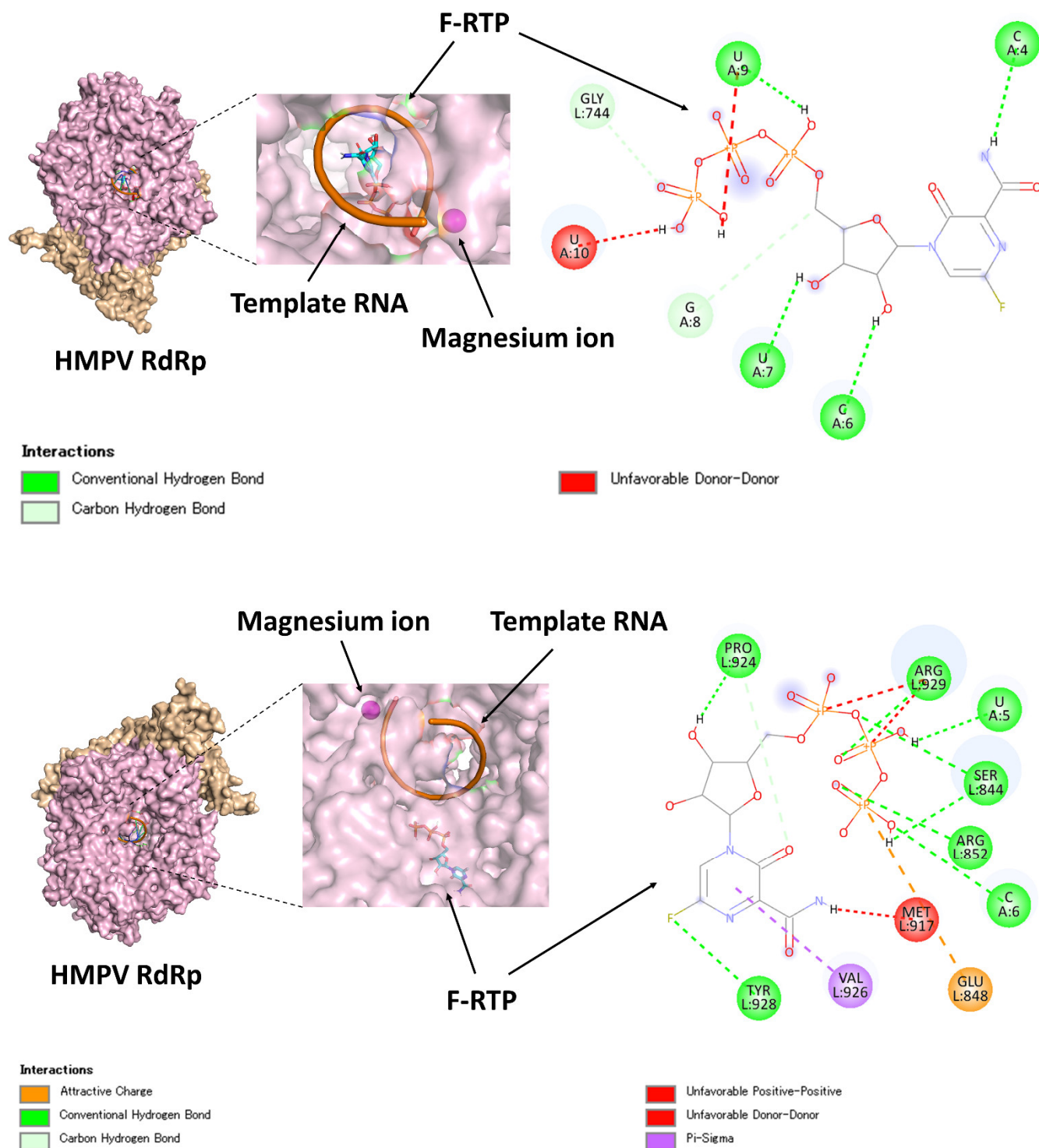
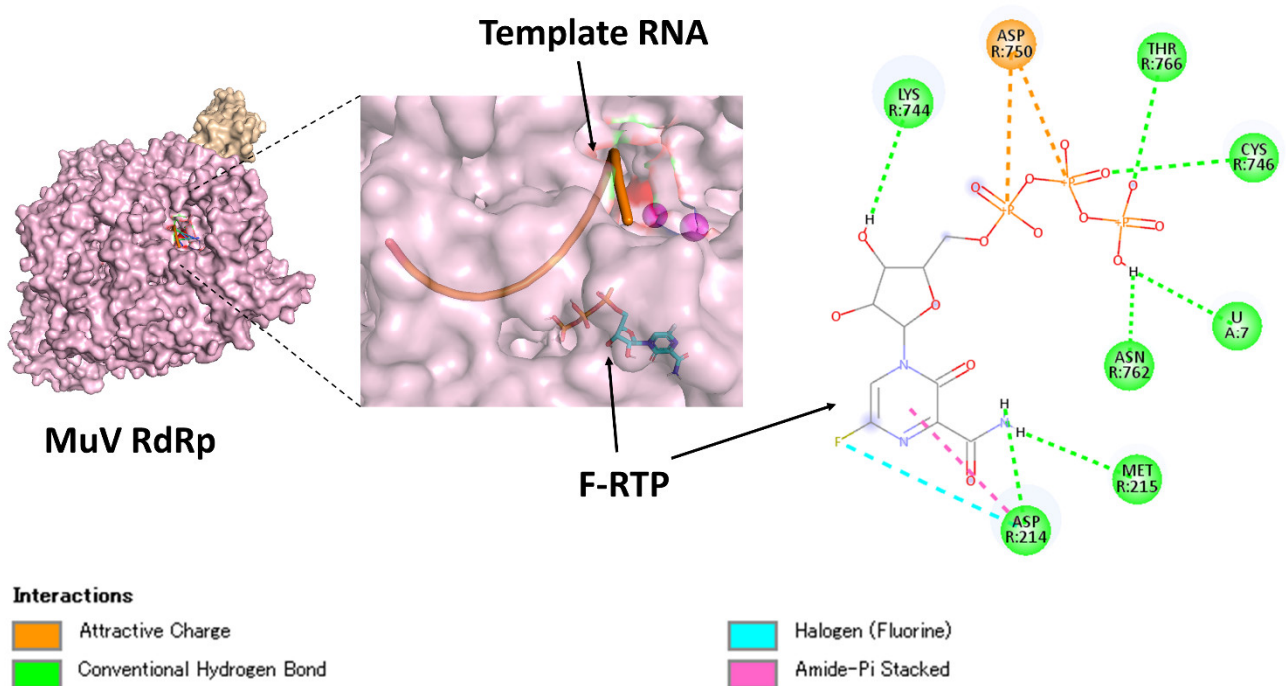
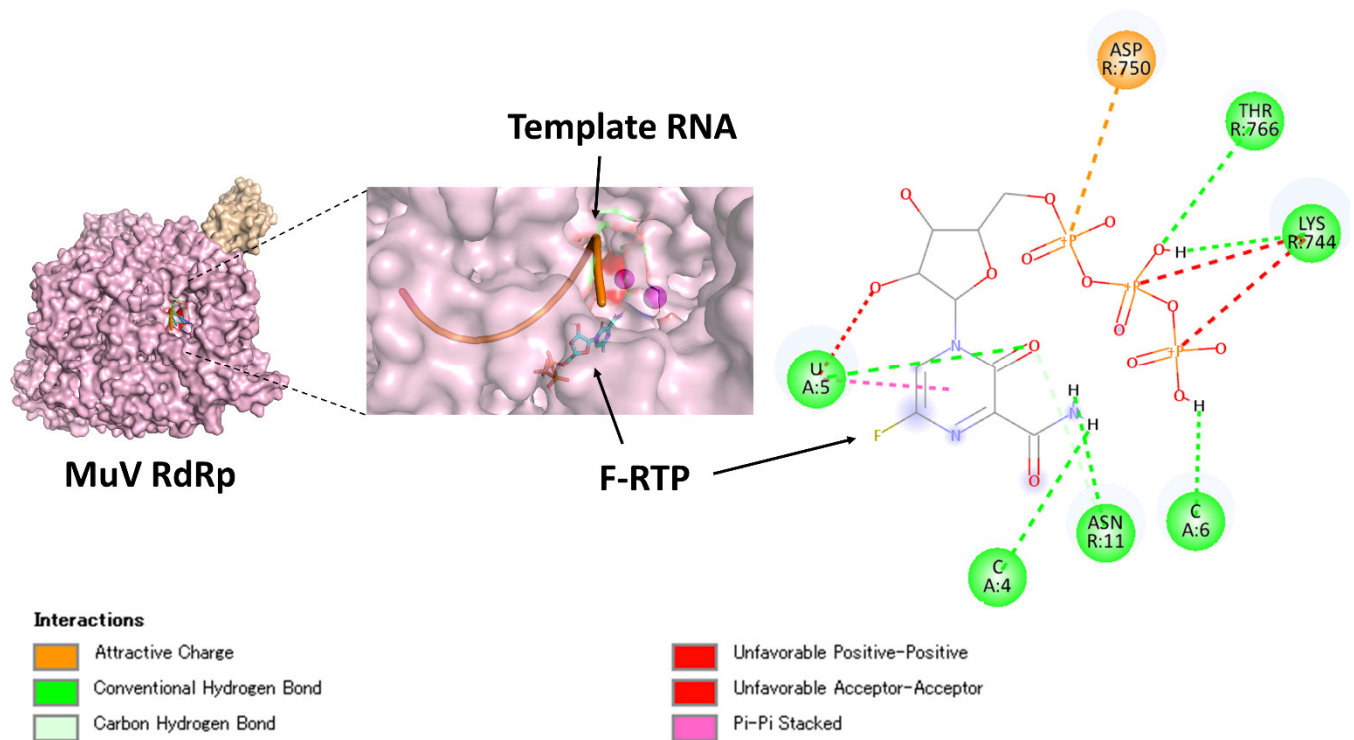


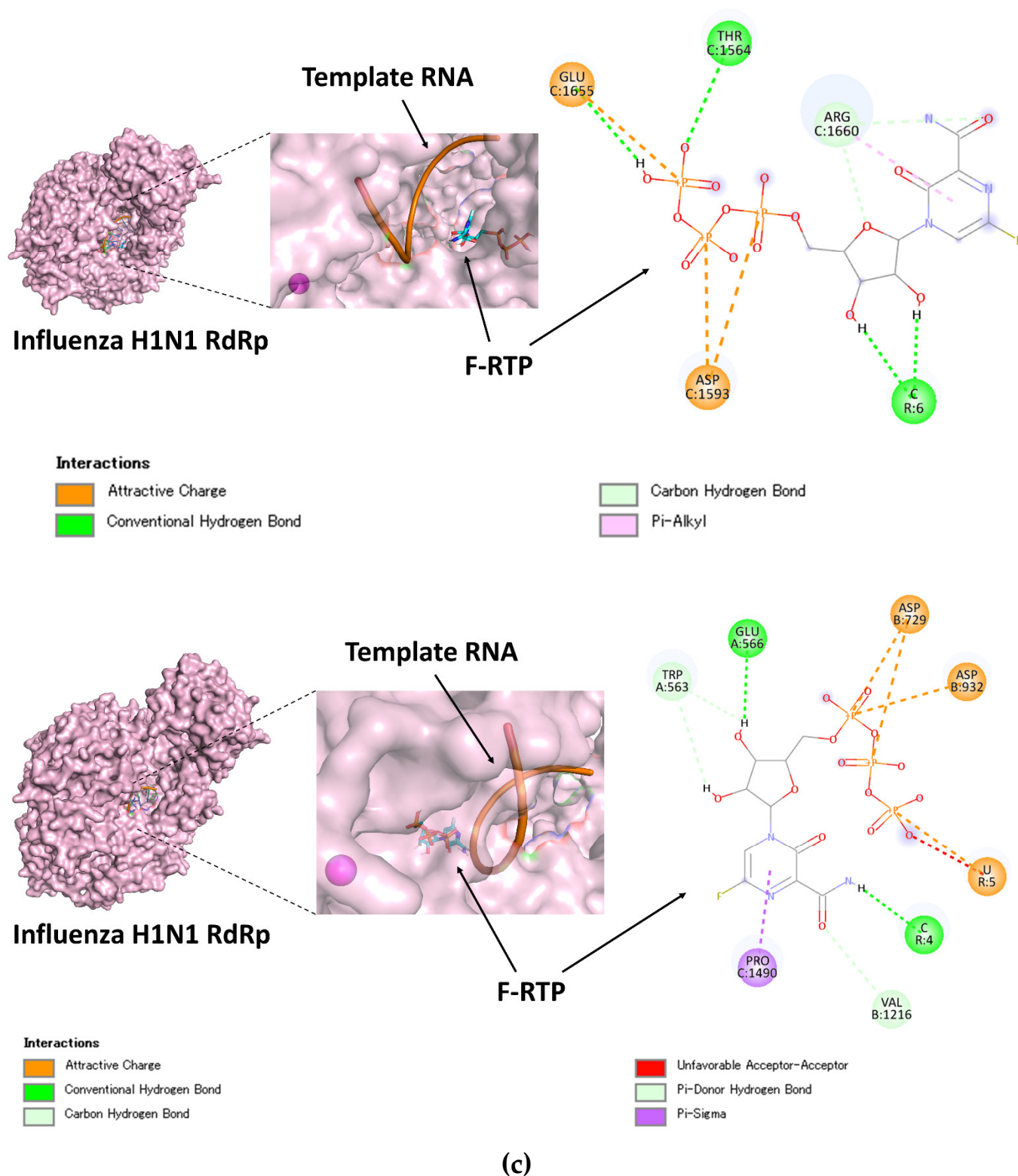
## Supplementary Figure



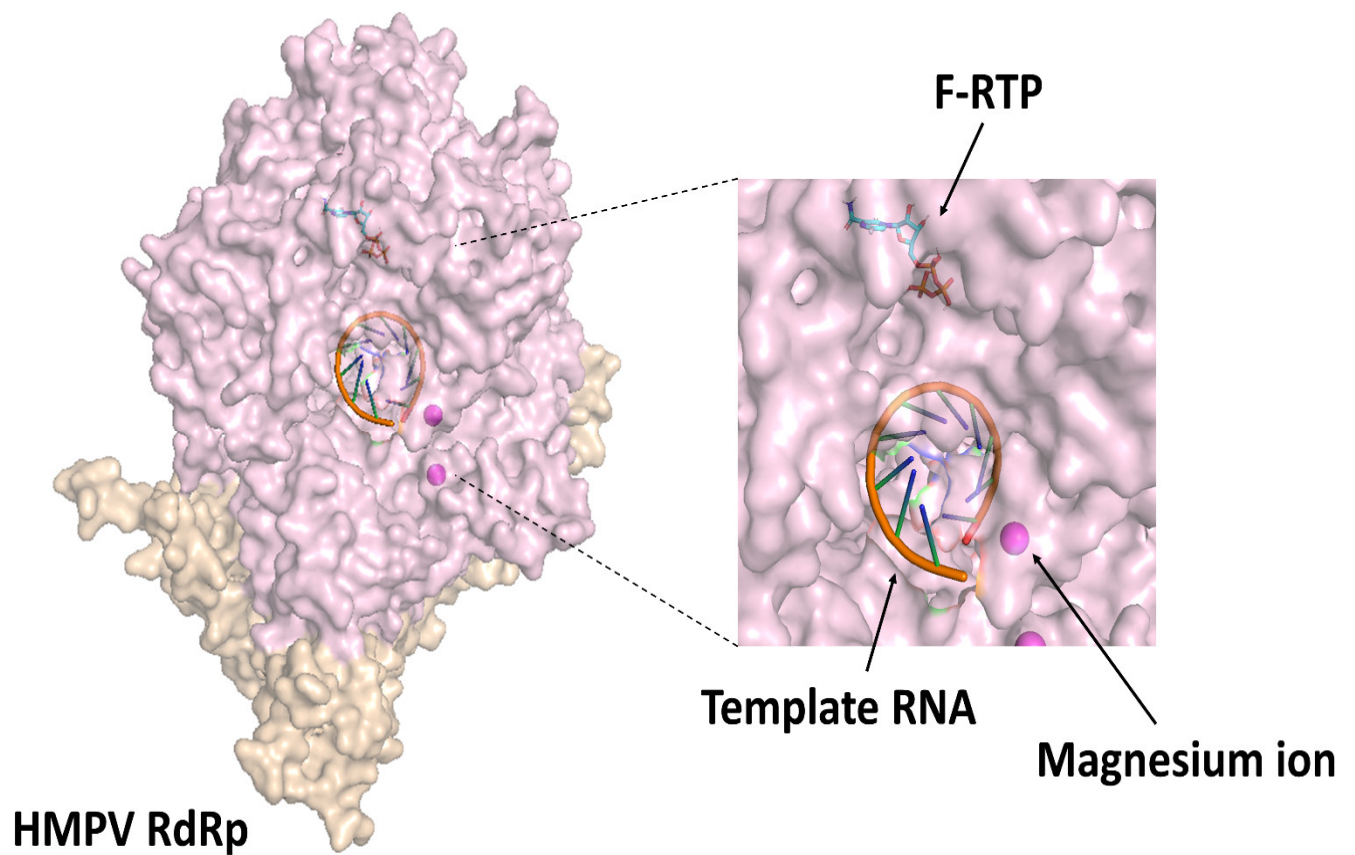
(a)



(b)

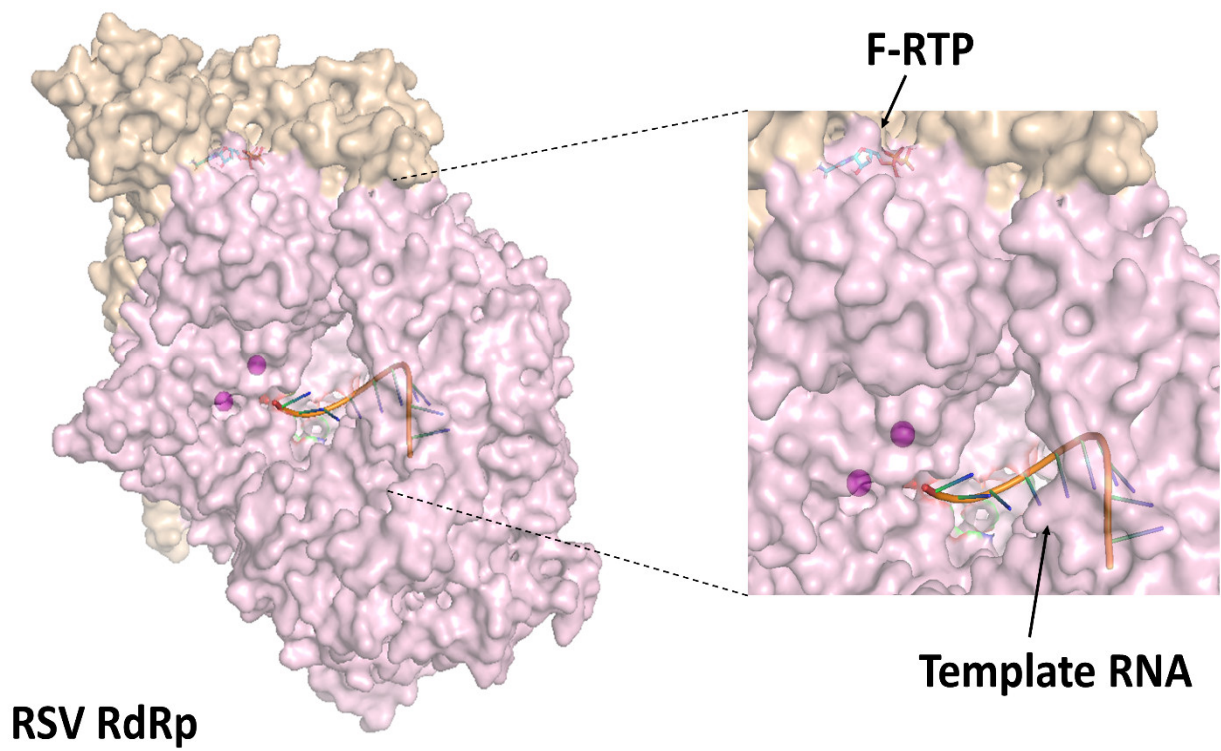
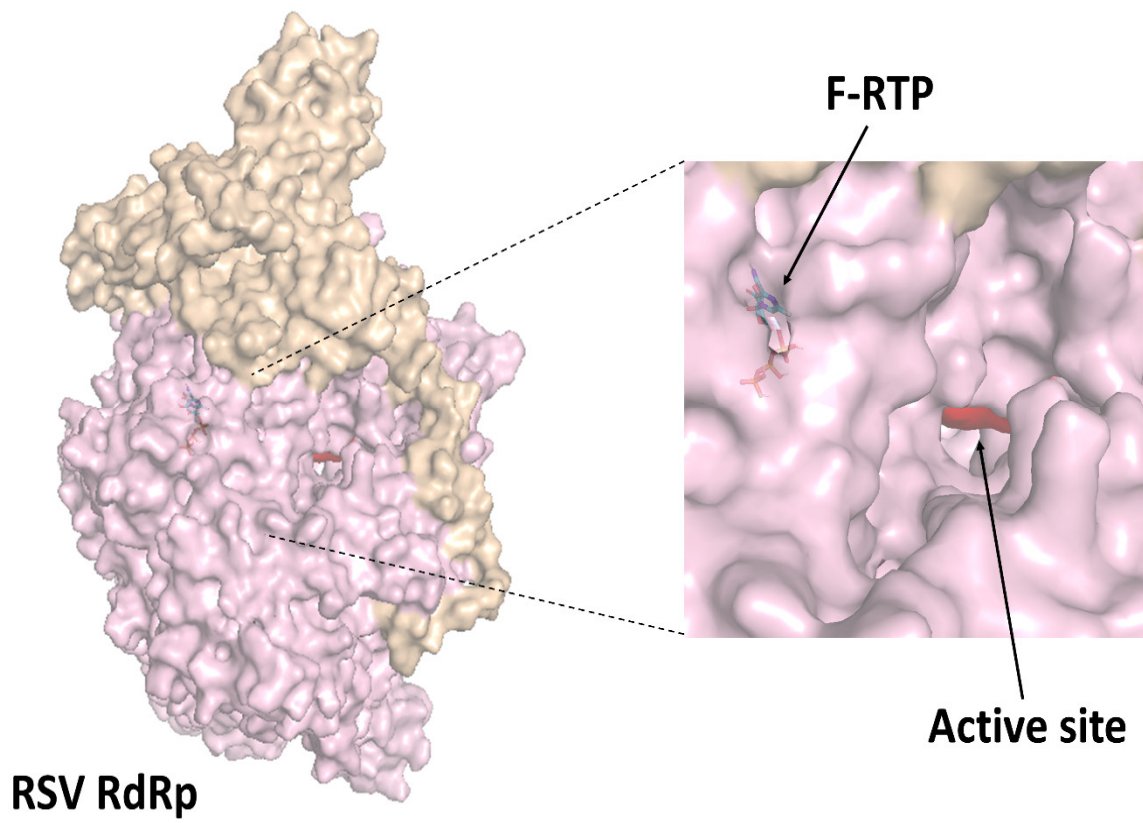


**Supplementary Figure S1.** Comparison between models selected by autodock alone (the upper figure) and those changed by the addition of LigScore (the lower figure). Each Diagram illustrates the binding conformations and interactions among favipiravir ribofuranosyl-5'-triphosphate (F-RTP), nucleotide triphosphate (NTP), magnesium ions, and (a) human metapneumovirus (HMPV) RNA-dependent RNA polymerase (RdRp), (b) mumps virus (MuV) RdRp, and (c) influenza H1N1 RdRp. The active sites on proteins are shown in red. Magnesium ions that bound to the RdRp are colored magenta.

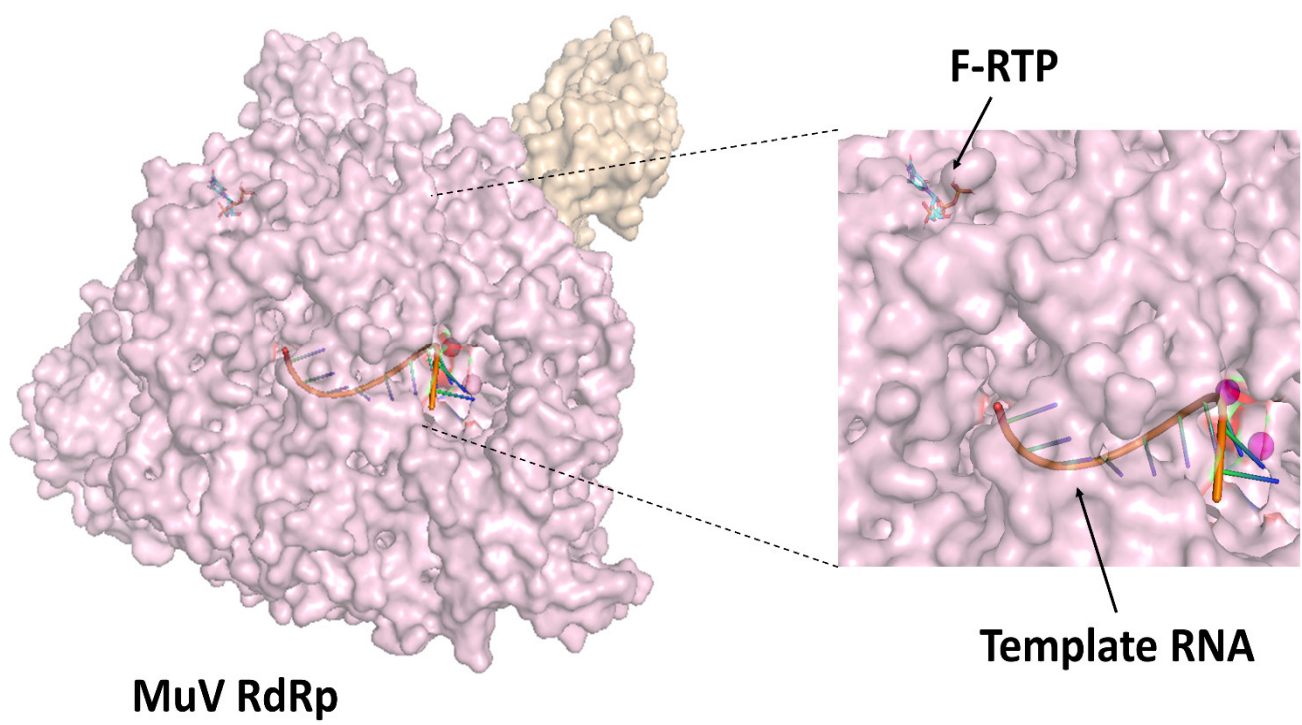
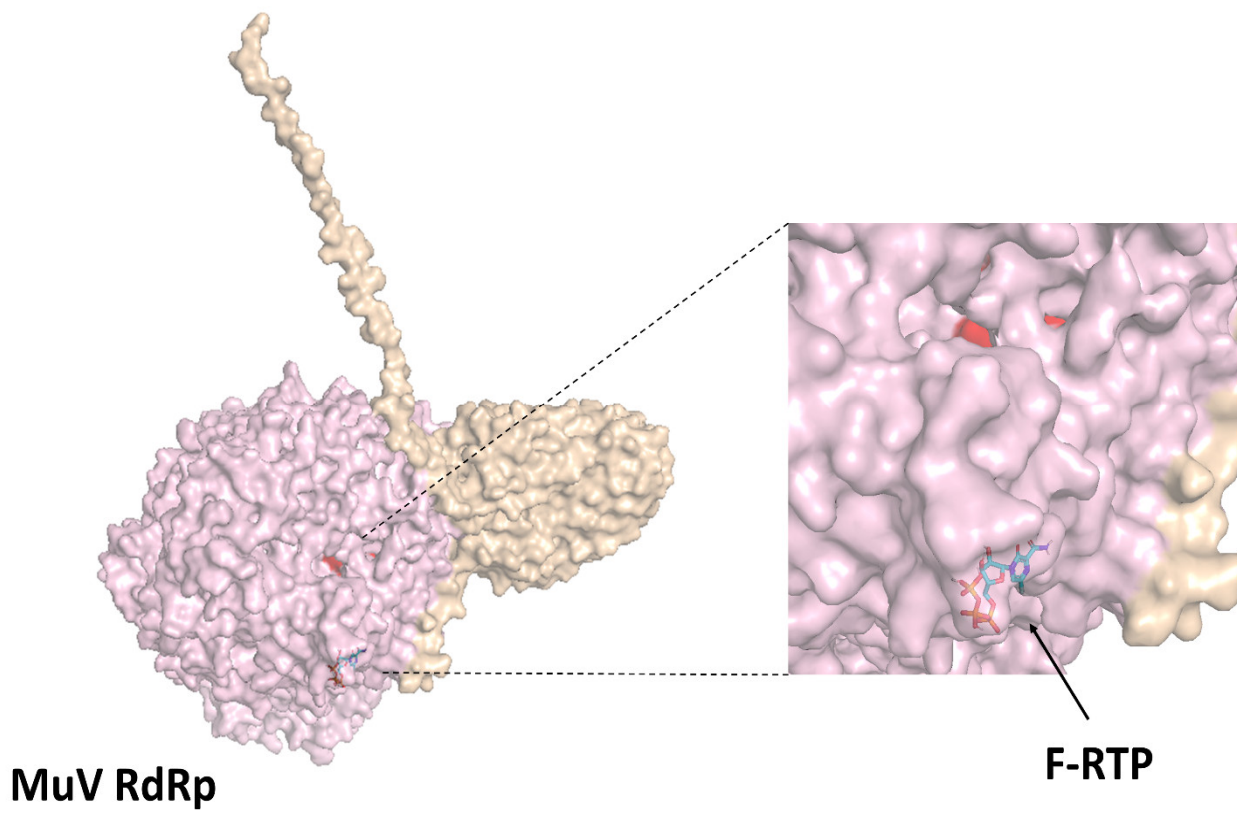


(a)



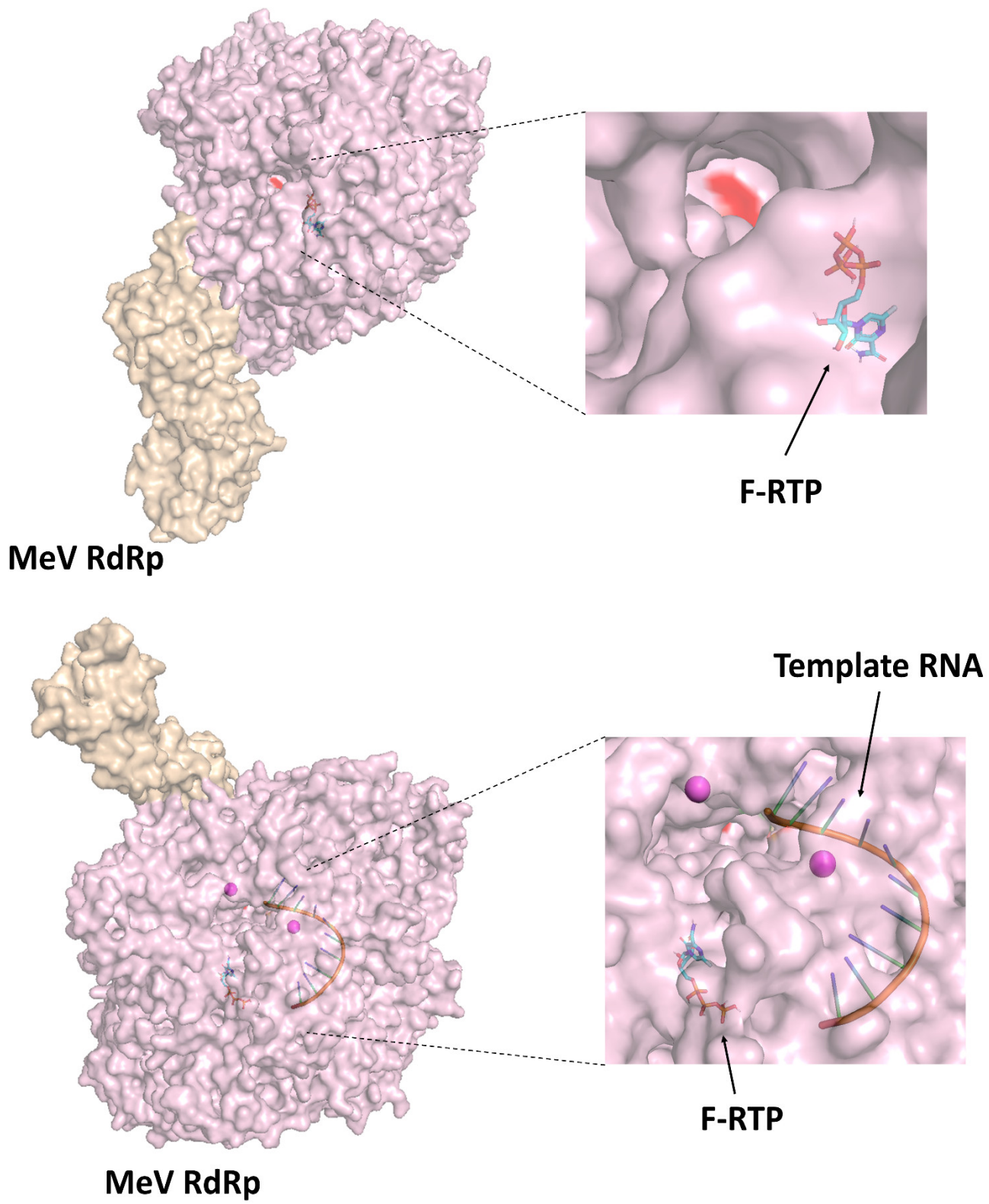


(b)

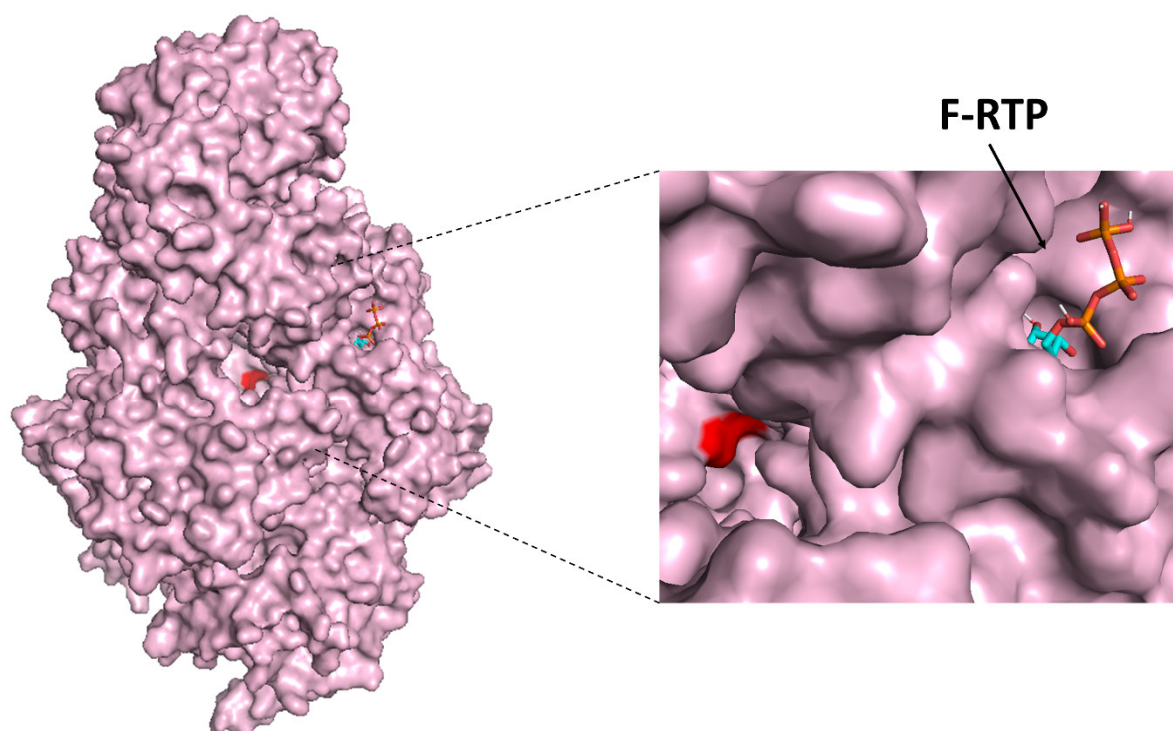


(c)





(d)



**Influenza H1N1 RdRp**

**(e)**

**Supplementary Figure S2.** Diagram illustrating the best-scored binding conformations of favipiravir ribofuranosyl-5'-triphosphate (F-RTP) with (a) human metapneumovirus (HMPV) RNA-dependent RNA polymerase (RdRp), (b) respiratory syncytial virus (RSV) RdRp, (c) mumps virus (MuV) RdRp, (d) measles virus (MeV) RdRp, and (e) influenza H1N1 RdRp based on LigScore. The red color on the surface of various proteins indicates active sites. Magnesium ions that bound to the RdRp are colored magenta.