Supplementary information, Figure S7

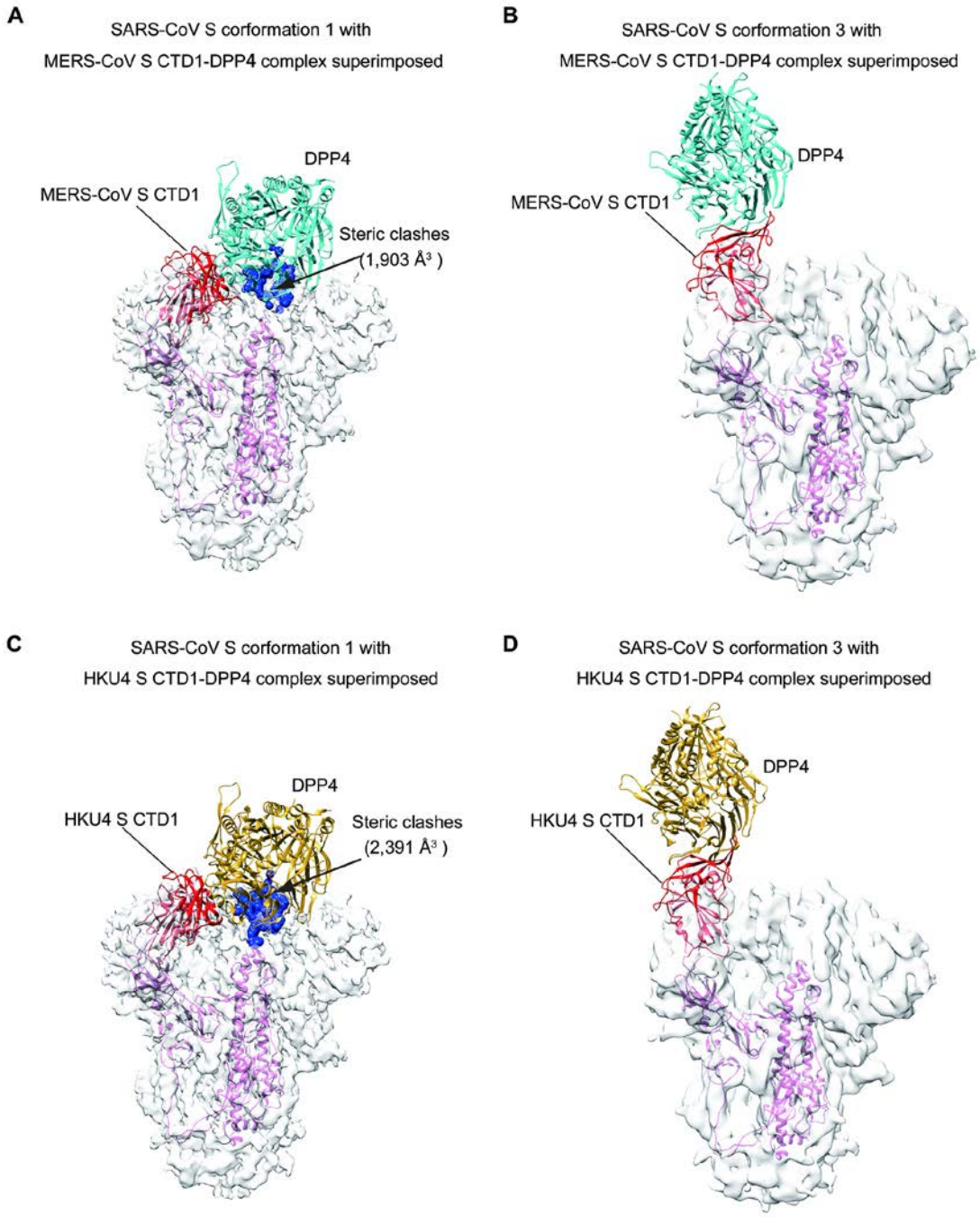

Figure S7 Structural modeling showing the "binding" of the MERS-CoV and HKU4 receptor to the S trimers. (A) Fitting of the MERS-CoV CTD1-DPP4 complex crystal structure into in the "down" conformation CTD1 of the SARS-CoV S density map resulted in steric clashes between the "bound" DPP4 and the S trimer. (B)

Fitting of the MERS-CoV CTD1-DPP4 complex crystal structure into the “up” conformation CTD1 of the SARS-CoV S EM map showing no steric clashes. (C-D), Similar fitting of the HKU4 CTD1-DPP4 complex crystal structure showing steric clashes for the binding to the “down” conformation CTD1 and no steric clashes for the binding to the “up” conformation CTD1. The steric clashes are highlighted in blue.