



## Research Article

# Bioinformatics Approach for COVID-19 (Coronavirus) Disease Prevention Treatment and Drug Validation

 Shruti Mishra,<sup>1,2</sup>  Prashant Ankur Jain,<sup>2</sup>  Shmmon Ahmad,<sup>3</sup>  Shivam Mishra<sup>4</sup>

<sup>1</sup>Glocal School of Life Allied Health Sciences, Glocal University, Saharanpur, India

<sup>2</sup>Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad, India

<sup>3</sup>Glocal School of Pharmacy, Glocal University, Saharanpur, India

<sup>4</sup>S. S. Khanna Girls Degree College, University of Allahabad, India

### Abstract

**Objectives:** To find out the effect of Hydroxychloroquine on COVID special protease.

**Methods:** PyMOL software used to find out all possible rotameters of residue and their probability. AutoDock software used to calculate and predict the interaction of molecules.

**Results:** Hydrochloroquine Bind and release over Protease 6y84 and 7buy and controlled their action in body.

**Conclusion:** Drug designing and docking is helpful for specific disease. It helps us in predicting the intermolecular frame work formed between a protein or a small molecule.

**Keywords:** Autodock, Chimera, COVID 19, SARS, PDB, PyMol

**Cite This Article:** Mishra S, Jain PA, Ahmad S, Mishra S. Bioinformatics Approach for COVID-19 (Coronavirus) Disease Prevention Treatment and Drug Validation. *EJMO* 2020;4(3):234–238.

The novel coronavirus 2019 (nCoV) has caused a global health crisis by causing coronavirus disease-19 pandemic in the human population. In December, 2019, a local outbreak of pneumonia of initially unknown cause was detected in Wuhan (Hubei, China), and was quickly determined to be caused by a novel corona virus, namely severe acute respiratory syndrome called corona virus, (SARS-CoV-2).<sup>[1–3]</sup> As of 22 May 2020, almost all countries and many territories have reported corona cases. Around the world wide over 5198307 confirmed cases and 334689 deaths report due to COVID-19.<sup>[4]</sup> In response to this public health emergency, Center for Systems Science and Engineering (CSSE) at Johns Hopkins University, Baltimore, MD, USA, developed an online interactive dashboard, hosted by the to visualize and track reported cases of corona virus disease

2019 (COVID-19) in real time.<sup>[5–7]</sup> On dated Jan 22, 2020 the dashboard, first shared publicly, illustrates the location and number of confirmed COVID-19 cases, deaths, and recoveries for all affected countries. Dashboard was developed to provide researchers, public health authorities, and the general public with a user-friendly tool to track the outbreak.<sup>[8]</sup> <sup>[9]</sup> All information collected and displayed are made freely available, initially through GitHub repository, and Google Sheets along with the feature layers of the dashboard, which are now included in the Esri Living Atlas (Fig. 1).<sup>[10]</sup>

A novel corona virus has resulted in an ongoing outbreak of viral pneumonia in China.<sup>[1–3]</sup> Person-to-person transmission has been demonstrated,<sup>1</sup> but, to our knowledge, transmission of the novel corona virus that causes corona virus disease 2019 (Fig. 2).

**Address for correspondence:** Shruti Mishra, MD. Glocal School of Life Allied Health Sciences, Glocal University, Mirzapur Pole, Delhi-Yamunotri State Highway 57, Saharanpur, India

**Phone:** +91 8567846738 **E-mail:** shrutimishra4january@gmail.com

**Submitted Date:** June 02, 2020 **Accepted Date:** July 08, 2020 **Available Online Date:** July 16, 2020

©Copyright 2020 by Eurasian Journal of Medicine and Oncology - Available online at [www.ejmo.org](http://www.ejmo.org)

**OPEN ACCESS** This work is licensed under a Creative Commons Attribution-NonCommercial 4.0 International License.



Corona virus from an asymptomatic carrier with normal chest computed tomography (CT) findings has not been reported. An outbreak of 2019 novel corona virus diseases (COVID-19) in Wuhan, Hubei Province, China has spread quickly nationwide.

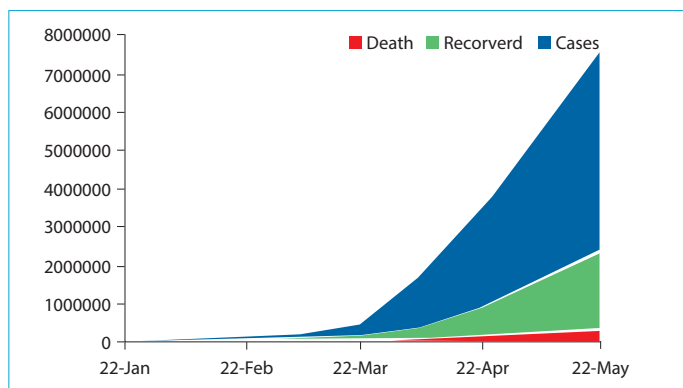
Here, results of a descriptive report, exploratory analysis of all cases diagnosed as of April 11, 2020. All COVID-19 cases reported through April 11, 2020 were found from China's Infectious.<sup>[12]</sup>

Disease Information System. Analyses included the following:

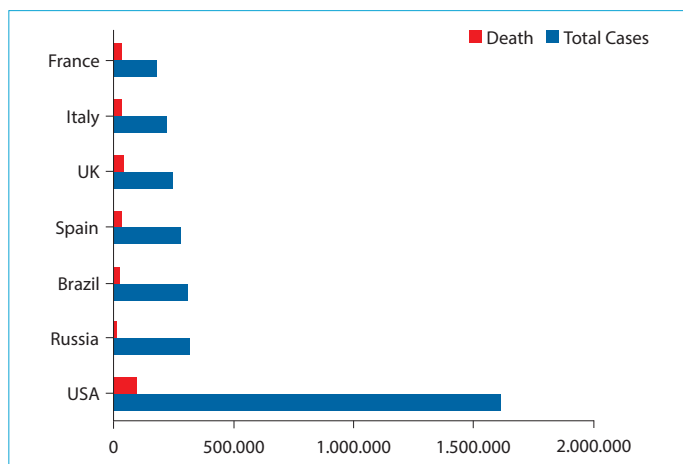
1. Calculation of case fatality and mortality rates,
2. Geo-temporal analysis of viral spread,
3. Epidemiological curve construction,
4. summary of patient characteristics,
5. Examination of age distributions and sex ratios.
6. Subgroup analysis.<sup>[9]</sup>

## Methods

PyMOL shows all possible rotamers of the residue and their



**Figure 1.** Globally COVID-19 total Cases, death and recovered.



**Figure 2.** Country wise COVID 19 number of cases and death.

probabilities.

The most likely rotamer of amino acid has a probability of 11.9% and the probability for the second and third most common rotamer. Thus, how many distinct rotamers exist for other amino acid finding, PyMOL shows the possible rotamers and action of two different conformation for species for this residue and take its surroundings into account for its probabilities. Every rotamer of arginine has a lot of red which indicates that arginine is probably not a good mutation in this position.<sup>[13]</sup> To avoid any of these mutations click clear. The mutagenesis wizard is very useful to explore possible positions of residues. And then go back to "No Mutation" and explore the various rotamers for several protein and amino acid.

The Open Babel project, a full-featured open chemical toolbox, designed to speak the many different representations of chemical data.<sup>[11]</sup> It allows everyone to search, convert, and analyze, or store data from molecular modeling, chemistry, solid-state materials, biochemistry, or related areas.<sup>[12]</sup> It provides both opportunity ready to use programs as well as a complete work, extensible and valid program tool kit for developing chemo-informatics software and programming. Open Babel implements a sophisticated and canonicalization algorithm that can operate molecules or molecular fragments. The atom symmetry classes are the initial graph invariants and encode topological and chemical properties.<sup>[12]</sup> A cooperative labeling procedure is used to investigate the automorphic permutations to find the canonical code.

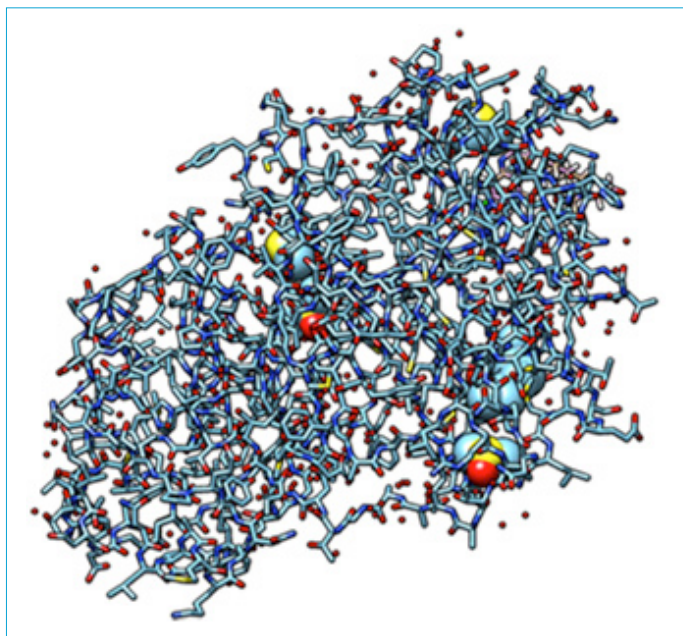
AutoDock software calculates and predicts the interaction between the ligand molecule and protein molecule based on predefined parameters. To be precise, the interactions between the molecules will be calculated at a user specified region in the protein, This region can be known by users, using the unique Grip map option. Ultimately,<sup>[13, 14]</sup> the software predicts the interaction and binding energy of the ligand molecule and the amino acids present within the GridBox only. Thus setting, the GridBox at the binding site or active site or other essential regions of the protein is very much important. Before executing the AutoDock. nce and AutoDock4.exe is successfully executed. The result will be given as the ten best confirmations. These can be viewed in the analyze options.<sup>[15, 16]</sup> The confirmations can be viewed in the order of their free energy binding, by choosing the Play, ranked by energy option. Analyzing the result takes a few steps that is given as a graphical representation. The panels a, b, c and d will open one after the other, in the same order as given. The ten conformations can be viewed by changing the conformations number in the panel A. The interaction energy of the given conforma-

tion can be viewed in the panel D. The number of hydrogen bonds formed between the ligand and protein can be viewed in the panel C.<sup>[13]</sup>

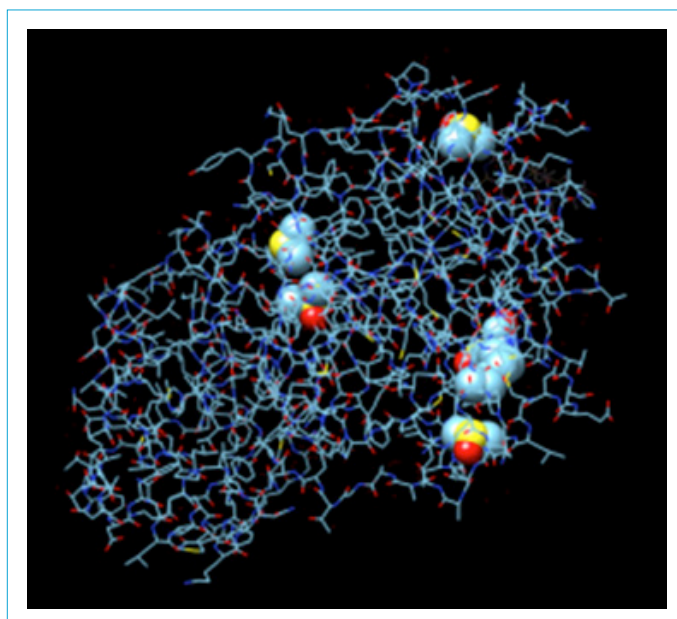
UCSF Chimera offers 3-D visualization of molecular structures and related data, including density maps, supramolecular assemblies, molecular dynamics trajectories, and multiple sequence alignments. The user can also create images and animations for publication and presentation. Besides supporting core visualization, the software is specifically designed for extensibility, to allow outside developers to incorporate new desirable functions.<sup>[18, 19]</sup> Current extensions include Multiscale Models to visualize large-scale molecular assemblies like viral coats, ViewDock to screen docked ligand orientations, Volume Viewer to visualize density maps, and Multalign Viewer to display sequence alignments, with crosstalk to any associated structures.<sup>[20]</sup>

## Result and Discussion

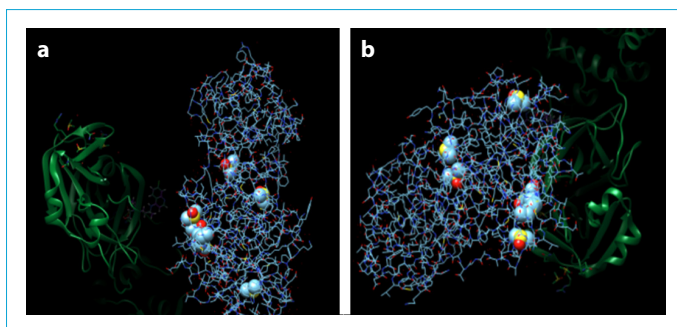
The mechanism of identifying a target synthesizing an active compound with suitable characteristic like minimal toxicity high bioavailability, cost effective and process of synthesis etc. And finally, a target is identified which plays a key role in process of the disease cure and identification. So, drug designing and docking is helpful for specific disease. Molecular docking helps us in predicting the inter molecular framework formed between a protein and a small molecule or a protein and protein and suggest the binding mode responsible for the inhibition of specific protein.



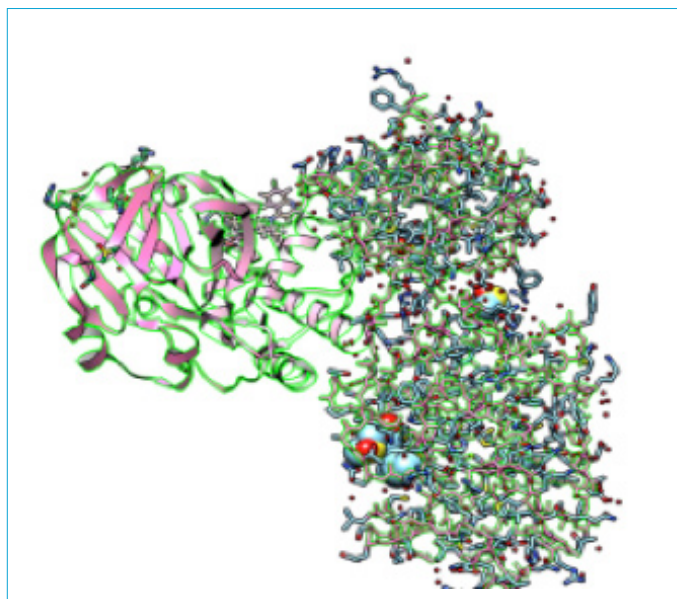
**Figure 3.** Interaction between PDB ID 6Y84 or 7BUY (COVID 19 Protease) and Hydroxychloroquine (2,4,7 chloroquinolin-4-yl) amino pentyl ethyl amino ethanol.



**Figure 4.** Binding of 6Y84 and 7 Hydroxychloroquine.

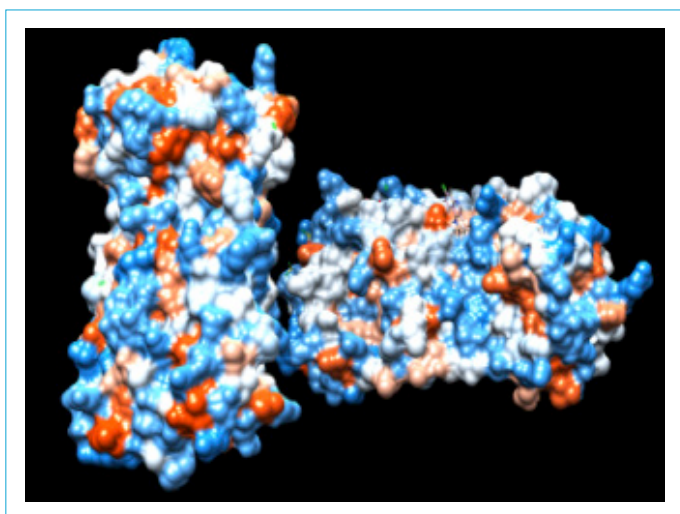


**Figure 5 (a, b).** Super impose, binding and coiling all together in Auto Docking.

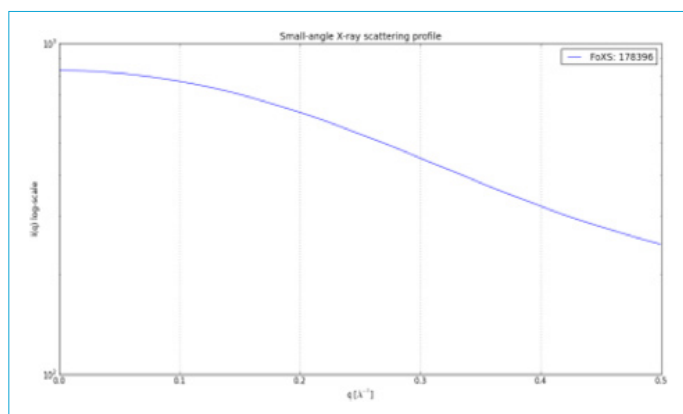


**Figure 6.** Full effect and inhibition process of 6Y84 COVID 19 protease and 7 Hydroxychloroquine drug action.





**Figure 7.** Working and effect of hydroxychloroquine.



**Figure 8.** Graphical representation of COVID 19 protease and hydroxychloroquine.

## Conclusion

As we all know COVID 19 now a days very severe infectious disease so we try to apply bioinformatics approach to validate and diagnosis of drug Hydroxychloroquine to overcome the effect of COVID 19 corona virus and try to find out the working effect and inhibition of Hydroxychloroquine drug and how its work over corona virus 6Y84 and 7 buy protease and after that its working in body and fight against COVID 19. Hydroxychloroquine bind and released over protease 6y84 and 7buy and control their action in body. We all very well know that proper care, sanitization and social distancing is a best way to cure our self from COVID-19.

## Disclosures

**Ethics Committee Approval:** The study was approved by the Local Ethics Committee.

**Peer-review:** Externally peer-reviewed.

**Conflict of Interest:** None declared.

**Authorship Contributions:** Concept – S.M., P.A.J.; Design – S.A., S.M.; Supervision – P.A.J.; Materials – S.M., S.A.; Data collection &/ or processing – S.A.; Analysis and/or interpretation – S.M.; Literature search – S.M.; Writing – S.A., S.M.; Critical review – P.A.J.

## References

- Ahmad S, Hafeez A, Siddqui SA, Ahmad M, Mishra S. A Review of COVID-19 (Coronavirus Disease-2019) Diagnosis, Treatments and Prevention. *EJMO* 2020;4:116–25.
- Singhal T. A Review of Coronavirus Disease-2019 (COVID-19). *Indian J Pediatr* 2020;87:281–6.
- Cascella M, Rajnik M, Cuomo A, et al. Features, Evaluation and Treatment Coronavirus (COVID-19) [Updated 2020 Apr 6]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2020 Jan-. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK554776/>
- WorldMeters, <https://www.worldometers.info/coronavirus/> (Accessed May 22, 2020).
- Johns Hopkins University, COVID-19 Map FAQ, <https://coronavirus.jhu.edu/map-faq> (Accessed May 23, 2020).
- WHO, Coronavirus disease 2019 (COVID-19) situation reports. <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports> (Accessed Feb 17, 2020).
- Universal Community Health Center, Coronavirus COVID-19 Global Cases. <https://www.uchcla.org/post/coronavirus-covid-19-global-cases> (Accessed May 23, 2020).
- DocPlayer.net. Pymol Tutorial. Go to This is the Protein Data Bank (PDB) - a database for protein structures. <http://docplayer.net/34862614-Pymol-tutorial-go-to-this-is-the-protein-data-bank-pdb-a-database-for-protein-structures.html> (Accessed May 23, 2020).
- Epidemiology Working Group for NCIP Epidemic Response, Chinese Center for Disease Control and Prevention. *Zhonghua Liu Xing Bing Xue Za Zhi = Zhonghua Liuxingbingxue Zazhi*, vol. 41, no. 2, 2020, pp. 145-151.
- Dong E, Du H, Gardner L. An interactive web-based dashboard to track COVID-19 in real time. *Lancet Infect Dis* 2020;20:533–4.
- Pirhadi S, Sunseri J, Koes DR. Open source molecular modeling. *J Mol Graph Model* 2016;69:127–43.
- O'Boyle, N.M., Banck, M., James, C.A. et al. Open Babel: An open chemical toolbox. *J Cheminform* 3, 33 (2011). <https://doi.org/10.1186/1758-2946-3-33>
- Meng XY, Zhang HX, Mezei M, Cui M. Molecular docking: a powerful approach for structure-based drug discovery. *Curr Comput Aided Drug Des* 2011;7:146–57.
- Forli S, Huey R, Pique ME, Sanner MF, Goodsell DS, Olson AJ. Computational protein-ligand docking and virtual drug screening with the AutoDock suite. *Nat Protoc* 2016;11:905–19.

15. Meng XY, Zhang HX, Mezei M, Cui M. Molecular docking: a powerful approach for structure-based drug discovery. *Curr Comput Aided Drug Des* 2011;7:146–57.
16. Taoufik, A, Lamchouri, F., Senhaji, S., Toufik, H., (2019). Molecular docking, ADME/Tox prediction, and in vitro study of the cell growth inhibitory activity of five  $\beta$ -carboline alkaloids. *Structural Chemistry*. 30. 10.1007/s11224-019-01308-x.
17. Rizvi SM, Shakil S, Haneef M. A simple click by click protocol to perform docking: AutoDock 4.2 made easy for non-bioinformaticians. *EXCLI J* 2013;12:831–57.
18. O'Donoghue SI, Goodsell DS, Frangakis AS, Jossinet F, Laskowski RA, Nilges M, Saibil HR, Schafferhans A, Wade RC, Westhof E, Olson AJ. Visualization of macromolecular structures. *Nat Methods* 2010;7:S42–55.
19. Pettersen E.F, Toddard T.D, Huang C.C, UCSF Chimera—A Visualization System for Exploratory, Research and Analysis, *Journal of Computational Chemistry* 25;1606–12.
20. McCafferty C.L, Verbeke E.J.V, *Structural Biology in the Multi-Omics Era*. ACS Publications. <https://pubs.acs.org/doi/10.1021/acs.jcim.9b01164#> (Accessed May 23, 2020).