



Research Article

The Molecular Docking Study of Potential Drug Candidates Showing Anti-COVID-19 Activity by Exploring of Therapeutic Targets of SARS-CoV-2

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Abstract

Objectives: The novel human coronavirus designated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) first emerged in late 2019 in Wuhan, China. This virus spread rapidly around the globe, causing the respiratory illness called coronavirus disease 2019 (COVID-19). In view of the multiple threats and disorder posed by the pandemic, scientists around the world have been racing to understand SARS-CoV-2 and investigate the pathophysiology of this disease to find potential treatments and effective therapeutic drug candidates.

Methods: The virtual interaction of the COVID-19 main protease (Mpro) in complex with the inhibitor N3 (Research Collaboratory for Structural Bioinformatics Protein Data Bank [PDB] ID: 6LU7) with antiviral and antimalarial drugs was measured, as well as that of the SARS spike glycoprotein-human angiotensin-converting enzyme II (ACE2) complex (PDB ID: 6CS2) with antimalarial drugs currently on the market using the AutoDock Vina suite (O. Trott, The Scripps Research Institute, La Jolla, CA, USA).

Results: The binding energy result obtained from the docking of 6LU7 with ligands of oseltamivir, ritonavir, remdesivir, ribavirin, favipiravir, chloroquine, and hydroxychloroquine was found to be -4.7, -7.3, -6.5, -5.6, -5.4, -5.1, -5.3 kcal/mol, respectively. The binding energy from the docking of 6CS2 with ligands of chloroquine, and hydroxychloroquine was -7.1 and -6.8 kcal/mol, respectively. The docking results suggested drug molecules of oseltamivir, ritonavir, remdesivir, ribavirin, and favipiravir had a greater capability to inhibit SARS-CoV-2 since they demonstrated high affinity interactions with the COVID-19 Mpro in complex with the N3 inhibitor. Chloroquine and hydroxychloroquine also showed prominent binding interaction with the SARS spike glycoprotein-human ACE2 complex.

Conclusion: The results of this study suggest that these drugs are promising candidates for antiviral treatment with high potential to fight the SARS-CoV-2 strain.

Keywords: Antiviral drugs, hydroxychloroquine, SARS-CoV-2 protease

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Since December 2019, much of the world has suffered from the outbreak of coronavirus disease 2019 (COVID-19), the disease caused by a novel human coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).^[1] From its origin in Wuhan, China, it spread rapidly around the globe to affect all but Antarctica.^[2] The World Health Organization declared it a pandemic in March 2020. As of April 14, 2020, 1,924,679 cases of COVID-19 infection

had been reported worldwide, with 119,955 patient deaths and 445,405 patients who recovered.^[3]

Novel approaches to drug design and discovery are being utilized to explore therapeutic drug candidates for COVID-19. Molecular docking is a promising tool for drug discovery and development through the study of the interaction of ligand (drug) molecules inside the binding pocket of a target protein (receptor).^[4] It offers the opportunity to

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study factors such as the identification of hit molecules, optimization of lead compounds, and virtual screening.^[5-8] Several existing drugs have demonstrated potential effectiveness against COVID-19, including oseltamivir,^[9] lopinavir,^[10] ritonavir,^[10] remdesivir,^[11] favipiravir,^[12] ribavirin,^[12] chloroquine, and hydroxychloroquine.^[13] Most of these drugs are HIV protease inhibitors.^[14] Docking with the COVID-19 Mpro in complex with the inhibitor N3 was explored in this study.^[15] It has also been reported that chloroquine and hydroxychloroquine showed anti-SARS-CoV action, which may be attributed to depletion of angiotensin-converting enzyme 2 (ACE2) glycosylation.^[16] At low pH, these drugs are also believed to interfere in post-translational modification in viral protease and glycosyl transferases in the endoplasmic reticulum or vesicles of the trans-Golgi complex.^[16] Therefore, docking of chloroquine and hydroxychloroquine with the COVID-19 Mpro (in complex with the inhibitor N3)^[15] and the SARS spike glycoprotein-human ACE2 complex was also performed.^[17]

Some of the Potential Therapeutic Targets for SARS-CoV and SARS-CoV-2

Several similarities have been recorded between SARS-CoV-2 and SARS-CoV. Following the characterization of the genome sequencing of SARS-CoV-2,^[18] various molecular modeling experiments have been launched in order to find a potential candidate to combat the novel coronavirus SARS-CoV-2. According to a phylogenetic analysis, SARS-CoV-2 is believed to have originated from a bat. Xu et al.^[18,19] performed molecular modeling experiments that revealed similarity in the 3-dimensional structures of SARS-CoV-2 and SARS-CoV in the receptor binding domain. This led to the design of various approaches to find a potential target for a drug candidate to be used in the fight against SARS-CoV-2. The analysis of the crystal structure and several biochemical studies revealed that the S protein (spike protein) of SARS-CoV possesses a strong affinity for binding to human ACE2 receptors.^[20] Some of the potential targets for drugs include an S protein, envelope protein (E protein), membrane protein (M protein), protease, nucleocapsid protein (N protein), hemagglutinin esterase, and helicase.^[21]

Spike Protein

The S protein consists of the ectodomain region (ED), the intracellular domain, and the transmembrane (TM) region.^[22] The S protein is a clove-shaped type I TM protein.^[22] The ED region is made up of 2 receptor binding domains (RBDs), the S1 subunit and the S2 trimeric stalk, associated with the C-terminal. The association of S proteins gives the virion a trimeric form, which gives it a crown-like structure and the name coronavirus.^[22] The S protein has a role in viral entry.

^[23] It has been reported that the S protein activated the host immune response. This protein is considered a potential target for a therapeutic drug because the S1 domain and host ACE2 for SARS-CoV, and dipeptidyl peptidase-4 for Middle East respiratory syndrome coronavirus, are associated with host and viral membrane fusion mediated by the S2 segment and enable the virus to release its RNA in the host cell.^[23]

Proteases

Two polyproteins, PP1a and PP1b, in the coronavirus genome contain 16 non-structural polyproteins (NSPs) and are encoded by the replicase gene.^[24] The release of these NSPs is mediated by the action of proteases. The chymotrypsin-like cysteine protease, also known as Mpro or 3-C like protease (3CLPro) cleaves at the C-terminal of polyproteins. The papain-like protease (PLpro) facilitates cleavage of polyproteins at the N-terminal.^[24] PLpro enables cleavage at the first 3 polyprotein sites, whereas CLpro enables cleavage at 11 sites.^[25]

The Cys-His dyad present on the active sites of 3CLPro/Mpro has been reported to show protease activity.^[26] This protease has the ability to effect cleavage at 11 sites in the p1 region of PP1a and PP1ab. It can generate mature protein, which facilitates replication^[27,28] and also helps to release NSPs.^[29] Some of the HIV protease inhibitors, including lopinavir and ritonavir, have also been found to inhibit the Mpro.^[30]

PLpro cleaves the pp1a polyprotein at the N-terminal to form NSP 1, 2, and 3.^[27,28] The catalytic domain of PLpro consists of 316 amino acids known to facilitate cleavage of substrates for replicase mediated by a consensus sequence (LXGG).^[29] High doses of zinc and its conjugates have been reported to inhibit CLpro and PLpro. Several protease inhibitors, including combinations of ritonavir and lopinavir, are being used to treat COVID-19.^[31]

Nucleocapsid Protein

The N protein consists of the N-arm, the central linker (CL), and the C-tail, which are also known as characteristic intrinsically disordered regions (IDRs).^[32] The major structural and functional domains of the N protein are the N-terminal domain (NTD) and the C-terminal domain (CTD). The NTD is known to facilitate RNA binding and the CTD plays an important role in dimerization.^[32,33] The CL region includes several phosphorylation sites, as well as arginine-serine.^[34] The C-tail region plays a vital role in interactions of N-M proteins and oligomerization of N protein.^[35] N protein has been reported to cause inhibition of cell growth in humans via inhibition of the cytokinesis process.^[36] The N protein peptide (N220) has been found to demonstrate a promis-

ing ability to destroy N protein-expressing cells in transgenic animals. Thus, it may be a potential target for developing a DNA vaccine.^[37]

Envelope Protein

The process of ion channel generation is mediated through oligomerization of E proteins. E protein, the smallest transmembrane structural protein of the coronaviruses, consists of a hydrophobic domain and a cytoplasmic tail. It is 8.4-12 kDa in size.^[38, 39] During viral assembly and release, E protein is known to facilitate viral morphogenesis. In the mammalian cells expressing SARS-CoV E protein, hexamethylenamiloride has been found to inhibit E protein-mediated ion channel activity.^[40] Along with assembly and release, E protein has also been found to be responsible for the virulence of the virus.^[39, 41]

Membrane Protein

M protein modulates the shape of the envelope of the virus as a result of interaction with proteins in the Golgi complex inside the virion and stabilizing the N protein.^[39, 42] M protein is known to promote intracellular homeostasis in a virus via various protein interactions.^[42] It consists of a short N-terminal and a long C-terminal.^[39] The entry of the virus takes place in association with the interaction of M-M, M-S, and M-N proteins. The introduction of a spike protein in a new virus takes place via M-S interactions.^[42] The stabilization of the nucleocapsid-RNA complex (ribonucleoprotein complex) is associated with M-N interactions. In addition to regulating the shape of the virus, M and N proteins also facilitate the generation and release of virus-like particles. M protein is known to potentiate sensitization of the host to the virus.^[42]

Helicase

The SARS-CoV helicase (NTPase) enzyme is a member of superfamily 1. It facilitates hydrolysis of all NTPs.^[43] Helicase may be a potential target for numerous drug candidates against various disorders.^[44] Toxicity is a major concern, however, in the design of helicase inhibitors, as non-specificity leads to a precipitation of toxic effects.^[43]

Molecular Docking Study of Some Drug Candidates with Main Protease of SARS-CoV-2

While there is as yet no specific treatment for COVID-19, several antiretroviral drugs have been reported to demonstrate some effectiveness, including ritonavir,^[45, 46] lopinavir alone or in combination with oseltamivir,^[46] remdesivir, chloroquine, and hydroxychloroquine.^[47] Of these, ritonavir, remdesivir, chloroquine, and hydroxychloroquine have shown efficacy at the cellular level.^[45] which will be evalu-

ated in future experimental studies. Molecular docking methodologies are a useful tool in drug discovery, as they permit rapid screening of candidates from drug libraries.^[48, 49] This docking study of some of the potential therapeutic drug candidates that are being used against COVID-19 worldwide was performed using computer-based techniques to assess the structure of ligand-protein complexes and biochemical pathways.

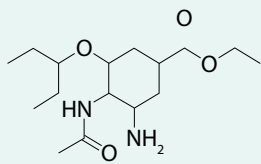
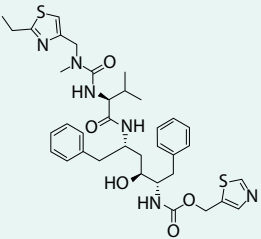
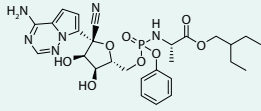
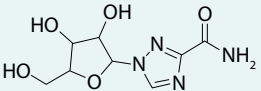
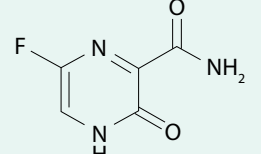
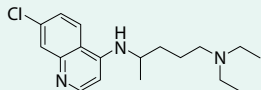
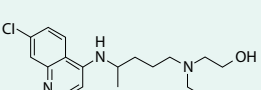
Methods

All of the docking experiments were performed using AutoDock Vina (O. Trott, The Scripps Research Institute, La Jolla, CA, USA) because (a) it offers more accuracy in predicting ligand-protein interactions than the previous version, AutoDock 4.2, (b) it offers a shorter running time as a result of multiple core processors, (c) and it offers greater accuracy for ligands with more than 20 rotatable bonds. All of the docking experiments were conducted using the blind docking method: using a grid box large enough to cover the whole protein structure to include any possible protein-ligand interactions.

All of the protein structures used in the docking experiments were retrieved from the Research Collaboratory for Structural Bioinformatics Protein Data Bank (PDB). All of the ligand structures were drawn using ChemDraw 14 and converted into PDB format using Chem3D 12.0 (PerkinElmer, Inc., Waltham, MA, USA). The ligands were converted to the energetically most stable structure using energy minimization with the Vega ZZ program (Drug Design Laboratory, University of Milan, Milan, Italy)^[51] and the SP4 force field and a conjugate gradient. The ligand and protein molecules were converted to their proper readable file format (pdbqt) using AutoDock tools 1.5.6. The docking was performed using an exhaustiveness value of 8. All of the other software parameters were the default values, and all of the bonds contained in the ligand were allowed to rotate freely while the receptor was rigid. The final visualization of the docked structure was performed using Discovery Studio Visualizer 2.5 (Accelrys Software Inc., San Diego, CA, USA).

Results

The results of these experiments revealed strong interactions of the potential drug candidates against the COVID-19 Mpro in complex with the inhibitor N3 and the SARS spike glycoprotein-human ACE2 complex of SARS-CoV-2. After successful docking of these drugs to the COVID-19 Mpro in complex with an inhibitor N3, various modes of drug-protein interactions are generated with a particular docking score (binding energy). The binding mode with the least binding energy is regarded as the best mode of binding,

Drug	Structure	Target (Protein)	Protein Data Base Code
Oseltamivir		COVID-19 main protease in complex with an inhibitor N3 ^[15]	6LU7
Ritonavir		COVID-19 main protease in complex with an inhibitor N3 ^[15]	6LU7
Remdesivir		COVID-19 main protease in complex with an inhibitor N3 ^[15]	6LU7
Ribavirin		COVID-19 main protease in complex with an inhibitor N3 ^[15]	6LU7
Favipiravir		COVID-19 main protease in complex with an inhibitor N3 ^[15]	6LU7
Chloroquine		1. COVID-19 main protease in complex with an inhibitor N3 ^[15] 2. SARS Spike glycoprotein-Human ACE2 complex ^[17]	6LU7 6CS2
Hydroxychloroquine		1. COVID-19 main protease in complex with an inhibitor N3 ^[15] 2. SARS Spike glycoprotein-Human ACE2 complex ^[17]	6LU7 6CS2

as it is most stable for the ligand. The binding energy results observed are summarized in Table 2. The interaction of specific amino acids taking part in the drug-protein interactions were also recorded. All of the docked structures were visualized in PyMOL 2.3 (Schrödinger LLC, New York, NY, USA) and Discovery Studio 4.0.

Three chains, A, B, and C, were present in the structure of the SARS spike glycoprotein-human ACE2 complex (PDB ID: 6CS2) with a central pocket for interaction with ligands. The binding pocket of the COVID-19 Mpro in complex with the inhibitor N3 (PDB ID: 6LU7) consists of 2 chains, chain A and chain C, which may be part of interactions with the ligand. The ligand showed selective interaction with either or both of the chains, depending on the availability of the

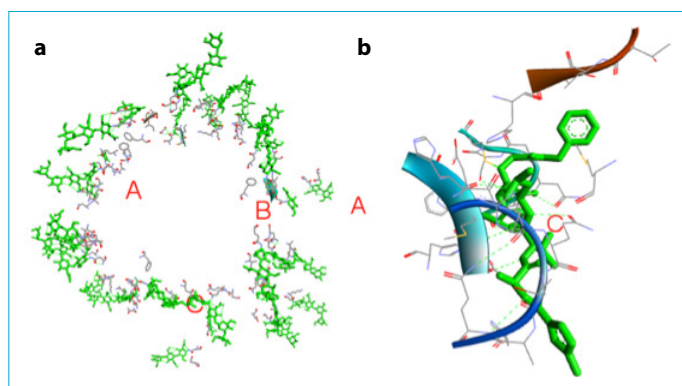
atoms for the particular interaction (Table 1).

Visualization of Docking Results

Chloroquine and hydroxychloroquine were docked with the COVID-19 Mpro in complex with the inhibitor N3 as well as the SARS spike glycoprotein-human ACE2 complex. The lowest energy conformations of all of the ligand molecules were docked with the protein. The ligand was illustrated as a red stick model and the protein is the surface. The amino acids taking part in the ligand-protein interaction were shown with blue stick ligands surrounded by the amino acids. The interactions represented by green dashed lines are the hydrogen-bonding interactions between the ligand and protein. Amino acids involved in the ligand-

Table 2. Target (protein) and the drug candidates (ligands) undergoing docking experiment with their best docking score (lowest binding energy)

Drug (ligand)	Proteins (receptor)	Affinity (kcal/mol)	Distance from rmsdl.b.	Distance from rmsdu.b.
Oseltamivir	COVID-19 main protease in complex with inhibitor N3 ^[15]	-4.7	0.000	0.000
Ritonavir	COVID-19 main protease in complex with inhibitor N3 ^[15]	-7.3	0.000	0.000
Remdesivir	COVID-19 main protease in complex with inhibitor N3 ^[15]	-6.5	0.000	0.000
Ribavirin	COVID-19 main protease in complex with inhibitor N3 ^[15]	-5.6	0.000	0.000
Favipiravir	COVID-19 main protease in complex with inhibitor N3 ^[15]	-5.4	0.000	0.000
Chloroquine	1. COVID-19 main protease in complex with inhibitor N3 ^[15]	-5.1	0.000	0.000
	2. SARS Spike glycoprotein-Human ACE2 complex ^[17]	-7.1	0.000	0.000
Hydroxychloroquine	1. COVID-19 main protease in complex with inhibitor N3 ^[15]	-5.3	0.000	0.000
	2. SARS Spike glycoprotein-Human ACE2 complex ^[17]	-6.8	0.000	0.000

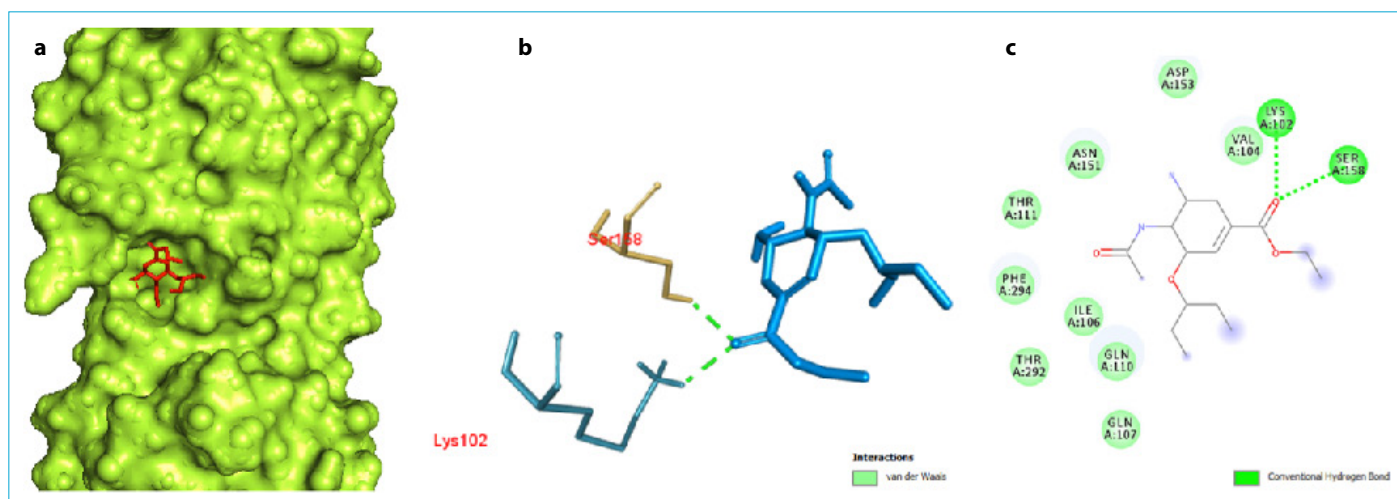
**Figure 1.** The ligand binding site of (a) SARS spike glycoprotein-human angiotensin-converting enzyme II complex with chain (labeled in red) and (b) the COVID-19 main protease in complex with the inhibitor N3. COVID-19: Coronavirus disease 2019; SARS: Severe acute respiratory syndrome.

protein interactions were shown as sticks of different colors and labeled in red. In order to visualize the ligands docked

to the protein structure, ligands were shown as red sticks in the binding pocket of the protein.

Discussion

Successful docking of all the ligands revealed significant binding with the target proteins. After visualizing the protein in Discovery Studio 12.0, it was found that the SARS spike glycoprotein-human ACE2 complex and the COVID-19 Mpro in complex with the inhibitor N3 consists of A, B, and C chains, as shown in (Fig. 1). In the COVID-19 Mpro, only the A and C chains are involved in interaction with ligands. Oseltamivir docked in the COVID-19 Mpro in complex with the inhibitor N3 showed significant binding, yielding a binding affinity of -6.1 kcal/mol. The interaction of oseltamivir with the protease (Fig. 2) showed a high affinity interaction in chain A, as the ligand fit inside the core pocket region of the protease. This is further evidenced by hydrogen bonding between the oxygen of a carbonyl

**Figure 2.** Oseltamivir docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with (a) best binding mode in the protein pocket (ligand illustrated as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) the binding interaction of oseltamivir with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

group (ester side chain) of oseltamivir with LYS 102 and SER 158. Some van der Waals interaction of oseltamivir with VAL 104, ASP 153, ASN 151, THR 111, PHE 294, ILE 106, THR 292, GLN 110, and GLN 107 was observed.

The docking of ritonavir with the COVID-19 Mpro in complex with the inhibitor N3 revealed that ritonavir (ligand) had a high-affinity interaction with the A chain of the protein: -7.3 kcal/mol (Fig. 3). To interact with the protein, ritonavir acquired the central pocket surrounded by chains A, B, and C, which led to several interactions between ritonavir and the amino acid residues of the proteins. The interaction resulted in a hydrogen bond between ritonavir and amino acid residues of the protein. The oxygen (amide group) demonstrated significant hydrogen bonding with THR 111. The benzene ring showed pi-anion and pi-pi interaction with ASP 153 and PHE 294, respectively.

The docking of remdesivir in the COVID-19 Mpro in complex with the inhibitor N3 revealed significant interactions in the central pocket of chain A with an affinity of -6.5 kcal/mol (Fig. 4). The major interaction between remdesivir and the protease was characterized by hydrogen bonding between nitrogen of a cyano group and PHE 294, and oxygen of a tetrahydrofuran ring with GLN 110. Some pi sigma interactions of the aromatic ring and ILE 249 and VAL 104 were observed.

Results obtained by docking ribavirin to the COVID-19 Mpro in complex with the inhibitor N3 showed binding in the pocket of chain A with an affinity of -5.6 kcal/mol (Fig. 5). Significant binding was observed, with 4 hydrogen bonds between nitrogen of a dihydrotriazole ring and TYR 239, hydrogen of an amide group (attached to dihydrotriazole) and TYR 237, hydrogen of a hydroxyl group (attached to a

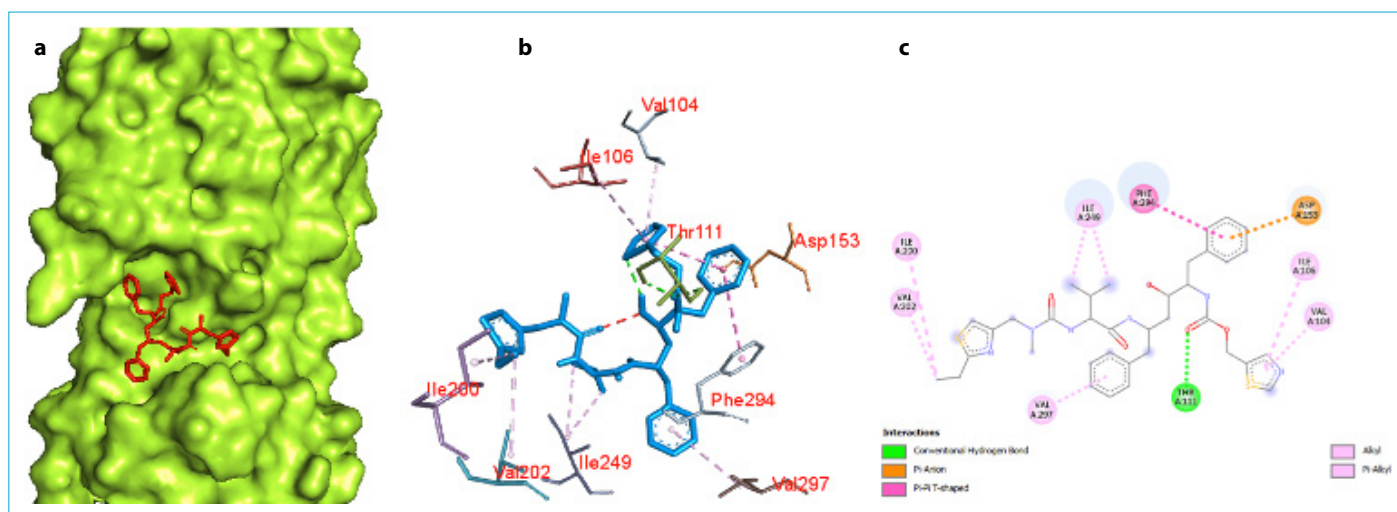


Figure 3. Ritonavir docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with (a) best binding mode in the protein pocket (ligand as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) binding interaction of ritonavir with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

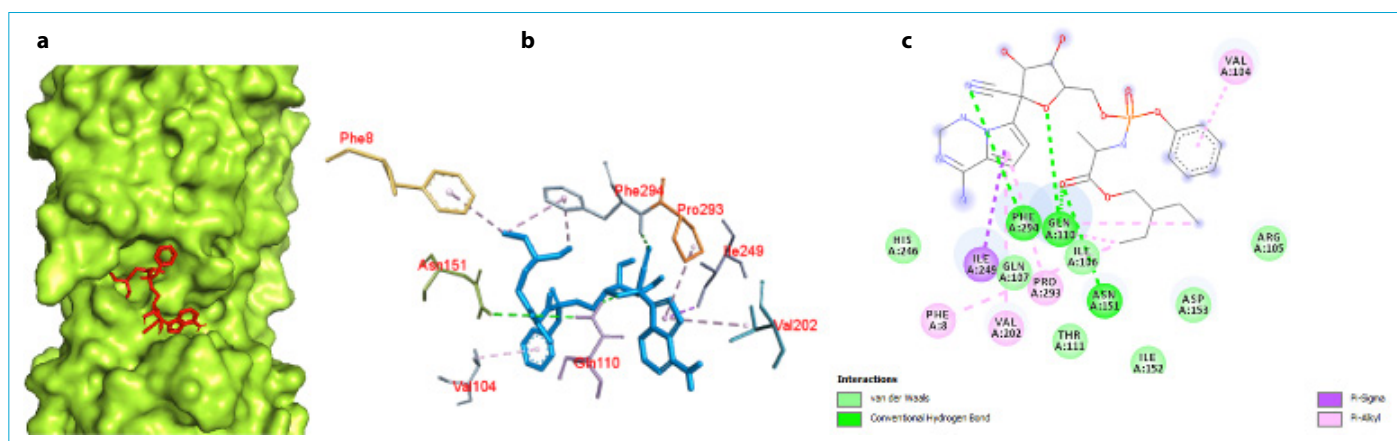


Figure 4. Remdesivir docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with (a) best binding mode in the protein pocket (ligand as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) binding interaction of remdesivir with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

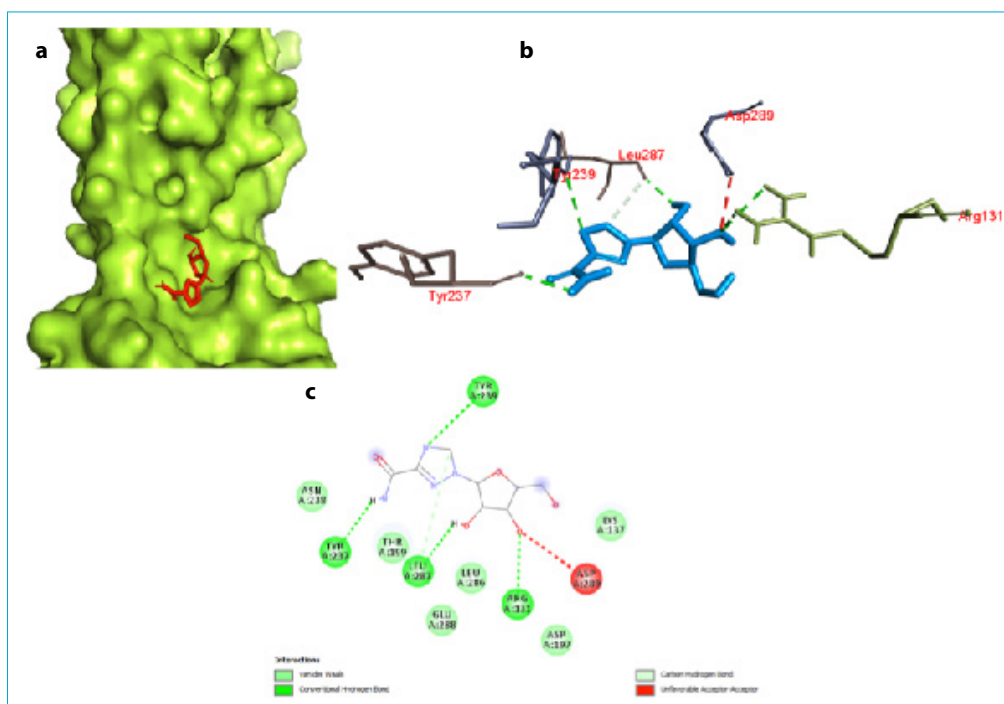


Figure 5. Ribavirin docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with **(a)** best binding mode in the protein pocket (ligand as red sticks), **(b)** amino acid residues involved in the interaction (ligand as blue sticks), and **(c)** binding interaction of ribavirin with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

tetrahydrofuran ring) and ARG 131 and oxygen (attached to a tetrahydrofuran ring) with ARG 131. An unfavorable acceptor interaction was also observed between oxygen (attached to tetrahydrofuran ring) and ASP 289.

With 6 hydrogen bonds, favipiravir showed promising activity with the Mpro of COVID-19, with an affinity of -5.4 kcal/mol. It showed strong interaction with the protease in

a binding pocket of chain A (Fig. 6). Thus, this interaction results in 6 hydrogen bonds, oxygen (attached to a pyrazine ring) and an oxygen carboxamide group (attached to a pyrazine ring) with GLN 110, THR 292, and THR 111. Similarly, hydrogen of a carboxamide group showed bonding with ASP 295 and ASN 151. Since the binding was characterized by 6 hydrogen bonds, this interaction can be seen as

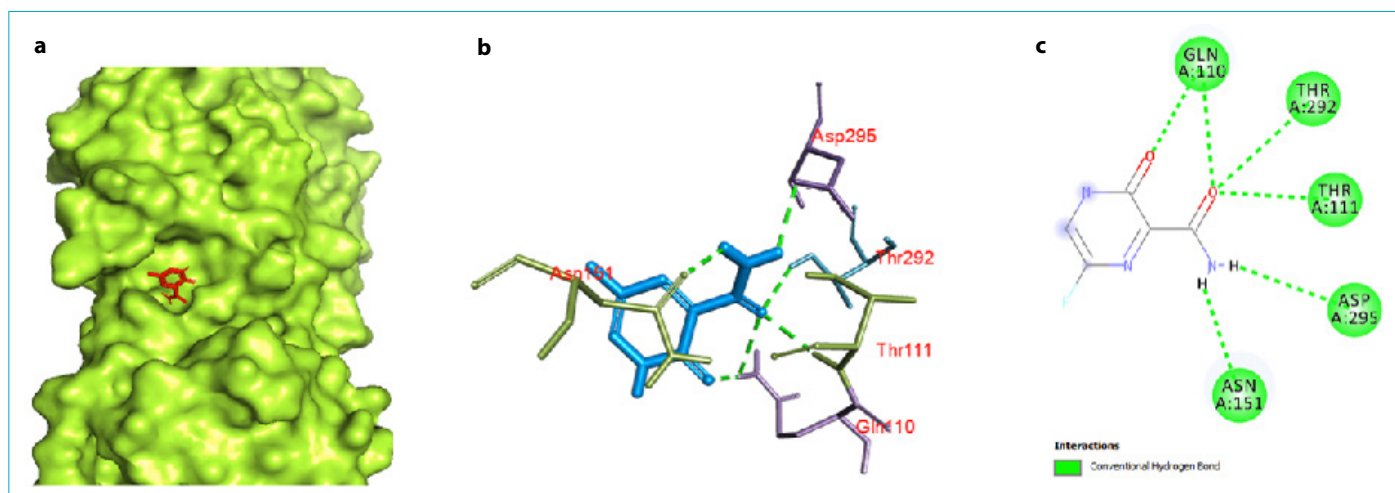


Figure 6. Favipiravir docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with **(a)** best binding mode in the protein pocket (ligand illustrated as red sticks), **(b)** amino acid residues involved in the interaction (ligand as blue sticks), and **(c)** the binding interaction of favipiravir with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

a possible mode of binding of favipiravir with the Mpro of COVID-19.

Docking of chloroquine was performed with both the COVID-19 Mpro in complex with the inhibitor N3 and the SARS spike glycoprotein-human ACE2 complex. The binding interaction of chloroquine with the COVID-19 Mpro was observed in the binding pocket of chain C with the affinity of -5.1 kcal/mol (Fig. 7). The interactions were primarily characterized by pi-alkyl interactions between a chlorobenzene ring with VAL 104 and ILE 106. The prominent interaction of chloroquine with the SARS spike glycoprotein-human ACE2 complex was observed with a binding affinity of -70 kcal/mol (Fig. 8). The interaction of chloroquine with the

SARS spike glycoprotein-human ACE2 complex was seen in pi-pi and pi-alkyl interactions between a benzene ring and chlorine (attached to the benzene ring) with TYR 738 and PHE 952, respectively. A large number of amino acids were involved in van der Waals interactions, including GLN 987, THR 988, GLN 984, THR 988, SER 985, PHE 741, GLY 981, THR 988, THR 991, GLN 987, GLN 984, and LEU 983. Thus, it was observed that chloroquine favored the SARS spike glycoprotein-human ACE2 complex over the COVID-19 Mpro in complex with the inhibitor N3.

Similarly, the docking study of hydroxychloroquine with both the COVID-19 Mpro in complex with the inhibitor N3 and the SARS spike glycoprotein-human ACE2 complex

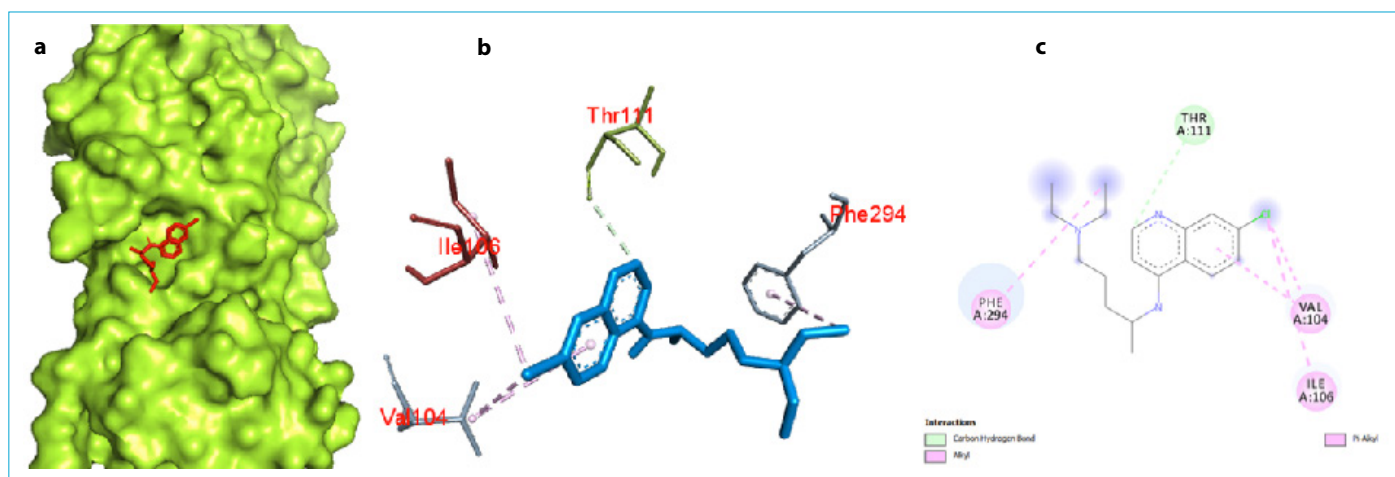


Figure 7. Chloroquine docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with (a) best binding mode in the protein pocket (ligand illustrated as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) the binding interaction of chloroquine with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

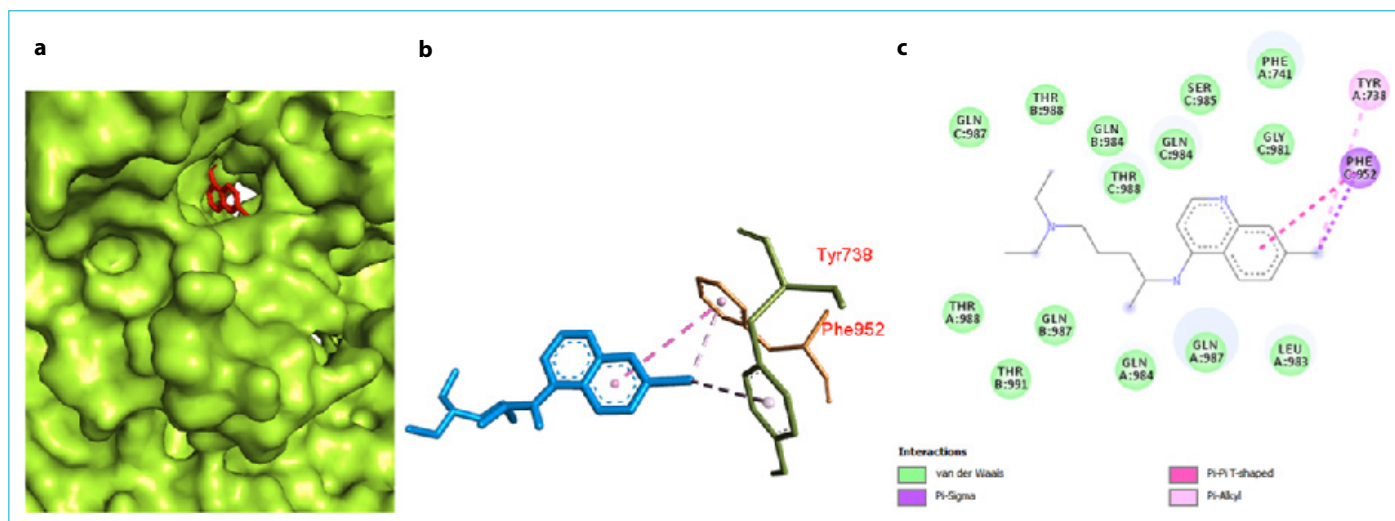


Figure 8. Chloroquine docked in the SARS spike glycoprotein-human angiotensin-converting enzyme complex (PDB ID: 6CS2) with (a) best binding mode in the protein pocket (ligand illustrated as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) the binding interaction of chloroquine with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019; SARS: Severe acute respiratory syndrome.

yielded several facts about binding interaction. Hydroxychloroquine docking with the COVID-19 Mpro revealed a binding affinity of -5.3 kcal/mol with a hydrogen bonding interaction between hydrogen of a hydroxyl group (in an aliphatic chain) with ASN 151 (Fig. 9). It also showed pi-pi and pi-alkyl interactions with residues of VAL 297, PRO 252 and ILE 249. Van der Waals interactions occurred with PRO 293, PHE 294, THR 111b and PHE 8. Similar to chloroquine, hydroxychloroquine also showed promising interaction with the SARS spike glycoprotein-human ACE2 complex (Fig. 10) with a binding affinity of -6.8 kcal/mol. This interaction is primarily attributed to the large number of amino acids involved in a van der Waals interaction due to a better fit of hydroxychloroquine inside the pocket of the protein.

One hydrogen bond between secondary amine hydrogen and GLN 992 was observed. A pi-sigma interaction was seen between the ring and THR 943. Based on the results, it appeared that the SARS spike glycoprotein-human ACE2 complex was a promising target for hydroxychloroquine against the COVID-19 Mpro in complex with the inhibitor N3. Based on this study, it can be said that hydroxychloroquine favored the SARS spike glycoprotein-human ACE2 complex over the protease for binding.

Conclusion

The docking results yielded various kinds of binding interactions of the drugs with the protein, and some were favorable. The antiviral drugs oseltamivir, ritonavir, remdesivir,

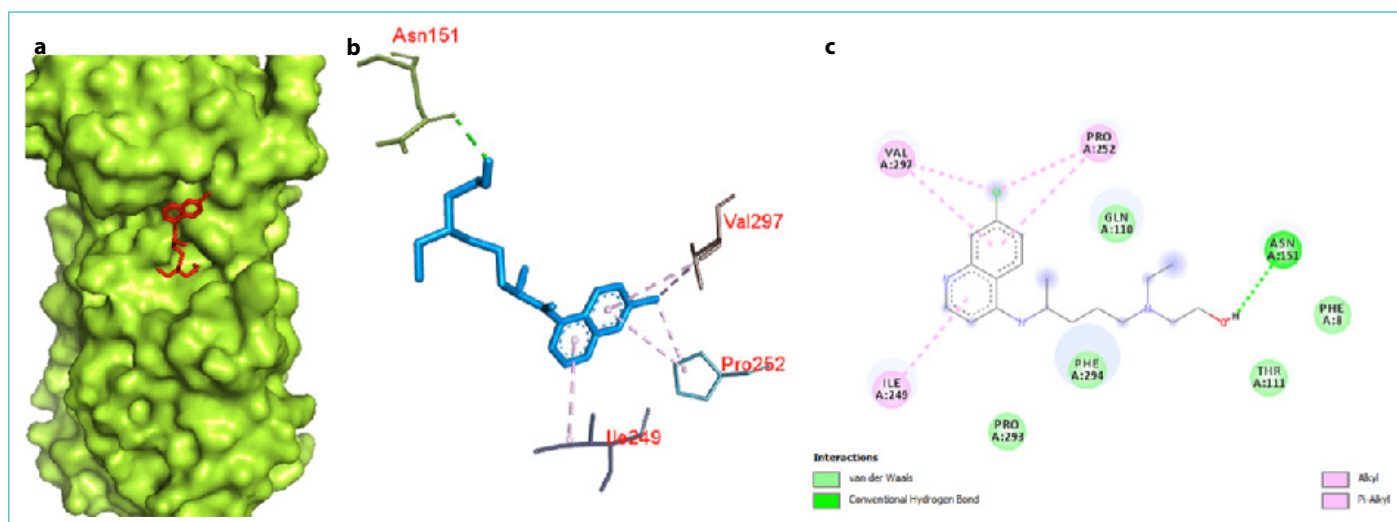


Figure 9. Hydroxychloroquine docked in the COVID-19 main protease in complex with the inhibitor N3 (PDB ID: 6LU7) with (a) best binding mode in the protein pocket (ligand illustrated as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) the binding interaction of hydroxychloroquine with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019.

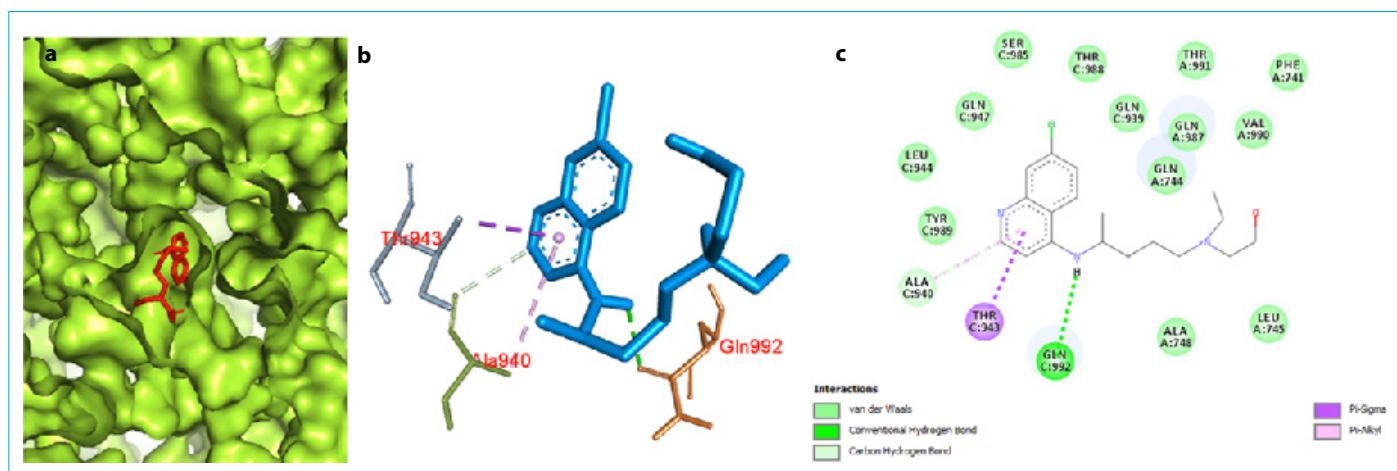


Figure 10. Hydroxychloroquine docked in the SARS spike glycoprotein-human angiotensin-converting enzyme complex (PDB ID: 6CS2) with (a) best binding mode in the protein pocket (ligand illustrated as red sticks), (b) amino acid residues involved in the interaction (ligand as blue sticks), and (c) the binding interaction of hydroxychloroquine with amino acid with a hydrogen bond (green dashed line). COVID-19: Coronavirus disease 2019; SARS: Severe acute respiratory syndrome.

ribavirin, and favipiravir showed high-affinity interactions with the COVID-19 Mpro in complex with the inhibitor N3, whereas the anti-malarial drugs chloroquine and hydroxychloroquine demonstrated prominent interaction with the SARS spike glycoprotein-human ACE2 complex. It may be that the anti-COVID-19 activity of antiviral drugs is a result of interaction with the COVID-19 Mpro and that the anti-COVID-19 effect of chloroquine and hydroxychloroquine is due to a high-affinity interaction with the SARS spike glycoprotein-human ACE2 complex.

Disclosures

Peer-review: Externally peer-reviewed.

Conflict of Interest: None declared.

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