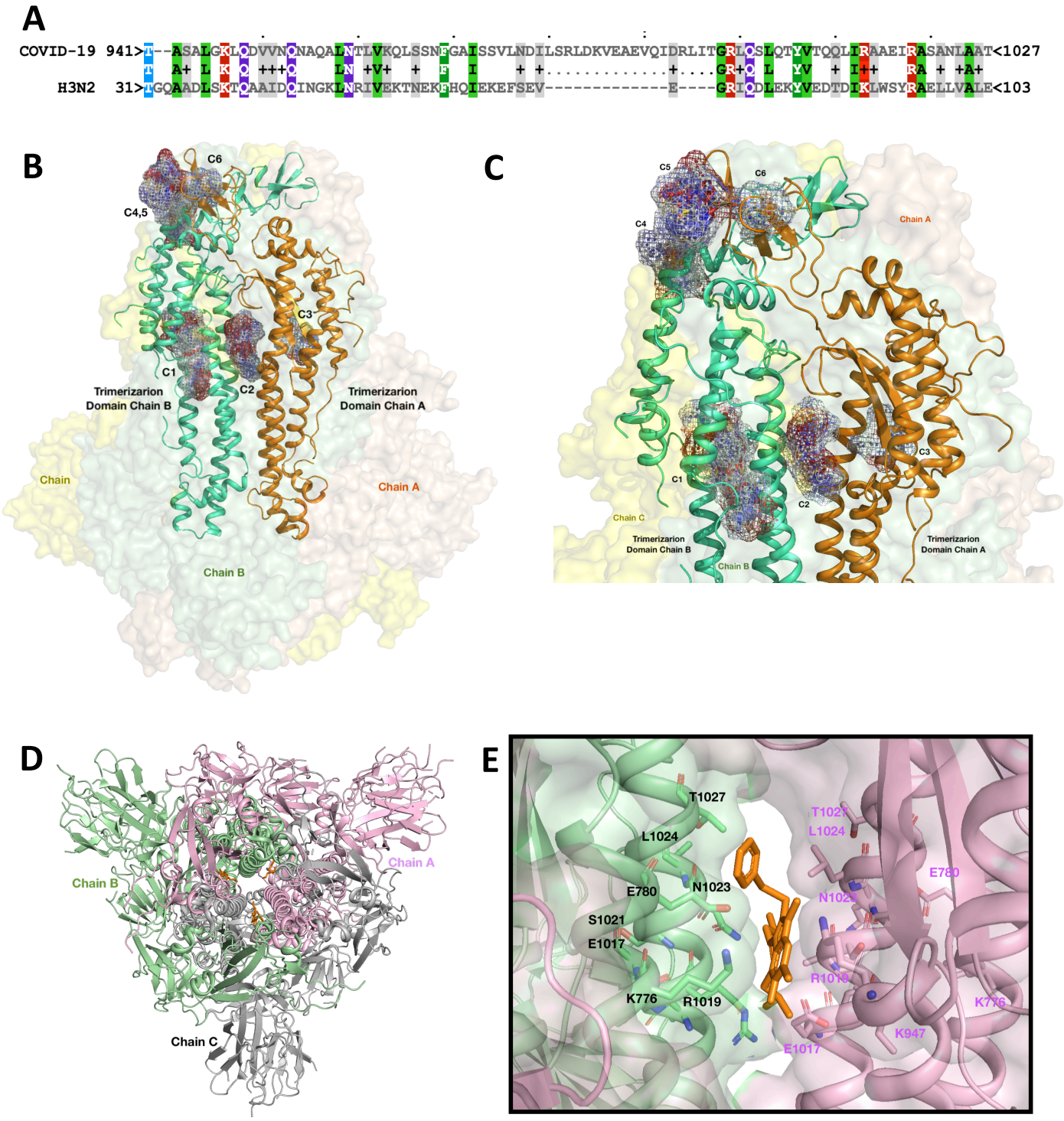

Figure S1: (A) Sequence alignment of Arbidol binding region of COVID-19 spike glycoprotein and H3N2 HA protein. Identical residues are coloured and similar residues are shaded in grey and indicated with + sign. **(B) Surface and cartoon structure of COVID-19 spike glycoprotein showing potential Arbidol binding sites as predicted.** The six unique Arbidol binding predicted clusters are shown is sticks and mesh, and labelled C1 - C6. The trimerization S2 domain region of Chain A and Chain B are shown in the orange and green cartoon, respectively. The structure of spike glycol protein homotrimer is shown in semi-transparent surface model and individual monomers (Chain A-C) are coloured accordingly. **(C)** Closer and tilt view of (A), colour coding and labelling are the same as above. **(D)** Bottom view of 3D structure of Arbidol in complex with COVID-19 spike glycoprotein (Refer. Fig. 1B). (Chain A-C coloured in pink, green and grey respectively) and Arbidol is shown as orange sticks. **(E)** Transparent surface model showing the Arbidol-binding site and the key side chain residues (labelled accordingly) of spike glycoprotein involved in the interaction with Arbidol (orange sticks).