An *in-silico* study on selected organosulfur compounds as potential drugs for SARS-CoV-2 infection *via* binding multiple drug targets

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**Abstract:** The emerging paradigm shift from ‘one molecule, one target, for one disease’ towards ‘multi-targeted small molecules’ has paved an ingenious pathway in drug discovery in recent years. This idea has been extracted for the investigation of competent drug molecules for the unprecedented COVID-19 pandemic which became the greatest global health crisis now. Perceiving the importance of organosulfur compounds against SARS-CoV-2 from the drugs under clinical trials, a class of organosulfur compounds effective against SARS-CoV were selected and studied the interaction with multiple proteins of the SARS-CoV-2. One compound displayed inhibition against five proteins (both structural and non-structural) of the virus namely, main protease, papain-like protease, spike protein, helicase and RNA dependent RNA polymerase. Consequently, this compound emanates as a potential candidate for treating the virulent disease. The pharmacokinetics, ADMET properties and target prediction studies carried out in this work further inflamed the versatility of the compound and urge to execute *in-vitro* and *in-vivo* analysis on SARS-CoV-2 in the future.
1. Introduction

The deplorable situation of the present world aroused by the dreadful behavior of an RNA virus named the Severe Acute Respiratory Syndrome Corona Virus-2 (SARS-CoV-2) is originated in the City of Wuhan, China in late 2019. The Corona Virus Disease (COVID-19) pandemic caused by the novel coronavirus (later named as SARS-CoV-2) massacred about four lakhs lives leaving more than eight million people in the infection with fever, dry cough, short breath and other respiratory ailments across 215 countries. Similar infections were reported in 2012 by the Middle East Respiratory Syndrome Corona Virus (MERS-CoV) and the Severe Acute Respiratory Syndrome Corona Virus (SARS-CoV) in 2003 but they were less contagious with 10,590 cases and 1632 fatalities collectively. According to the World Health Organization (WHO), there are no approved medicines or vaccines for COVID-19 as of now while extensive researches are undergoing to explore the treatment proceeding including the clinical trials of more than 300 compounds. The leading approach for the development of curative medication is drug repurposing as it allows for the rapid acceptance with a profit of low cost, known and optimized synthetic route and often facile to leapfrog the preliminary stages of clinical trial.

In hand the list of various known drugs for repurposing, the promising approach is to go down the line of SARS-CoV drugs. The phylogenetic analysis of SARS-CoV-2 revealed about 89.1% genomic similarity with SARS-CoV which is also a beta corona virus. Closely scrutinizing the proteins involved in the SARS-CoV-2 infection, the Spike Protein (Spro) promotes the entry of the virus into the human cell by binding with the type 1 transmembrane metallocarboxypeptidase known as Angiotensin Converting Enzyme-2 (ACE-2). The receptor binding motif of SARS-CoV and SARS-CoV-2 spike proteins are the same and they possess the sequence similarity of 76% by showcasing more similar adherence in the receptor binding domain. Spro is a structural protein located on the periphery of the virus and other main structural proteins are envelope protein, membrane proteins and nucleocapsid protein. The non-structural proteins are more in number, sixteen, and they are responsible for the viral multiplication and other specific purposes for infection. Once inside the cell, the viruses commence the synthesis of its RNA by the enzyme called RNA-dependent RNA polymerase (RdRp). Knowing the fact that SARS-CoV and SARS-CoV-2 share RdRp sequence with about 96% similarity, the inhibition of this protein is a prospective strategy of drug action. The other promising drug targets are Chymotrypsin Like Protease (3CLpro) otherwise called Main Protease (Mpro) and Papain Like Protease (PLpro) which help in virus replication. These two protease enzymes of the SARS-CoV-2 exhibit 96% and 83% percentage similarity respectively with that of SARS-CoV with similar active site sequences. Helicase is another target for antiviral drugs as it plays a vital role in replication and the central dogma of the virus. Spotlighting the structural similarity between SARS-CoV and SARS-CoV-2, we selected organosulfur compounds as drug candidates against SARS-CoV-2 which were previously found to be effective against SARS-CoV infection.

Organosulfur compounds are an important class of molecules with the sulfur-containing functional groups such as sulfones, sulfonamides, disulfides, sulfoxides, thiophene, thiazole
etc\textsuperscript{10}. The impact of organosulfur compounds in the pharmaceutical sector is impeccable right from the example of penicillin. Clinical trial of a range of organosulfur compounds such as Ritonavir, arbidol\textsuperscript{11}, baricitinib\textsuperscript{12} etc. is currently underway against SARS-CoV-2. Given the potential of organosulfur compounds as an antiviral drug, we selected eight organosulfur compounds (Figure 1) which are already reported to show antiviral activity against SARS-CoV, a very close analogue of SARS-CoV-2, and studied the inhibitory action against several druggable targets of SARS-CoV-2 to investigate the possibility of multiple targets binding of the selected candidates. As the mutation rate and thus evolution rate is more for RNA viruses\textsuperscript{13}, multiple target binding increases the efficiency of the drug by reducing the effect of viral resistance against one protein\textsuperscript{14}. Therefore, the molecular docking study of each compound is carried out with five different target proteins. The ADMET properties, target prediction and Lipinski’s rule are also predicted for the selected compounds to explore more about the pharmacokinetics and druggability.

![Figure 1](image-url)

**Figure 1.** Structure of the selected organosulfur compounds for the current study

2. **Materials and Methods**

2.1 **Ligand preparation**

The structure of all the organosulfur compounds was drawn in ChemDraw and the 3D structure was generated by UCSF Chimera\textsuperscript{15} from the SMILE string. The structures of all the reference compounds were obtained in UCSF Chimera through their PubChem ID. All the structures were energy minimized through the same software and converted the PDB structure to PDBQT format by using AutoDock Tools.

2.2 **Molecular docking**

Molecular docking study was carried out by using AutoDock Vina\textsuperscript{16} to explore the binding affinity and the involved interactions in between all eight organosulfur compounds and the five druggable protein targets of SARS-CoV-2 namely Main proteases (Mpro, Chain A), Papain-like proteases (PLpro, Chain A), Spike-protein (Spro, Chain B), Helicase protein, RNA dependent RNA polymerase (RdRp). The crystal structure of Mpro (PDB ID: 6Y84), PLpro
(PDB ID: 6W9C), Spro (PDB ID: 6LZG), RdRp (PDB ID: 6M71) and helicase (PDB ID: 6JYT) were retrieved from the protein databank (http://www.rcsb.org)\textsuperscript{17}. The hydrogen atoms and gasteiger charges were added to each protein, subsequently, all the proteins were saved in PDBQT format by using the AutoDock v4.2 program\textsuperscript{18}. For Mpro protein grid box (30 Å × 30 Å × 30 Å) centered at (X12, Y-8, Z20 Å), for PLpro grid box (30 Å × 30 Å × 30 Å) centered at (X-42, Y29, Z30 Å), SPro grid box (30 Å × 30 Å × 30 Å) centered at (X-36, Y33, Z12 Å), RdRp grid box (30 Å × 30 Å × 30 Å) centered at (X120, Y122, Z127 Å at 0.375 Å spacing) and for helicase protein grid box (42 Å x 30 Å x 86 Å) centered at (X424, Y29, Z25 Å at 0.375 Å spacing) were prepared and saved the output grid file in txt format. A docking run was given from the command prompt. Best docked conformation and minimum binding energy were considered for further analysis. UCSF chimera was used for the visualization of the docked conformation and results. The results and 2D interaction plots were analyzed by using Discovery studio visualizer\textsuperscript{19}.

2.3 Physicochemical properties
The physicochemical properties according to Lipinski’s rule were calculated for all the selected organosulfur compounds to predict the pharmacokinetics property. SwissADME tool was used to calculate the properties from the SMILES structures of each compound. (http://www.swissadme.ch/)\textsuperscript{20}.

2.4 ADMET studies
Predicting in-silico pharmacokinetic properties of a new drug is very crucial for further studies. ADMET (Absorption, Distribution, Metabolism, Excretion and Toxicity) prediction provides some important information for new compounds. ADMET studies have been carried out by using the computational pkCSM tool (http://biosig.unimelb.edu.au/pkcsm/prediction)\textsuperscript{21}.

2.5 Molecular target prediction
For the validation of targets, we used molecular target studies by using the Swiss Target Prediction tool (http://www.swisstargetprediction.ch/)\textsuperscript{22} which is a web server that predicts the putative targets of the given molecule by utilizing 2D and 3D similarity index with known ligands. The smile formats of the compounds were entered to obtain the targets.

3. Results and Discussion
In the current study, a set of organosulfur compounds known for targeting SARS-CoV Mpro were selected and to carry out the molecular docking studies to assess their potential against SARS-CoV-2. To examine the possibility of binding with multiple targets, we selected five SARS-CoV-2 proteins namely Mpro, PLpro, Spro, RdRp and helicase, and docked with the selected compounds along with their known inhibitors as the reference compounds such as indinavir for Mpro, darunavir for PLpro, arbidol for Spro, remdesivir for RdRp and ivermectin for helicase. Utilizing molecular docking study, the binding energy of the organosulfur compounds with the reference drug compounds is calculated and the results are tabulated in Table 1.
Table 1. Binding energy (kcal/mol) of the organosulfur compounds along with the reference compounds against various proteins of SARS-CoV-2 by molecular docking study

| S. No. | Compound name | Binding energy (kcal/mol) against SARS-CoV-2 proteins |
|--------|---------------|------------------------------------------------------|
|        |               | Mpro | PLpro | Spro | RdRp | Helicase |
| 1      | 1             | -8.6 | -6.2  | -7.2 | -6.8 | -7.7     |
| 2      | 2             | -7.0 | -5.8  | -6.7 | -6.5 | -6.9     |
| 3      | 3             | -7.3 | -5.9  | -6.8 | -6.8 | -7.2     |
| 4      | 4             | -5.9 | -5.1  | -5.6 | -5.4 | -5.6     |
| 5      | 5             | -5.6 | -4.8  | -5.3 | -5.0 | -5.2     |
| 6      | 6             | -7.6 | -6.1  | -6.4 | -6.3 | -6.6     |
| 7      | 7             | -7.2 | -6.1  | -6.7 | -6.3 | -6.3     |
| 8      | 8             | -6.5 | -5.2  | -5.4 | -5.8 | -5.9     |
| 9      | Indinavir     | -7.7 | -    | -    | -    | -        |
| 10     | Darunavir     | -    | -6.6  | -    | -    | -        |
| 11     | Arbidol       | -    | -    | -6.1 | -    | -        |
| 12     | Remdesivir    | -    | -    | -    | -7.4 | -        |
| 13     | Ivermectin    | -    | -    | -    | -    | -8.5     |

3.1 Molecular docking study

3.1.1 Docking studies of the organosulfur compounds with the SARS-CoV-2 Mpro

Molecular docking study of the organosulfur compounds with the Mpro of SARS-CoV-2 exhibited promising results with several of them. Indinavir, a well-known drug that has already been reported to inhibit Mpro of the SARS-CoV-2\(^{23}\) was studied as a reference compound. Docking score of the organosulfur compounds along with the reference compound is tabulated in Table 1 and docking conformations of the reference compound and the organosulfur compound with the highest binding affinity \(i.e. 1\) is represented in Figure 2. All the compounds were found to bind in the active site of Mpro where Cys145 and His41 are the catalytic residues. Indinavir docked with a conformation that makes five hydrogen bonds with Thr26, Ser46, Asn142, Cys145 and Gln189 along with pi-alkyl interaction with Pro168, van der Waals interaction with His41 and other residues (see Figure 2b). When the lowest binding energy for the reference compound was observed to be -7.7 kcal/mol, the organosulfur compound, 1 docked with a minimum binding energy of -8.6 kcal/mol with three conventional hydrogen bonds with His41 (catalytic residue), Cys44 and Gly143. The interactions include two pi-sulfur interactions with Met49 and Met165; eight van der Waals interaction with Thr25, Thr45, Ser46, Leu141, Ser144, His164, Glu166 and Gln189; carbon-hydrogen bond with Asn142 and Cys145 which is also an active site residue (Figure 2d). The compound 6 binds with the binding energy -7.6 kcal/mol which is close to the binding energy of the reference compound with conventional hydrogen bond with both the active site residues His41 and Cys145 along with other van der Waals interaction. A pi-sulfur interaction is also observed with His41 making the binding stronger (Figure S1b in the Supplementary Information). Thus, 6 claims to be a fairly good candidate to inhibit Mpro of SARS-CoV-2. 3 docked with Mpro with a binding energy -7.3 kcal/mol even though hydrogen bonding with the catalytic dyad is absent. Nevertheless, 3 forms a pi-pi stacking interaction with His41, pi donor hydrogen bond with Cys145,
conventional hydrogen bond with Gly143, pi-sulfur bond with Met165, pi-sigma bond with Glu166 and van der Waals interaction with other residues (Figure S1d in the Supplementary Information). Based on these observations, 1, 6 and 3 can be a potential drug against the SARS-CoV-2 acting via Mpro inhibition.

Figure 2. Best-docked conformation and 2D diagram of amino acid interaction of the SARS-CoV-2 Mpro complexed with indinavir (a, b) and compound 1 (c, d)

3.1.2 Docking studies of the organosulfur compounds with the SARS-CoV-2 PLpro
The molecular docking study of organosulfur compounds with the SARS-CoV-2 PLpro revealed that the three compounds, namely 1, 6 and 7 exhibited reasonably strong interaction with binding energy in the range of the reference compound darunavir which is a known organosulfur drug for SARS-CoV-2. Darunavir docked into the binding pocket of the protein with catalytic triad Cys111, His272 and Asp286. Darunavir bound with the PLpro with the lowest binding energy of -6.6 kcal/mol when all the selected compounds could achieve
only higher energy than this. The interactions of Darunavir with the protein include four hydrogen bonds with Asn109, Gln269, Lys274 and Asp 286; two pi-sigma interactions with Trp106 and His272 besides the pi-alkyl and van der Waals interaction with other residues as depicted in the **Figure 3b**. Compounds 1, 6 and 7 showed the lowest binding energy of -6.2, -6.1 and -6.1 kcal/mol, respectively among the set. Out of the three potent molecules, 1 bound with protein by forming a hydrogen bond with the residues Trp106 and Ala288; pi-pi stacking with His272 and Trp106 and also van der Waals interaction with Asp286, Lys105, Gly287 and Leu289 (**Figure 3d**). Although 6 and 7 exhibited the same binding energy with PLpro, 6 made more interactions with the catalytic residues. The interactions are two hydrogen bonds with Trp106 and Cys111; pi-pi stacking interaction with Trp106, pi-alkyl interaction with Leu289 and also van der Waals interaction with His272 and other neighboring residues (**Figure S2b** in the Supplementary Information). Whereas 7 made no interaction with the catalytic triad but it exhibited hydrogen bonding with Asp37, Lys94 and Tyr97; amide pi stacked interaction with Gly142 along with few pi-alkyl and van der Waals interaction (**Figure S2d** in the Supplementary Information). Hence 1 and 6 found to be better candidates to inhibit PLpro of the SARS-CoV-2.
3.1.3 Docking studies of the organosulfur compounds with the SARS-CoV-2 Spike protein (Spro)

The docking scores of organosulfur compounds selected for the study of inhibition of Spro of the SARS-CoV-2 are shown in Table 1. Antiviral organosulfur drug for Influenza virus, arbidol, which has been repurposed against the SARS-CoV-2, is taken as the reference compound and is already in the clinical trial. The docking score of arbidol with Spro is -6.1 kcal/mol when five compounds namely 1, 2, 3, 6, and 7 in our list showed lower binding energy values than the reference compound. The active site of the protein comprised the amino acid residues Phe486, Gln493 and Asn501. Arbidol displayed one hydrogen bonding with Gly496, pi-pi interaction with Tyr449, van der Waals interaction with the catalytic residues Gln493, Asn501 and also with other residues (Figure 4b). Compound 1 interacted with Spro more strongly with the binding energy -7.2 kcal/mol by making a hydrogen bond with Gly496; pi-pi stacking with Tyr 505 along with the van der Waals interaction with Glu406, Tyr453, Tyr495, Asn501 and Gly502 (Figure 4d). 3 has the strongest interaction with the protein, after 1, by -6.8 kcal/mol. The compound made two hydrogen bonding with Gln498 and Tyr449; pi-sulfur and pi-pi T shaped interaction with Tyr505; the active site residue Gln493 and Asn501 interacted with the protein through van der Waals interaction (Figure S3d in the Supplementary Information). Compound 2 binds with the binding energy -6.7 kcal/mol and made pi-sulfur interaction with Tyr505; hydrogen bonding with Tyr449 and Gln498, and it managed to make a van der Waals interaction with the catalytic residue Asn501 and other residues (Figure S3d in the Supplementary Information). 7 is another compound that also showed good results with the docking score -6.7 kcal/mol. This compound is interacting with the catalytic residues Gln493 and Asn501 through van der Waals interaction by making the hydrogen bond with Glu406 (Figure S3f in the Supplementary Information). Analyzing these results, it can be observed that organosulfur compounds exhibited considerably low binding
energy with Spro of the SARS-CoV-2 warranting further *in vitro* and *in vivo* investigation to consider them as potential drugs for COVID-19.

Figure 4. Best-docked conformation and 2D diagram of amino acid interaction of the SARS-CoV-2 Spro complexed with arbidol (a, b) and compound 1 (c, d)

3.1.4 Docking studies of the organosulfur compound with the SARS-CoV Helicase

For this study, we have taken the crystal structure of SARS-CoV helicase protein which shares almost 99.83 % similarity over the complete length of sequences with the helicase protein of SARS-CoV-2 virus. The docking scores of the eight organosulfur compounds and the reference compound are represented in Table 1. The docked structure with the lowest binding energy and best conformation of the top-scoring organosulfur compound namely 1 along with one reference drug ivermectin, with their corresponding 2D interaction plots are shown in Figure 5. The docked conformation indicates that these molecules bind within the active site of the helicase protein of SARS-CoV. Figure 5b illustrates that the reference compound
ivermectin binds via two carbon-hydrogen bonds with residues Arg178, Asp534, four alkyl hydrophobic interactions with Pro408, Ala312, Ala313, Ala316 and van der Waals interactions and these conformation resulted in the lowest binding energy of -8.5 kcal/mol. Compound 1 binds with two conventional hydrogen bonds involving Lys202 and Arg178, two Pi-alkyl interactions with Lys202 and Ala520, one pi-anion interaction with Glu201, and van der Waals interactions as shown in Figure 5d giving -7.7 kcal/mol binding energy. Compound 2 stabilizes the complex through one hydrogen bond with Lys202, one pi-anion with Glu201, one carbon-hydrogen interaction with Asn177, pi-alkyl interaction with Lys202 and van der Waals interactions with other residues as represented in the 2D plot Figure S4b in Supplementary Information. Compound 2-helicase complex resulted in -6.9 kcal/mol binding energy. 3 was found to bind within the active site of the helicase through one hydrogen bond with Lys202, alkyl hydrophobic interaction with Arg178, pi-alkyl interaction with Lys202, pi-anion interaction with Glu201 and van der Waals interactions with other residues as shown in Figure S4d in Supplementary Information providing -7.2 kcal/mol binding energy. If we compare the values of the docking score, we can observe the reference compound ivermectin has the lowest binding energy with -8.5 kcal/mol followed by organosulfur compound 1, then 3 and finally 2. Three organosulfur compounds (1, 2 and 3) show good inhibitory activity towards the helicase protein of the SARS-CoV suggesting that these three organosulfur compounds might also be potent against helicase protein of the SARS-CoV-2.
Figure 5. Best-docked conformation and 2D diagram of amino acid interaction of SARS-CoV helicase complexed with ivermectin (a, b) and compound 1 (c, d).

3.1.5 Docking studies of the organosulfur compounds with the SARS-CoV-2 RdRp
Molecular docking studies of our organosulfur compound library against the RdRp protein of the SARS-CoV-2 revealed that the three organosulfur compounds, namely 1, 2 and 3 exhibited lowest binding energy along with the reference compound remdesivir\(^\text{26}\). The docked conformations of the RdRp-organosulfur compounds are depicted in Figure 6 and the docked scores are mentioned in Table 1. Remdesivir, a potent SARS-CoV-2 RdRp inhibitor binds in the active site (see Figure 6a) through hydrogen bonding with Tyr619 and Asp760, pi-sulfur interaction with Asp618, Asp761, pi-alkyl interactions with Lys621 and Pro620, alkyl hydrophobic interaction with Phe793, respectively, along with other interactions such as pi-sigma and van der Waals interactions with other residues as depicted in the 2D plot and this significant number of interactions resulted in the lowest binding energy of -7.4 kcal/mol. The docked structure showed that 1 formed four hydrogen bonds with Cys622, Arg553, Ser682, Asn691, and different non-covalent interaction such as pi-alkyl interaction with Lys621, pi-anion interaction with Asp623 and van der Waals interactions as shown in Figure 6d resulting lowest binding energy of -6.8 kcal/mol among all eight organosulfur compounds. 2 is involved in three hydrogen bond interaction with Trp800, Ser814, Cys813, two pi-anion interactions with Asp761, Glu811 and van der Waals interaction as represented in Figure S5b in the Supplementary Information consequently resulting -6.5 kcal/mol binding energy. Compound 3 formed two H-bond interactions with Lys621 and Ser795, one pi-alkyl interaction with Val166, one pi-sigma interaction with Pro620, two pi-cation interactions with Asp618, Lys798 and van der Waals interactions as depicted in Figure S5d eventually this complex resulted in minimum binding energy -6.8 kcal/mol. Here we observed that among the eight organosulfur compounds, three compounds namely 1, 2 and 3 showed promising binding activity with RdRp of the SARS-CoV-2. Based on these observations, the above mentioned three organosulfur compounds can be potential RdRp inhibitors to combat the SARS-CoV-2 infection.
In order to identify the potential inhibitors for the SARS-CoV-2, molecular docking studies were carried out over eight potential organosulfur compounds against multiple target proteins namely Mpro, PLpro, Spro, RdRp and helicase. Among these compounds, 1 exhibited the lowest binding energy against all five proteins, which suggests that 1 could be the potential drug candidate for treating COVID-19. Apart from 1, 3 and 6 exhibited promising binding affinities towards the above mentioned five proteins which suggests that these two organosulfur also can act as antiviral drugs against the SARS-CoV-2. We were keen to do further investigation on the physicochemical, pharmacokinetic properties and target prediction studies.
of 1 which showed the lowest binding energy among all the eight organosulfur compounds against five target proteins of SARS-CoV-2. The predicted pharmacokinetic properties of other organosulfur compounds are tabulated in Table S1-S5 in the Supplementary Information.

3.2 Physicochemical properties study based on the Lipinski’s rule
The physicochemical properties of the compounds were studied to predict the pharmacokinetics of the drug by the Lipinski’s rule. The guidelines for an orally active drug according to the Lipinski’s rule are (i) molecular weight (MW) <500 Daltons, (ii) octanol-water partition coefficient (clogP) <5, (iii) polar surface area (PSA) <150 Å², (iv) number of hydrogen bond donors (HBD) <5, (v) number of hydrogen bond acceptors (HBA) <5 and (vi) Number of rotatable bonds (RB) <10²⁷. The calculated values for the same for the selected organosulfur compounds are tabulated in Table 2 and the result shows that all the compounds strictly follow Lipinski’s rule with zero violation. This indicates that the compounds have the potential for drug-like activities.

Table 2. Physicochemical properties of the organosulfur compounds.

|     | 1         | 2        | 3        | 4        | 5        | 6        | 7        | 8        |
|-----|-----------|----------|----------|----------|----------|----------|----------|----------|
| MW  | 336.36    | 372.24   | 419.24   | 205.24   | 239.68   | 375.65   | 320.39   | 340.48   |
| clogP| 2.32      | 3.76     | 3.82     | 0.72     | 2.76     | 4.58     | 2.56     | 3.88     |
| PSA (Å²) | 108.71    | 65.62    | 65.62    | 118.42   | 67.43    | 71.61    | 129.90   | 57.64    |
| No. of HBD | 1         | 0        | 0        | 2        | 0        | 0        | 2        | 1        |
| No. of HBA | 3         | 2        | 2        | 3        | 3        | 4        | 2        |         |
| No. of RB | 3         | 2        | 2        | 0        | 3        | 3        | 2        | 9        |
| Violations | Zero      | Zero     | Zero     | Zero     | Zero     | Zero     | Zero     | Zero     |

3.3 Prediction of the absorption, distribution, metabolism, excretion, and toxicity (ADMET) profile
We carried out ADMET property profiling to explore the drug likeliness of compound 1 which exhibited efficient binding energy among the eight organosulfur compounds against RdRp, PLpro, Mpro, Spro and helicase proteins of SARS-CoV_2 in the molecular docking study. In-silico pharmacological prediction of 1 was performed using the pkCSM server to assess the overall ADMET properties (see Table 3). A favorable ADMET profile is necessary for the molecules in drug discovery. 1 showed water solubility and high Caco-2 permeability, which indicates that this drug can be absorbed orally. 1 showed good human intestinal absorption and skin permeability. Compound 1 was predicted to be a substrate of P-glycoprotein as well as P-glycoprotein I and II inhibitor

The Volume of distribution at steady state (VDss) prediction indicates a low theoretical dose of 1 will be required to get it uniformly distributed in blood plasma. Blood-brain barrier (BBB) permeability prediction showed that 1 readily cross the BBB and drug can penetrate the central nervous system.

It is well known that cytochrome P450s can regulate the metabolism of various drugs. In that respect, it is worth noting that inhibitors of CYP2D6/CYP3A4 can hamper the
pharmacological properties of drugs. 1 inhibits neither CYP2D6 nor CYP3A4, whereas it is predicted to be a substrate of CYP3A4. Further, it was observed that 1 is not a substrate of ROCT-2 which means that this drug can be excreted through other routes such as bile, sweat and breathe.

We have also assessed the toxicity index of the organosulfur compound 1. The toxicity prediction from the Ames test (Salmonella typhimurium reverse mutation assay) revealed that 1 could be considered as a mutagenic agent. High toxicity was predicted in Tetrahymena pyriformis. 1 was shown to inhibit the human ether-a-go-go-related gene II (hERG II). However, 1 was found to be associated with hepatotoxicity. The maximum recommended tolerated dose (MRTD) in human prediction shows that 1 does not violate MRTD. 1 is predicted to be a high acute toxic compound as it falls under minnow toxicity. Additionally, compound 1 is not associated with skin sensitivity.

**Table 3. Predicted ADMET properties of the compound 1**

| Properties       | Model name               | Predicted values | Unit          |
|------------------|--------------------------|------------------|---------------|
| **Absorption**   | Water solubility         | -4.303           | log mol/L     |
|                  | Caco2 permeability       | 0.98             | Log Papp in $10^{-6}$ cm/s |
|                  | Human intestinal absorption | 94.882         | % Absorbed |
|                  | Skin permeability        | -2.76            | log Kp        |
|                  | P-glycoprotein substrate | Yes              | Yes/No       |
|                  | P-glycoprotein I inhibitor | Yes            | Yes/No       |
|                  | P-glycoprotein II inhibitor | Yes         | Yes/No       |
| **Distribution** | VDs                      | -0.009           | log L/kg      |
|                  | Fraction unbound (human) | 0.078            | Fu            |
|                  | BBB permeability         | -0.518           | log BB        |
|                  | CNS permeability         | -2.189           | log PS        |
| **Metabolism**   | CYP2D6 substrate         | No               | Yes/No       |
|                  | CYP3A4 substrate         | Yes              | Yes/No       |
|                  | CYP1A2 inhibitor         | Yes              | Yes/No       |
|                  | CYP2C19 inhibitor        | Yes              | Yes/No       |
|                  | CYP2C9 inhibitor         | Yes              | Yes/No       |
|                  | CYP2D6 inhibitor         | No               | Yes/No       |
|                  | CYP3A4 inhibitor         | No               | Yes/No       |
| **Excretion**    | Total clearance          | -0.128           | log ml/min/kg |
|                  | Renal OCT2 substrate     | No               | Yes/No       |
| **Toxicity**     | AMES toxicity            | Yes              | Yes/No       |
|                  | Maximum tolerated dose (Human) | 0         | log mg/kg/day |
|                  | hERG I inhibitor         | No               | Yes/No       |
|                  | hERG II inhibitor        | Yes              | Yes/No       |
|                  | Oral rat acute toxicity (LD₅₀) | 2.064     | mol/kg       |
|                  | Oral rat chronic toxicity (LOAEL) | 1.114    | log mg/kg_bw/day |
|                  | Hepatotoxicity           | Yes              | Yes/No       |
|                  | Skin sensitivity         | No               | Yes/No       |
|                  | T. pyriformis toxicity   | 0.834            | µg/L          |
|                  | Minnow toxicity          | 0.11             | log mM        |
3.4 Identification of target class for compound 1 via target prediction studies

Most of the drug performs its mechanism of action by interacting with the proteins, enzymes and other biomacromolecules. However, many drugs have more than one target. *In-silico* predictions of drug targets based on resemblance with known drugs are very useful to find out the number of targets. Here we observed that 1 has 68% kinases as a target. As shown in Figure 7, compound 1 interacts with a broad range of proteins and enzymes. The detailed information on the target, common name, UniProt ID, ChEMBL ID, target class, probability and known actives in 2D/3D are shown in Table S6 in the Supplementary Information.

![Pie chart showing target classes for compound 1](image)

**Figure 7.** Molecular target predictions for compound 1 obtained from the Swiss target prediction report. The frequency of the target classes (top 25) is depicted in the pie chart.

4. Conclusion

When the entire world fight against the global pandemic of SARS-CoV-2, the major challenge towards the scientists is to annihilate the viral effect. This study is based on the identification of potential drug molecules against the deadly virus from the list of known drugs against SARS-CoV which has a very similar structure of SARS-CoV-2. As the viral drug targets are susceptible to mutations at higher rates, our aim was to investigate the compounds which could bind with multiple targets. From the list of selected organosulfur compounds, we could find compounds that interacted with multiple targets and surprisingly one compound, 1 found to be very efficient on inhibiting all the five SARS-CoV-2 targets namely RdRP, helicase, Mpro, PLpro and Spro with a significant binding affinity. Hence, this compound can be an effective candidate against SARS-CoV-2 for a longer term as it is capable of binding with multiple targets and inhibiting its activity, thus reducing the effect of drug resistance. The physicochemical properties of all the compounds are studied and found that all the compounds are druggable with zero violations from the Lipinski’s rule. The ADMET profile and the target prediction studies were also carried out for the most potential candidate 1 and observed that this can be a promising drug against the SARS-CoV-2. *In-silico* ADMET studies of 1 revealed that it has promising pharmacokinetic properties and does not fall under high-risk chemical
groups. Target prediction analysis also showed that compound 1 exhibits excellent drug-like properties. Based on the results obtained, we look forward to performing the in vitro and in vivo studies to evaluate the potency of compound 1 and other hits as plausible therapeutic agents for the pandemic COVID-19 through multi-target binding.

Acknowledgments. The authors acknowledge financial supports from the Indian Institute of Technology Palakkad and Indian Institute of Technology Indore. This work was supported by the Department of Science and Technology-Science & Engineering Research Board, Govt. of India (ECR/2017/002082 to S. Sadhukhan, and the Ramanujan Fellowship to M. Porel).

Conflicts of interest. The authors declare no conflict of interest.

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Supplementary Information

An in-silico study on selected organosulfur compounds as potential drugs for SARS-CoV-2 infection via binding multiple drug targets

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Figure S1. Best docked conformation and 2D diagram amino acid interaction of SARS-CoV-2 Mpro complexed with the compound 6 (a, b) and 3 (c, d)
Figure S2. Best docked conformation and 2D diagram of amino acid interaction of SARS-CoV-2 PLpro complexed with the compound 6 (a, b) and 7 (c, d)
Figure S3. Best docked conformation and 2D diagram of amino acid interaction of SARS-CoV-2 Spro complexed with the compound 3 (a, b), 2 (c, d) and 7 (e, f)
Figure S4. Best docked conformation and 2D diagram of amino acid interaction of SARS-CoV helicase complexed with the compound 2 (a, b) and 3 (c, d)
Figure S5. Best docked conformation and 2D diagram of amino acid interaction of SARS-CoV-2 RdRp complexed with the compound 2 (a, b) and 3 (c, d)
### Table S1. Predicted absorption properties of organosulfur compounds (2 to 8)

| Properties                              | 2       | 3       | 4       | 5       | 6       | 7       | 8       |
|-----------------------------------------|---------|---------|---------|---------|---------|---------|---------|
| Water solubility log mol/L              | -5.557  | -5.56   | -2.818  | -3.092  | -6.081  | -3.646  | -3.435  |
| Caco2 permeability Log 10^6 cm/s        | 1.711   | 1.687   | 0.601   | 2.109   | 1.472   | 0.035   | 0.938   |
| Human intestinal absorption (%)         | 93.522  | 94.461  | 77.867  | 94.285  | 92.593  | 65.186  | 89.533  |
| Skin permeability log Kp                | -2.522  | -2.533  | -3.113  | -2.403  | -2.638  | -2.735  | -2.806  |
| P-glycoprotein substrate                | Yes     | Yes     | No      | No      | No      | No      | Yes     |
| P-glycoprotein I inhibitor              | No      | No      | No      | No      | Yes     | No      | Yes     |
| P-glycoprotein II inhibitor             | Yes     | Yes     | No      | No      | No      | No      | Yes     |

### Table S2. Predicted distribution properties of organosulfur compounds (2 to 8)

| Properties                              | 2       | 3       | 4       | 5       | 6       | 7       | 8       |
|-----------------------------------------|---------|---------|---------|---------|---------|---------|---------|
| VDss (log L/kg)                         | 0.326   | 0.345   | -0.328  | -0.344  | 0.387   | -1.519  | 1.642   |
| Fraction unbound (human) (Fu)           | 0.039   | 0.044   | 0.477   | 0.251   | 0       | 0.131   | 0.167   |
| BBB permeability (log BB)               | 0.249   | 0.248   | -0.479  | 0.257   | 0.264   | -0.52   | 0.162   |
| CNS permeability (log PS)               | -1.252  | -1.276  | -3.045  | -1.713  | -2.014  | -2.295  | -0.715  |

### Table S3. Predicted metabolism of organosulfur compounds (2 to 8)

| Properties                              | 2       | 3       | 4       | 5       | 6       | 7       | 8       |
|-----------------------------------------|---------|---------|---------|---------|---------|---------|---------|
| CYP2D6 substrate                        | No      | No      | No      | No      | No      | No      | Yes     |
| CYP3A4 substrate                        | Yes     | Yes     | No      | Yes     | No      | Yes     | No      |
| CYP1A2 inhibitor                        | Yes     | Yes     | Yes     | Yes     | Yes     | No      | Yes     |
| CYP2C19 inhibitor                       | Yes     | Yes     | No      | Yes     | Yes     | No      | No      |
| CYP2C9 inhibitor                        | Yes     | Yes     | No      | No      | Yes     | No      | No      |
| CYP2D6 inhibitor                        | No      | No      | No      | No      | No      | No      | Yes     |
| CYP3A4 inhibitor                        | No      | No      | No      | No      | No      | No      | No      |
Table S4. Predicted excretion of organosulfur compounds (2 to 8)

| Properties                        | 2    | 3    | 4    | 5    | 6    | 7    | 8    |
|-----------------------------------|------|------|------|------|------|------|------|
| Total clearance log ml/min/kg     | -0.096 | -0.293 | 0.046 | 0.234 | 0.188 | -0.055 | 0.92 |
| Renal OCT2 substrate              | No   | No   | No   | No   | Yes  | No   | Yes  |

Table S5. Predicted toxicity of organosulfur compounds (2 to 8)

| Properties                        | 2    | 3    | 4    | 5    | 6    | 7    | 8    |
|-----------------------------------|------|------|------|------|------|------|------|
| AMES toxicity                     | Yes  | Yes  | Yes  | No   | No   | No   | Yes  |
| Maximum tolerated dose (Human) (log mg/kg/day) | 0.01 | -0.007 | 0.372 | 0.732 | 0.318 | 0.973 | 0.596 |
| hERG I inhibitor                  | No   | No   | No   | No   | No   | No   | No   |
| hERG II inhibitor                 | Yes  | Yes  | No   | No   | No   | No   | Yes  |
| Oral rat acute toxicity (LD50) (mol/kg) | 2.227 | 2.23 | 2.38 | 2.636 | 3.242 | 2.624 | 2.405 |
| Oral rat chronic toxicity (LOAEL) (log mg/kg bw/day) | 0.947 | 1.047 | 1.081 | 1.281 | 1.06 | 1.927 | 1.683 |
| Hepatotoxicity                    | No   | No   | No   | No   | No   | Yes  | Yes  |
| Skin sensitivity                  | No   | No   | No   | No   | No   | No   | No   |
| T. pyriformis toxicity (µg/L)     | 1.058 | 1.021 | 0.263 | 0.848 | 1.016 | 0.285 | 0.726 |
| Minnow toxicity log mM            | -0.803 | -0.862 | 2.243 | 1.263 | -2.785 | -0.762 | -0.213 |
Table S6. SwissTargetPrediction report obtained using compound 1 as the query molecule

| Target Name | Common name | Uniprot ID | ChEMBL ID | Target Class | Probability* | Known activies (3D/2D) |
|-------------|-------------|------------|-----------|--------------|--------------|------------------------|
| Cyclin- dependent kinase 2/ cyclin A | CDK2/CCNA1/CCNA2 | P24941/78396/20248 | CHEMBL2094128 | Other cytosolic protein | 0.104671941128 | 176 / 0 |
| Cyclin-dependent kinase 2 | CDK2 | P24941 | CHEMBL301 | Kinase | 0.104671941128 | 237 / 0 |
| Dual-specificity tyrosine-phosphorylation regulated kinase 1A | DYRK1A | Q13627 | CHEMBL2292 | Kinase | 0.104671941128 | 145 / 0 |
| Dual specificity protein kinase CLK4 | CLK4 | Q9HAZ1 | CHEMBL4203 | Kinase | 0.104671941128 | 74 / 0 |
| Dual specificity protein kinase CLK1 | CLK1 | P49759 | CHEMBL4224 | Kinase | 0.104671941128 | 88 / 0 |
| Dual specificity protein kinase CLK2 | CLK2 | P49760 | CHEMBL4225 | Kinase | 0.104671941128 | 38 / 0 |
| Dual specificity protein kinase CLK3 | CLK3 | P49761 | CHEMBL4226 | Kinase | 0.104671941128 | 35 / 0 |
| Dual specificity tyrosine-phosphorylation-regulated kinase 1B | DYRK1B | Q9Y463 | CHEMBL5543 | Kinase | 0.104671941128 | 53 / 0 |
| Serine/threonine-protein kinase PLK4 | PLK4 | O00444 | CHEMBL3788 | Kinase | 0.104671941128 | 24 / 0 |
| Mitogen-activated protein kinase kinase kinase kinase 4 | MAP4K4 | O95819 | CHEMBL6166 | Kinase | 0.104671941128 | 16 / 0 |
| P2X purinoceptor 7 | P2RX7 | Q99572 | CHEMBL4805 | Ligand-gated ion channel | 0.104671941128 | 215 / 0 |
| Tyrosine-protein kinase BTK | BTK | Q06187 | CHEMBL5251 | Kinase | 0.104671941128 | 34 / 0 |
| Mineralocorticoid receptor | NR3C2 | P08235 | CHEMBL1994 | Nuclear receptor | 0.104671941128 | 143 / 0 |
| Ribosomal protein S6 kinase 1 | RPS6KB1 | P23443 | CHEMBL4501 | Kinase | 0.104671941128 | 252 / 0 |
| 15-hydroxyprostaglandin dehydrogenase [NAD+] | HPGD | P15428 | CHEMBL1293255 | Enzyme | 0.104671941128 | 59 / 0 |
| Tyrosine-protein kinase receptor FLT3 | FLT3 | Q36888 | CHEMBL1974 | Kinase | 0.104671941128 | 234 / 0 |
| Ribosomal protein S6 kinase alpha 1 | RPS6KA1 | Q15418 | CHEMBL2553 | Kinase | 0.104671941128 | 11 / 0 |
| Rho-associated protein kinase 1 | ROCK1 | Q13464 | CHEMBL3231 | Kinase | 0.104671941128 | 123 / 0 |
| MAP kinase ERK2 | MAPK1 | P28482 | CHEMBL4040 | Kinase | 0.104671941128 | 348 / 0 |
| Melatonin receptor 1A | MTNR1A | P48039 | CHEMBL1945 | Family A G protein-coupled receptor | 0.104671941128 | 506 / 0 |
| Melatonin receptor 1B | MTNR1B | P49286 | CHEMBL1946 | Family A G protein-coupled receptor | 0.104671941128 | 439 / 0 |
| Quinone reductase 2 | NQO2 | P16083 | CHEMBL3959 | Enzyme | 0.104671941128 | 67 / 0 |
| Leucine-rich repeat serine/threonine-protein kinase 2 | LRRK2 | Q55007 | CHEMBL1075104 | Kinase | 0.104671941128 | 114 / 0 |
| Poly [ADP-ribose] polymerase 10 | PARP10 | Q53GL7 | CHEMBL2429708 | Enzyme | 0.104671941128 | 7 / 0 |
| Cyclin-dependent kinase 4 | CDK4 | P11802 | CHEMBL331 | Kinase | 0.104671941128 | 56 / 0 |
| Inosine-5’-monophosphosphate dehydrogenase 2 | IMPDH2 | P12268 | CHEMBL2002 | Oxidoreductase | 0.104671941128 | 168 / 0 |
| Potassium-transporting | ATP4B | P51164 | CHEMBL2095173 | Primary active | 0.104671941128 | 14 / 0 |
| Target | Common name | Uniprot ID | ChEMBL ID | Target Class | Probability* | Known actives (3D/2D) |
|--------|-------------|------------|-----------|--------------|--------------|-----------------------|
| ATPase | ATP4A       | P20648     | ChemBL2815 | Transporter  | 0.104671941128 211 / 0 |
| Nerve growth factor receptor Trk-A | NTRK1     | P04629     | ChemBL3594 | Kinase       | 0.104671941128 373 / 0 |
| Carbonic anhydrase IX | CA9       | Q16790     | ChemBL4158 | Lyase        | 0.104671941128 27 / 0 |
| Fatty acid synthase | FASN      | P49327     | ChemBL1075166 | Transferase  | 0.104671941128 15 / 0 |
| Beta-adrenergic receptor kinase 2 | GRK3      | P35626     | ChemBL1075319 | Voltage-gated ion channel | 0.104671941128 36 / 0 |
| Transient receptor potential cation channel subfamily M member 8 (by homology) | TRPM8     | Q7Z2W7     | ChemBL2111377 | Protease | 0.104671941128 251 / 0 |
| Gamma-secretase | PSEN2      | P49810     | ChemBL2094135 | Protease | 0.104671941128 42 / 0 |
| CDC7/DBF4 (Cell division cycle 7-related protein kinase/Activator of S phase kinase) | DBF4      | Q9UBU7     | ChemBL2111377 | Kinase | 0.104671941128 251 / 0 |
| Myeloperoxidase | MPO       | P05164     | ChemBL2439 | Enzyme | 0.104671941128 20 / 0 |
| Dual specificity mitogen-activated protein kinase kinase 1 | MAP2K1   | Q02750     | ChemBL3587 | Kinase | 0.104671941128 45 / 0 |
| G-protein coupled receptor kinase 2 | GRK2      | P25098     | ChemBL4079 | Kinase | 0.104671941128 57 / 0 |
| Dopamine transporter (by homology) | SLC6A3    | Q01959     | ChemBL238 | Electrochemical transporter | 0.104671941128 91 / 0 |
| Phosphodiesterase 4B | PDE4B     | Q07343     | ChemBL275 | Phosphodiesterase | 0.104671941128 172 / 0 |
| Neuropeptide Y receptor type 5 | NPY5R     | Q15761     | ChemBL4561 | Family A G protein-coupled receptor | 0.104671941128 165 / 0 |
| Dipeptidyl peptidase IV | DPP4      | P27487     | ChemBL284 | Protease | 0.104671941128 128 / 0 |
| Vanilloid receptor | TRPV1     | Q8NER1     | ChemBL4794 | Voltage-gated ion channel | 0.104671941128 370 / 0 |
| Protein kinase C gamma (by homology) | PRKCG     | P05129     | ChemBL2938 | Kinase | 0.104671941128 36 / 0 |
| MAP kinase signal-integrating kinase 2 | MKNK2     | Q9HBH9     | ChemBL4204 | Kinase | 0.104671941128 39 / 0 |
| MAP kinase-interacting serine/threonine-protein kinase MNK1 | MKNK1     | Q9UBU5     | ChemBL4718 | Kinase | 0.104671941128 22 / 0 |
| Glucocorticoid receptor | NR3C1     | P04150     | ChemBL2034 | Nuclear receptor | 0.104671941128 189 / 0 |
| Serine/threonine-protein kinase mTOR | MTOR     | P42345     | ChemBL2842 | Kinase | 0.104671941128 365 / 0 |
| Serine/threonine-protein kinase PLK2 | PLK2      | Q9NYY3     | ChemBL5938 | Kinase | 0.104671941128 21 / 0 |
| Cyclin-dependent kinase 2/cyclin E1 | CCNE1/CDK2 | P24864     | ChemBL1907605 | Kinase | 0.104671941128 80 / 0 |
| PI3-kinase p110-delta subunit | PIK3CD    | O00329     | ChemBL3130 | Enzyme | 0.104671941128 259 / 0 |
| PI3-kinase p110-beta subunit | PIK3CB    | P42338     | ChemBL3145 | Enzyme | 0.104671941128 189 / 0 |
| PI3-kinase p110-alpha subunit | PIK3CA    | P42336     | ChemBL4005 | Enzyme | 0.104671941128 562 / 0 |
| NAD-dependent deacetylase sirtuin 3 | SIRT3     | Q9NTG7     | ChemBL4461 | Eraser | 0.104671941128 73 / 0 |
| Target Common name | Uniprot ID | ChEMBL ID | Target Class | Probability | Known actives (3D/2D) |
|---------------------|------------|-----------|---------------|--------------|-----------------------|
| NAD-dependent deacetylase sirtuin 2 | SIRT2 | Q8IXJ6 | CHEMBL4462 | Eraser | 0.104671941128 148 / 0 |
| NAD-dependent deacetylase sirtuin 1 | SIRT1 | Q96EB6 | CHEMBL4506 | Eraser | 0.104671941128 69 / 0 |
| Progesterone receptor | PGR | P06401 | CHEMBL208 | Nuclear receptor | 0.104671941128 182 / 0 |
| Serine/threonine-protein kinase PIM1 | PIM1 | P11309 | CHEMBL2147 | Kinase | 0.104671941128 179 / 0 |
| 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 | PFKFB3 | Q16875 | CHEMBL2331053 | Enzyme | 0.104671941128 205 / 0 |
| Serine/threonine-protein kinase PIM2 | PIM2 | Q9P1W9 | CHEMBL4523 | Kinase | 0.104671941128 97 / 0 |
| Purinergic receptor P2Y1 | P2RY1 | P47900 | CHEMBL4315 | Family A G protein-coupled receptor | 0.104671941128 11 / 0 |
| Nitric oxide synthase, inducible | NOS2 | P35228 | CHEMBL4481 | Enzyme | 0.104671941128 105 / 0 |
| Epidermal growth factor receptor erbB1 | EGFR | P00533 | CHEMBL203 | Kinase | 0.104671941128 610 / 0 |
| ALK tyrosine kinase receptor | ALK | Q9UM73 | CHEMBL4247 | Kinase | 0.104671941128 85 / 0 |
| Translocator protein (by homology) | TSPO | P30536 | CHEMBL5742 | Membrane receptor | 0.104671941128 156 / 0 |
| Hepatocyte growth factor receptor | MET | P08581 | CHEMBL3717 | Kinase | 0.104671941128 472 / 0 |
| Hydroxyacid oxidase 2 (by homology) | HAO2 | Q9NYQ3 | CHEMBL2169732 | Enzyme | 0.104671941128 1 / 0 |
| Neprilysin (by homology) | MME | P08473 | CHEMBL1944 | Protease | 0.104671941128 44 / 0 |
| Cathepsin (B and K) | CTSB | P07858 | CHEMBL4072 | Protease | 0.104671941128 121 / 0 |
| MAP kinase-activated protein kinase 2 | MAPKAPK2 | P49137 | CHEMBL2208 | Kinase | 0.104671941128 114 / 0 |
| Glycogen synthase kinase-3 beta | GSK3B | P49841 | CHEMBL262 | Kinase | 0.104671941128 521 / 0 |
| MAP kinase ERK1 (by homology) | MAPK3 | P27361 | CHEMBL3385 | Kinase | 0.104671941128 47 / 0 |
| Ribosomal protein S6 kinase alpha 5 | RPS6KA5 | O75582 | CHEMBL4237 | Kinase | 0.104671941128 25 / 0 |
| CDC7/DBF4 (Cell division cycle 7-related protein kinase/Activator of S phase kinase) | CDC7 | O00311 | CHEMBL5443 | Kinase | 0.104671941128 132 / 0 |
| Heat shock factor protein 1 | HSF1 | Q00613 | CHEMBL5869 | Other cytosolic protein | 0.104671941128 2 / 0 |
| Matrix metalloproteinase 9 | MMP9 | P14780 | CHEMBL321 | Protease | 0.104671941128 362 / 0 |
| Branched-chain-amine transferase, mitochondrial | BCAT2 | O15382 | CHEMBL3616354 | Transferase | 0.104671941128 23 / 0 |
| Thyrotopin-releasing hormone receptor (by homology) | TRHR | P34981 | CHEMBL1810 | Family A G protein-coupled receptor | 0.104671941128 29 / 0 |
| Tyrosine-protein kinase ABL | ABL1 | P00519 | CHEMBL1862 | Kinase | 0.104671941128 254 / 0 |
| Interleukin-8 receptor B | CXCR2 | P25025 | CHEMBL2434 | Family A G protein-coupled receptor | 0.104671941128 59 / 0 |
| Tyrosine-protein kinase SRC | SRC | P12931 | CHEMBL267 | Kinase | 0.104671941128 301 / 0 |
| Protein kinase C alpha | PRKCA | P17252 | CHEMBL299 | Kinase | 0.104671941128 38 / 0 |
| Target Common name | Uniprot ID | ChEMBL ID | Target Class | Probability | Known actives (3D/2D) |
|-------------------|------------|-----------|--------------|-------------|-----------------------|
| Cyclin-dependent kinase 1 | CDK1 | P06493 | CHEMBL308 | Kinase | 0.104671941128 | 116 / 0 |
| Vascular endothelial growth factor receptor 1 | FLT1 | P17948 | CHEMBL1868 | Kinase | 0.104671941128 | 87 / 0 |
| Androgen Receptor | AR | P10275 | CHEMBL1871 | Nuclear receptor | 0.104671941128 | 185 / 0 |
| Sodium/ glucose cotransporter 1 | SLC5A1 | P13866 | CHEMBL4979 | Electrochemical transporter | 0.104671941128 | 145 / 0 |
| Cyclin-dependent kinase 2/ cyclin E | CCNE2 CDK2 CCNE1 | O96020 P24941 P24864 | CHEMBL2094126 | Other cytosolic protein | 0.104671941128 | 103 / 0 |
| Cyclin-dependent kinase 1/ cyclin B | CCNB3 CDK1 CCNB1 CCNB2 | Q8WWL7 P06493 P14635 O95067 | CHEMBL2094127 | Other cytosolic protein | 0.104671941128 | 72 / 0 |
| Tyrosine- protein kinase JAK2 | JAK2 | O60674 | CHEMBL2971 | Kinase | 0.104671941128 | 384 / 0 |
| PI3-kinase p110-gamma subunit | PIK3CG | P48736 | CHEMBL3267 | Enzyme | 0.104671941128 | 295 / 0 |
| Matrix metalloproteinase 2 | MMP2 | P08253 | CHEMBL333 | Protease | 0.104671941128 | 348 / 0 |
| Serotonin 6 (5-HT6) receptor | HTR6 | P50406 | CHEMBL3371 | Family A G protein-coupled receptor | 0.104671941128 | 71 / 0 |
| 5-lipoxygenase activating protein | ALOX5AP | P20292 | CHEMBL4550 | Other cytosolic protein | 0.104671941128 | 528 / 0 |
| Tyrosine- protein kinase JAK3 | JAK3 | P52333 | CHEMBL2148 | Kinase | 0.104671941128 | 203 / 0 |
| Tyrosine- protein kinase JAK1 | JAK1 | P23458 | CHEMBL2835 | Kinase | 0.104671941128 | 237 / 0 |
| Serine/ threonine-protein kinase PLK1 | PLK1 | P53350 | CHEMBL3024 | Kinase | 0.104671941128 | 102 / 0 |
| Melanin-concentrating hormone receptor 1 | MCHR1 | Q99705 | CHEMBL344 | Family A G protein-coupled receptor | 0.104671941128 | 24 / 0 |
| ADAM17 | ADAM17 | P78536 | CHEMBL3706 | Protease | 0.104671941128 | 168 / 0 |
| UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit | OGT | O15294 | CHEMBL5955 | Enzyme | 0.104671941128 | 7 / 0 |
| Phospholipase A-2-activating protein | PLAA | Q9Y263 | CHEMBL6114 | Unclassified protein | 0.104671941128 | 11 / 0 |
| Matrix metalloproteinase 13 | MMP13 | P45452 | CHEMBL280 | Protease | 0.104671941128 | 263 / 0 |