Was observed eleven hydrogen bonding formation between reduces Gln 110 bonded with N and O atoms, Thr 111 bonded with N atom, Asp 295 bonded with N and O atoms, Thr 292 bonded with N and O atoms, Gln 127 bonded with O atom, Ser 158 bonded with N atom, Asn bonded with N and N atoms, Asp 153 bonded with N atom of the Zidovudine are observed. Also, Asp 153, Ser 158, Asn 151, Thr 292, Thr 111 and Phe 294 are contact with negatively and positively charged in the Zidovudine binding environment. It was found that the ligand Zidovudine shows the best affinity towards of the 2019-nCoV compared to other known antiviral drugs: Colistin, Valrubicin, Icatibant, Bepotastine, Epirubicin, Epoprostenol, Vapreotide, Aprepitant in which the binding energy for Coronavirus 2019-nCoV and them is -11.206, -10.934, -9.607, -10.273, -9.091, 10.582, -9.892 and -11.376 kcal/mol that shows weak binding affinity between them and 2019-nCoV.