Searching inhibitors for the potent COVID-19 RdRp/ ACE2/ SGp through molecular docking and other computational approaches

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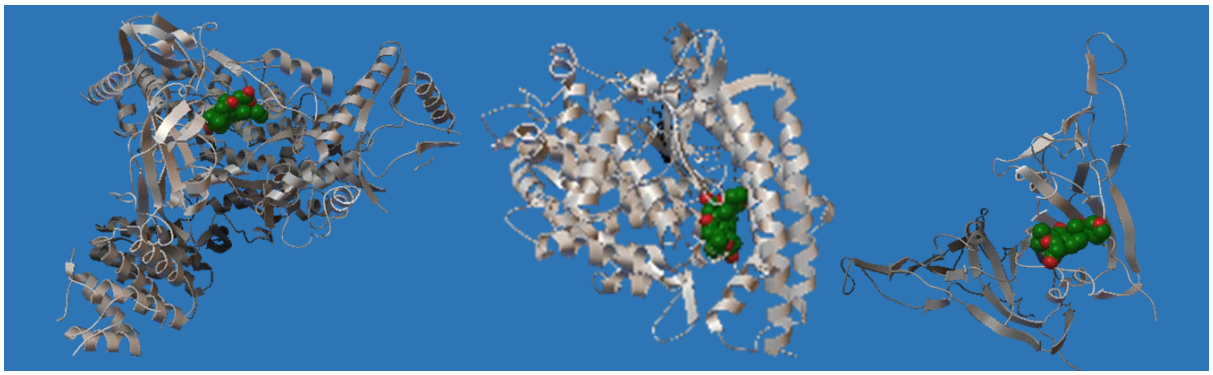
Objective of the research

After the first infected patient identified in Wuhan, China in December, 2019 with the severe acute respiratory syndrome coronavirus 2 with a new name COVID-19 (popularly known as coronavirus disease 2019), the disease spread globally due to high contagious nature and became an ongoing pandemic. Also, the lack of vaccines and efficacious drugs to treat infected patients is a great problem to cope this pandemic. The approved drugs for other health problems are applied with the hope to treat the infected patients and also simultaneous research are going on to develop novel drugs/vaccines against COVID-19. With our available computational resources, we are trying to identify the therapeutically potent of available drugs along with novel molecules present in plants/fruits against the COVID-19. In our recent results, we have found molecules that showed better dock score in compared to the hydroxychloroquine claimed to be effective against COVID-19.

Some docking images:



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