Abstract

Introduction:

The first outbreak of Covid-19 virus has caused serious health concerns worldwide. The lack of diagnoses or vaccines continues to be a challenge, accelerating the discovery of new therapeutic molecules. Computer-aided design has helped speed up the process of drug discovery and development by reducing costs and time.

Methods:

First, the coordinates of the junction hole in the RBD virus with the code PDB 6M17 were identified using DeepSite and sent to the LIGANN server to generate a decoding molecular library. High-performance screening for new molecules binding to the RBD virus was performed using BindScope, and high-binding molecules were selected for further investigation. The CB-Dock server is used to precisely connect the selected molecules to provide the complete spike, viral component and ACE 2 receptor. Drug similarities of these new molecules were identified using Swiss-ADME, and molecules that show high or close binding to RBD. Analyzes of virus-protein structural changes (human SARS-CoV-2 receptor spike-ACE 2) were performed via PatchDock and FireDock servers.

Results:

Based on the existing library and docking, 4 fragments were obtained that were joined at the junction with a suitable bond. How these fragments are connected The fragments have been investigated and linked, and the docking results show that the right linker can lead to the formation of the right compounds with the right bond energy. Among the linked compounds, two better links were introduced with the final compounds.

Conclusion:

Finding new compounds with medicinal properties through the development of small parts can be considered as a way to discover a new drug. Therefore, the results of virtual screening of the proposed fragments through the neural network and docking them through the cavity-receptor method turned into finding a fragment with a suitable bond. Finally, with the development of these fragments, compounds based on basic drug similarity filters were proposed. After examining the structural changes of the receptor after the developed compounds, it can be concluded that the proposed compounds have the ability to cause structural changes after attachment to the active areas of the receptor.

Keywords:

covid19 , virtual screening , spike protein , fragment library , FBDD .