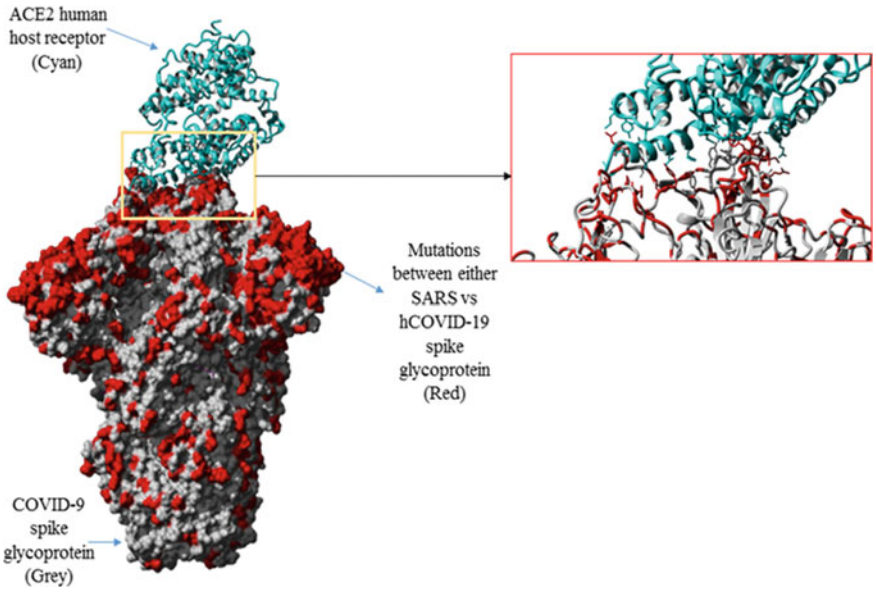

Fig. 7.3 Superimposed structure of viral spike glycoprotein of COVID-19 (grey) and SARS CoV with ACE2 (cyan) and a complex structure also showing mutational site (red) either in COVID-19 or SARS CoV [17]

7.4 Discussion

The ongoing COVID-19 pandemic makes us painfully realize that our current situation is only based on isolation from society and maintain hygienic condition to protect us from this unpredictable behavior of this virus. Earlier the outbreaks of SARS CoV in 2003 and MERS-CoV in 2012 has provide us extensive research efforts, but unfortunately there were no any drug which protect us from any type zoonotic coronavirus. Earlier, strains of these viruses were not much highly spreadable and unable to infect worldwide. But, this virus has very fluctuating and unstable strain due to their epitopic nature of the virus that make a challenges to worldwide scientific community to develop antiviral therapeutics. Due to this nature of virus earlier there was no any prototype of drug for coronavirus was progressed. After 17 years of SARS CoV epidemic and current COVID-19, emerging coronaviruses are very similar with their infection site. Therefore, our approach based on systematic comparison with these two viruses and associated mutation.

In this study, we presented a bioinformatics based methodology for systematic interaction and identification of similarity between COVID-19 and SARS CoV viral spike protein in association with ACE2 receptor binding domain. The host ACE2 has been proved by many studies to be the specific receptor for the Spike RBD of SARS-CoV [18]. The latest research shows that the host receptor of COVID-19 is consistent with SARS-CoV, exhibiting that the Spike RBD sequence of COVID-19