Molecular Docking Analysis of Novel SARS-CoV-2 Inhibitors Based on Structural Homology

Han, Jonah (School: Independence High School)

The recent COVID-19 pandemic caused by SARS-CoV-2 has threatened billions of lives across the globe and demands immediate attention. Although vaccines have recently started deployment, there exists a lack of efficacious drugs, which may be preferred under certain situations or threats. This study presents a structural homological analysis of the SARS-CoV-2 RNA-Dependent RNA Polymerase (RdRp) in order to identify novel inhibitors. The RdRp structures primarily comprise the viral nonstructural protein nsp12, which was screened for structures that are physically similar. A number of inhibitors for these similar structures were identified, docked, and analyzed for binding affinity in the active site of the RdRp. 3 inhibitors (Compound 5, Compound 10, and Compound 15) exhibited significantly low Gibbs free energy values (when compared to currently approved FDA drugs like Remdesivir), thus indicating binding affinity and strength. Although these compounds require further testing and verification, they present a promising potential drug for the treatment of COVID-19. Further research could explore correlations between protein similarity and viral behavior, as well as the drugs that could be used to inhibit them. This research could also be extended by in vitro or in vivo verification of the properties discussed, in addition to a more expansive search for drug candidates.

Awards Won: