# Potential therapeutic agents against CoVID-19 based on molecular docking

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**Abstract:** The commotion caused due to the outburst of the coronavirus is in an extreme need for the development of a therapeutic agent/biomarker against the causative agent. In this study, we have studied the virtual interaction between COVID-19 protease (6LU7) and different commercially available drug molecules using the Autodock Vina software. The docking results showed a higher affinity of three drug molecules Simeprevir, Glecaprevir and Pseudopterosin F towards the binding pocket of the protease predicted by the software. We propose that these drugs can be used as therapeutic agents/diagnostic agents in this case.

**Introduction:** The end of 2019 witnessed an outbreak of a fatal infection caused by the novel coronavirus in Wuhan, China. The subsequent periods beheld the spread of the virus across the boundaries of countries and continents. As of March 20th 2,44,962 confirmed cases and 10,022 deaths were reported across the world (https://infographics.channelnewsasia.com/covid-19/map.html). With the unavailability of any proven antiviral drugs against the novel coronavirus medical professionals have attempted to just supportive care for the past periods. However, researchers across the world have reported that viral restraining mechanisms can be a possible solution until the perfect drug against the virus is developed. The three dimensional structures of the viral proteins were unavailable until the recent availability of the PDB ID: 6LU7 protease in the RCSB public domain (1,2). HIV inhibitory drugs although have been found to exhibit appreciative interactions with the protease the binding energies obtained are quite high. Here, we screened a number of commercial drugs and studied their virtual interactions with the protease.

**Method:** In this study we chose 3-chymotrypsin like protease (3CL-protease)which is the main protease used to cleave polyproteins into replication-related proteins, as the target receptor. The three dimensional protein structure (PDB ID: 6LU7) was obtained from the RCSB Protein Data Bank.

Based on the literature survey we tested Remdesivir, Indinavir, vidarabine and cytarabine for its affinity towards the 3CL-protease. We downloaded the three

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dimensional structures of each drug from the PubChem database in Structure Data Format (SDF) format.

The molecular docking and visualisation was performed using the Autodock Vina. Preparation of the target protein and the ligand molecules were performed as per the methodology laid down by the blind docking mode of the software. The ligands were downloaded in sdf format and were converted to pdb format using the discovery studio software. These were then used to run the docking in Autodock Vina.

**Result:** The docking scores of the ligands with the covid-19 protease is listed in table1. Three drugs called Simeprevir, Glecaprevir and Pseudopterosin F show higher affinities towards the protease with the highest docking scores. Apart from these the docking scores of the already known anti-HIV drug (indinavir) that is considered appreciable against the covid-19, was found to have a docking score of -7.9.

Finally, there may be a number of molecules showing higher affinities to the protein but due to the emergency situation arising in the world which needs to be controlled, it is preferred to choose commercially available drugs, although possibilities of many efficient drugs can be further explored in future.

Table1: The Docking scores of the ligand moles used against the protease 6LU7

| Sl No. | Ligand Name | Affinity (kcal/mol) |
|---|---|---|
| 1 | **Simeprevir** | **-8.3** |
| 2 | **Glecaprevir** | **-8.1** |
| 3 | **Pseudopterosin F** | **-8.1** |
| 4 | Pseudopterosin D | -8 |
| 5 | Indinavir | -7.9 |
| 6 | L_756423 | -7.8 |
| 7 | Pseudopterosin A | -7.8 |
| 8 | Pseudopterosin E | -7.8 |
| 9 | Amprenavir | -7.5 |
| 10 | Pseudopterosins | -7.5 |
| 11 | Pseudopterosin G | -7.3 |
| 12 | Pseudopterosin B | -7.1 |
| 13 | Pseudopterosin C | -7.1 |
| 14 | Pleconaril | -7 |

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|---|---|---|
| 15 | Pseudopterosin X | -6.9 |
| 16 | Manoalide | -6.6 |
| 17 | Pseudopterosin W | -6.6 |
| 18 | Opaviraline | -6.4 |
| 19 | Vidarabine (Ara A) | -6.3 |
| 20 | Zanamivir | -6.3 |
| 21 | Adefovir | -6.1 |
| 22 | Cytarabine (Ara C) | -5.8 |
| 23 | Metisazone | -5.7 |
| 24 | Tromantadine | -5.6 |
| 25 | Chloroquine | -5.6 |
| 26 | Acyclovir | -5.5 |
| 27 | Hydroxychloroquine | -5.5 |
| 28 | JE_2147 | -5.2 |
| 29 | Moroxydine | -5.2 |
| 30 | Ritonavir | -4.9 |
| 31 | Foscarnet | -4.3 |
| 32 | N_Hydroxyguanidine | -4 |
| 33 | Lopinavir | -3.8 |
| 34 | Okadaic acid | -2.7 |
| 35 | Laninamivir octanoate | -2.1 |

**References**


1. Berman, H. M. et al. The Protein Data Bank. Nucleic Acids Res. 28, 235–242 (2000).
2. Liu, X., Zhang, B., Jin, Z., Yang, H. & Rao, Z. The crystal structure of 2019-nCoV main protease in complex with an inhibitor N3. (2020) doi:10.2210/pdb6lu7/pdb.