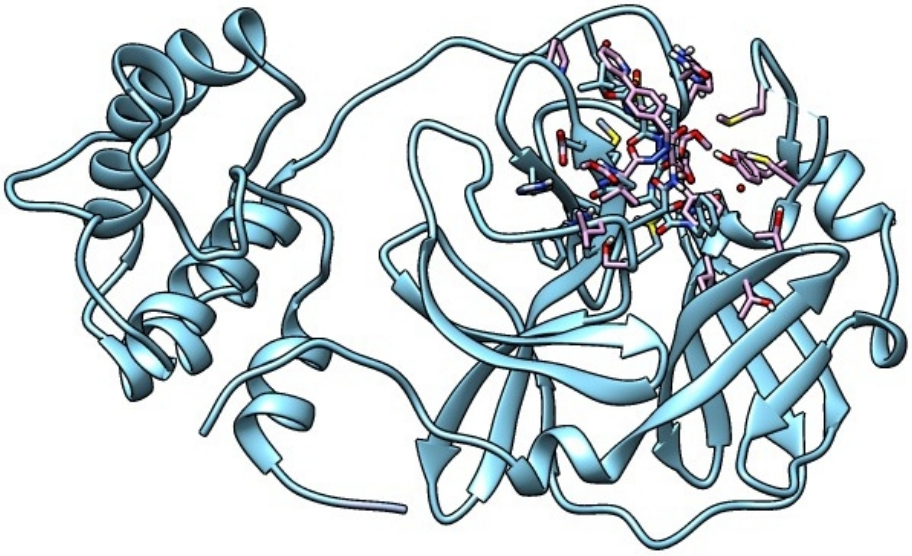


Figure S1: Superimposed protein three dimensional X-ray crystal structures of SARS-CoV-2 M^{pro}, (PDB ID: 6Y2F in blue) and (PDB ID: 5R7Z in light yellow).

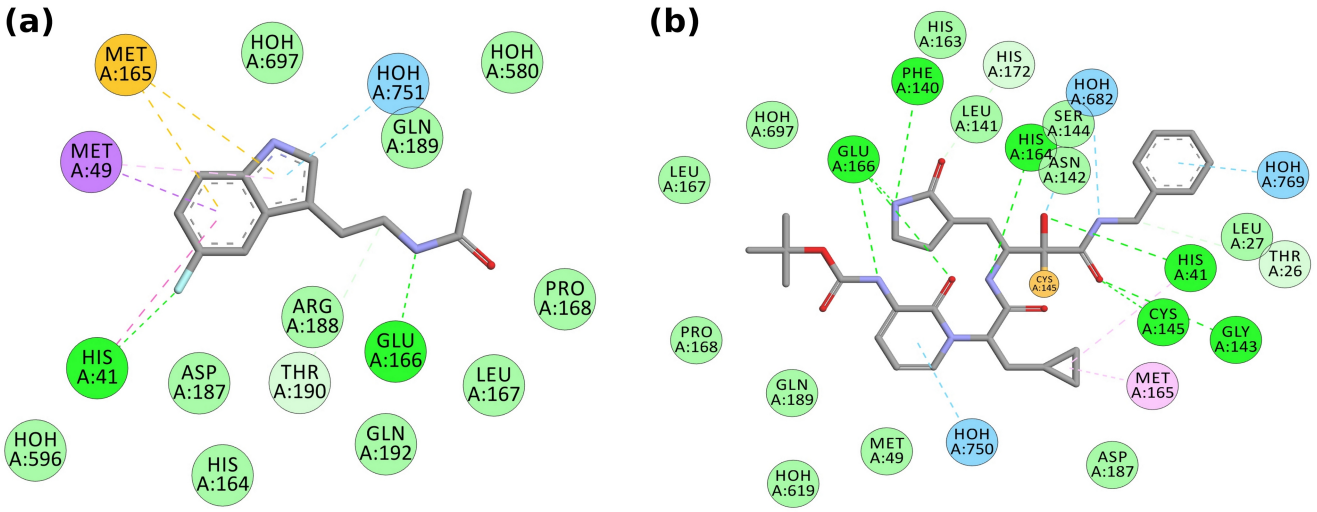
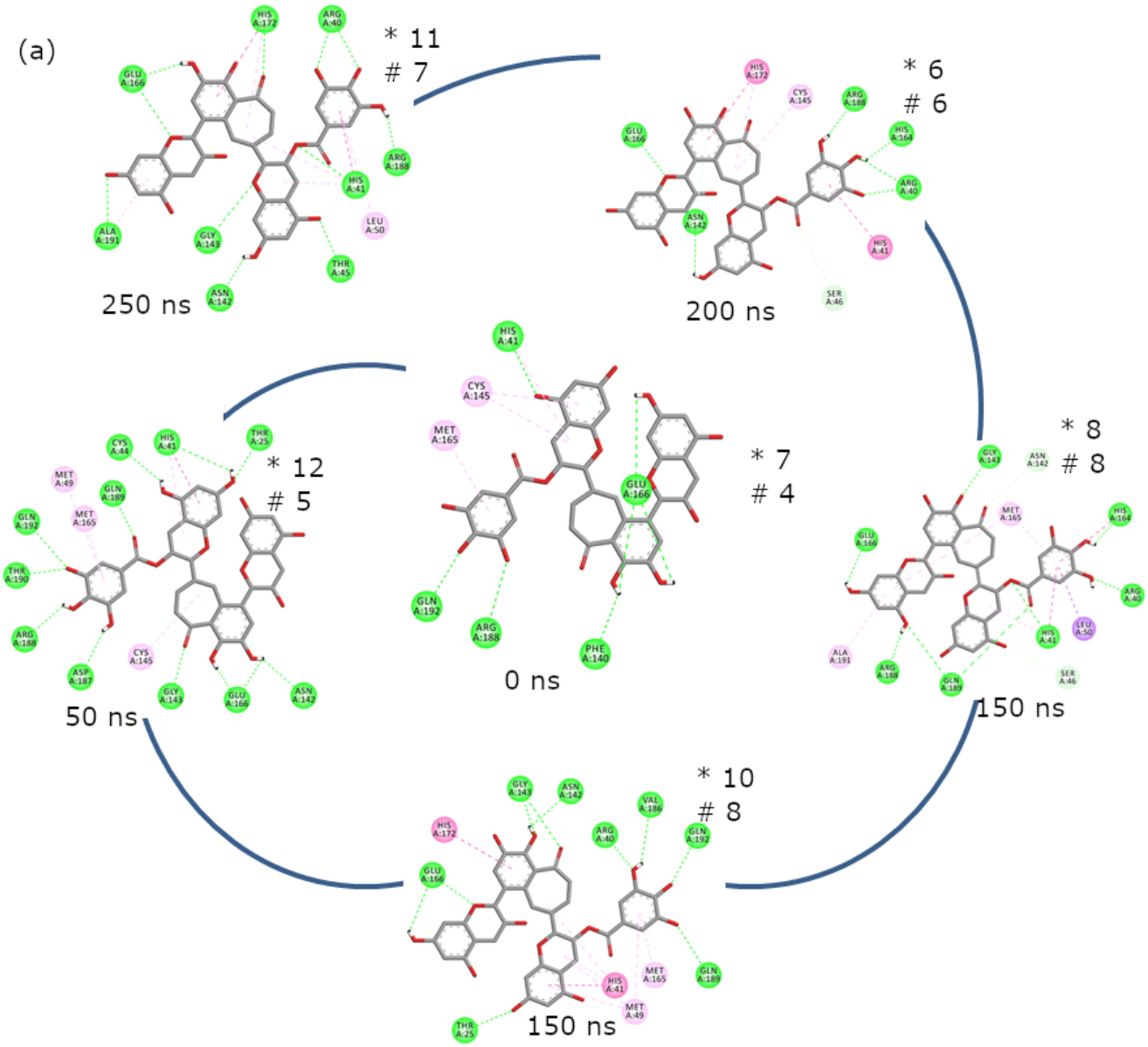
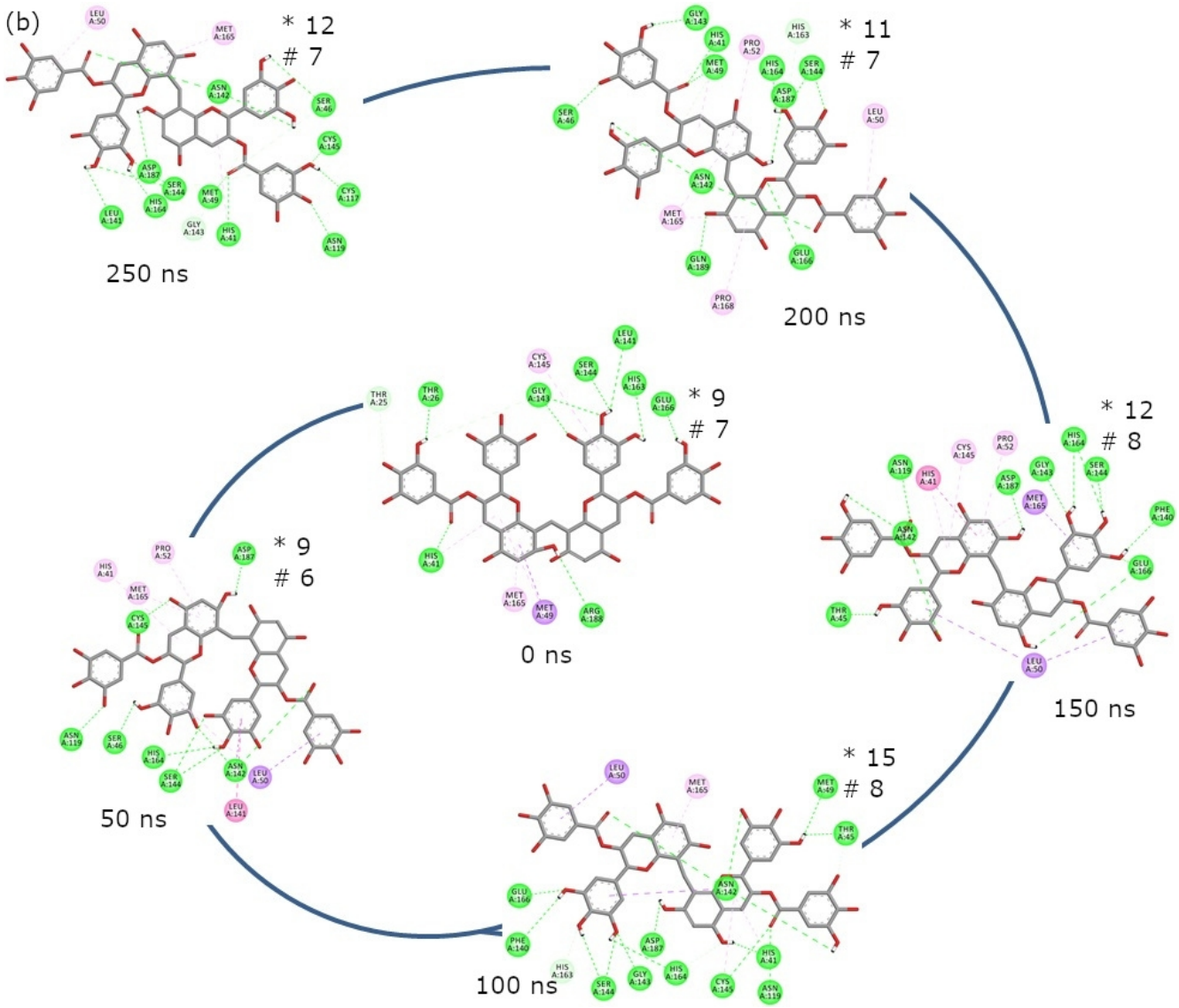
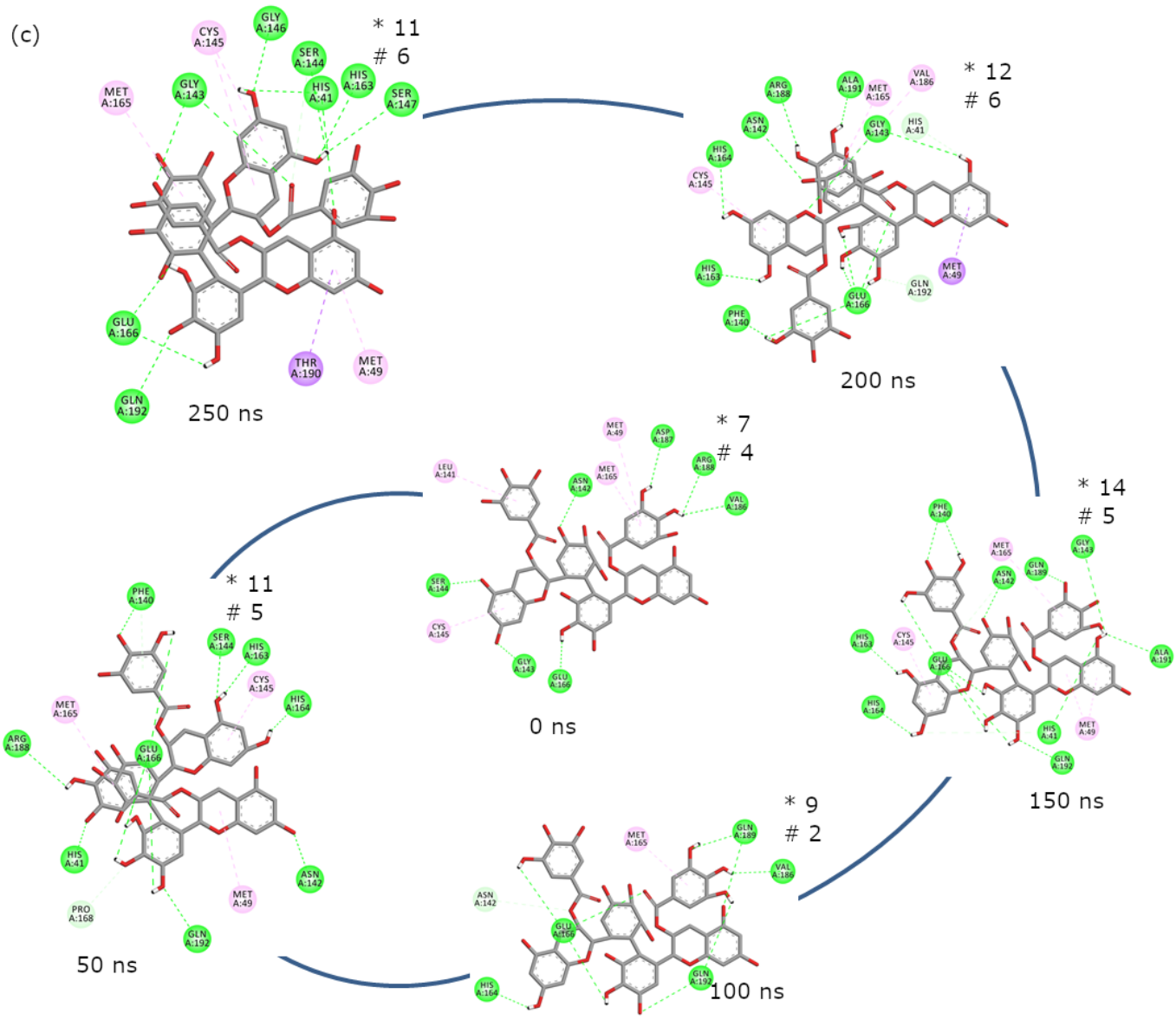
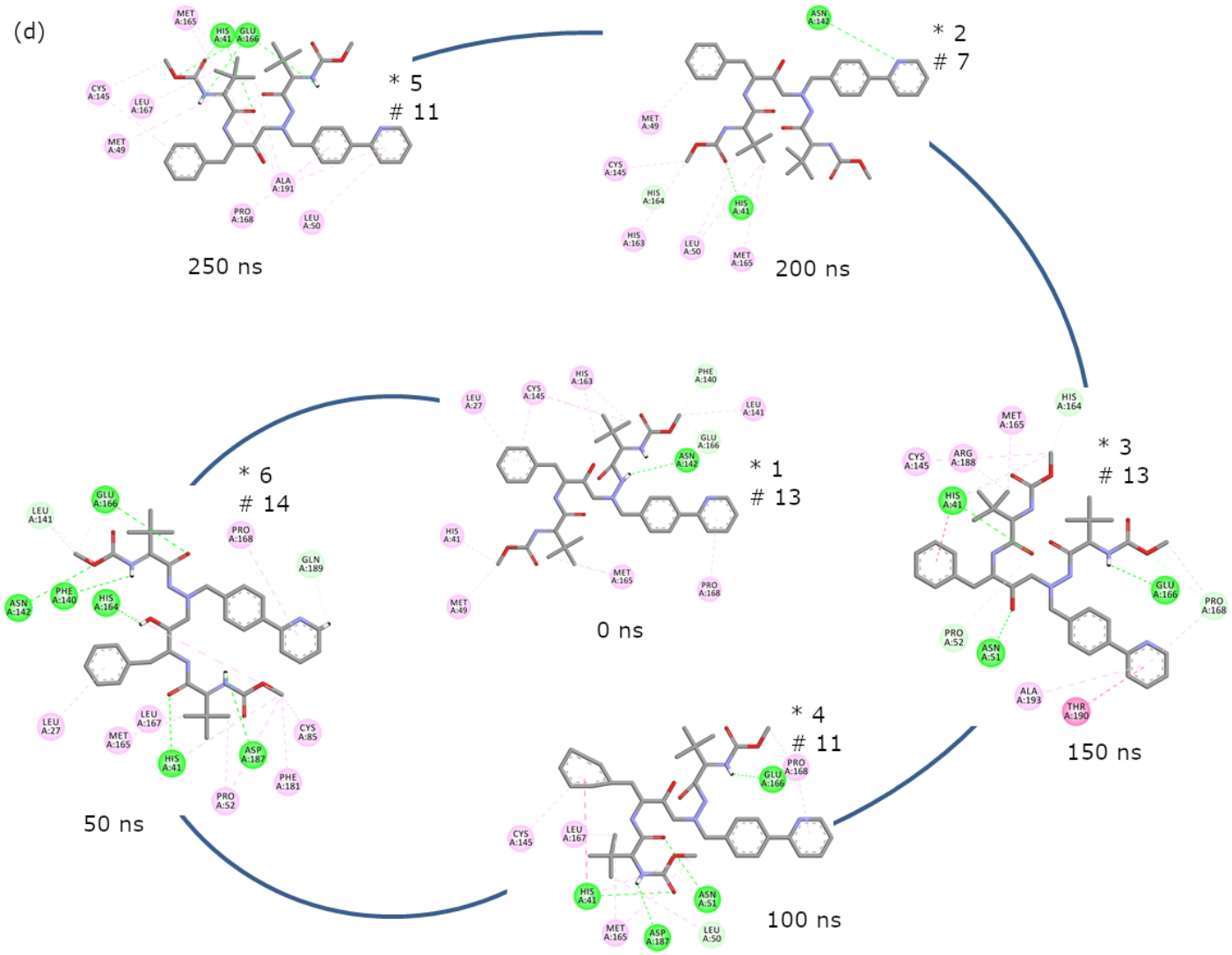


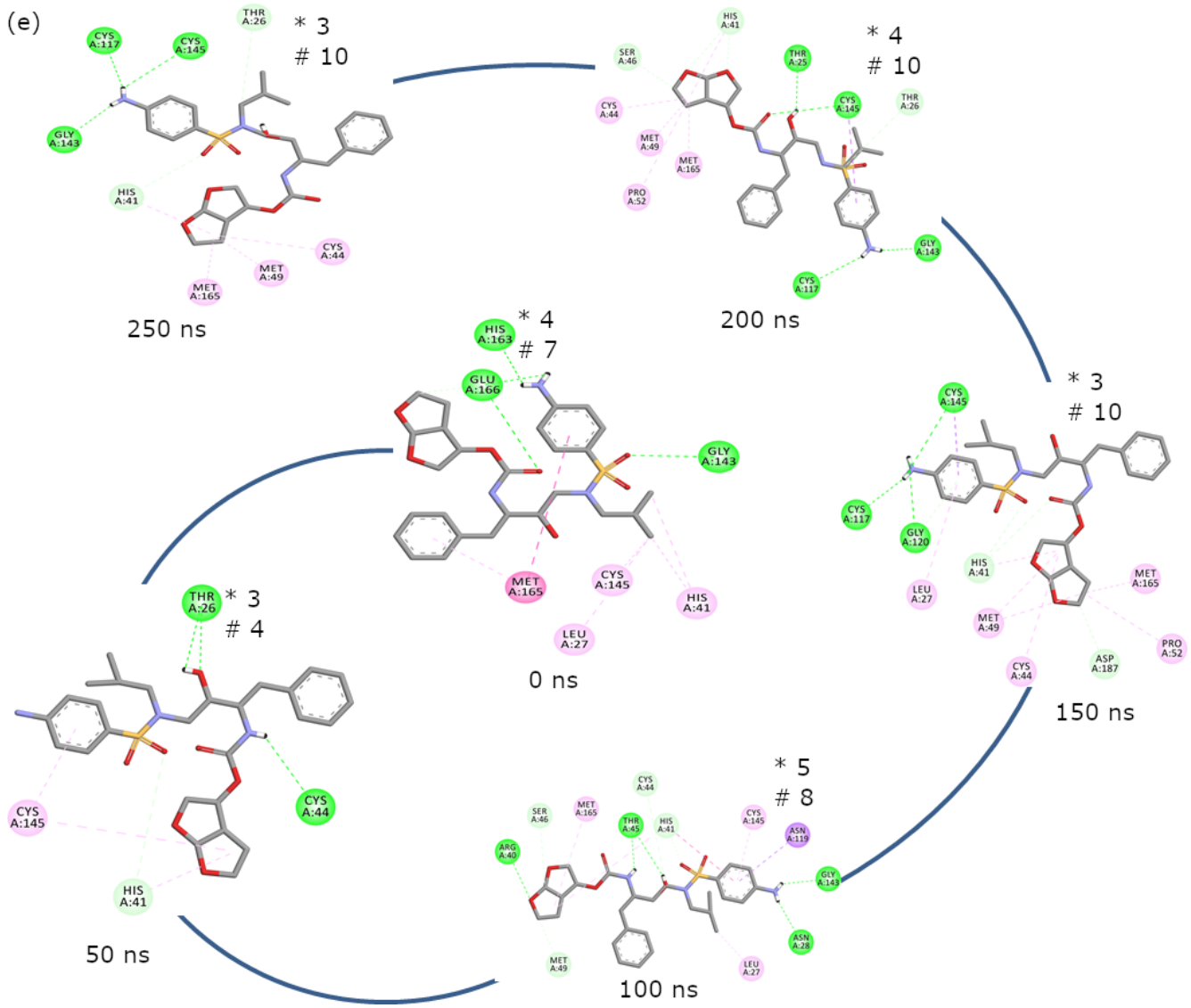
Figure S2: Binding pattern of co-crystallized ligand of SARS-CoV-2 M^{pro}, (a) PDB ID: 5R7Z (b) PDB ID: 6Y2F.


(a)
* 11
# 7
250 ns
* 6
# 6
200 ns
* 8
# 8
150 ns
* 10
# 8
150 ns
* 12
# 5
50 ns
* 7
# 4
0 ns


(b)
* 12
# 7
250 ns
* 11
# 7
200 ns
* 12
# 8
150 ns
* 15
# 8
100 ns
* 9
# 6
50 ns
* 9
# 7
0 ns


(c)
* 11
# 6
250 ns
* 12
# 6
200 ns
* 14
# 5
150 ns
* 9
# 2
100 ns
* 11
# 5
50 ns
* 7
# 4
0 ns


(d)
* 5
# 11
250 ns
* 2
# 7
200 ns
* 3
# 13
150 ns
* 4
# 11
100 ns
* 1
# 13
0 ns
* 6
# 14
50 ns


(e)
* 3
# 10
250 ns
* 4
# 10
200 ns
* 3
# 10
150 ns
* 5
# 8
100 ns
* 3
# 4
50 ns
* 4
# 7
0 ns

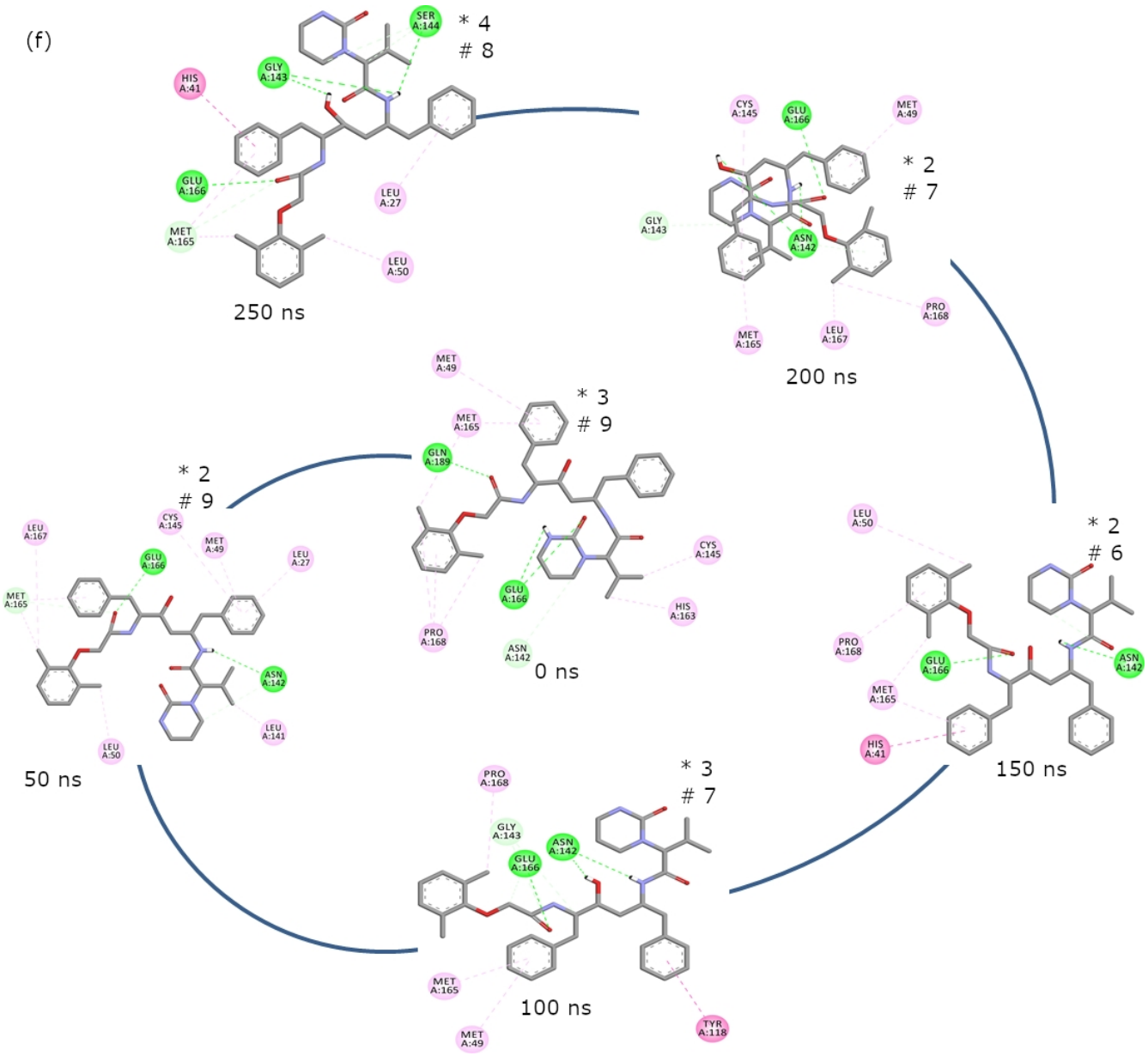


Figure S3: 2D interactions showing hydrogen bonds (green) and hydrophobic interactions (Pink, light pink, blue, and cyan) at different time period of MD-simulations in the binding pocket of the SARS-CoV-2 M^{pro} visualized by Discovery studio. (a) Theaflavin-3-O-gallate (b) Oolonghomobisflavan-A (c) Theasinensin-D (d) Atazanavir (e) Darunavir, and (f) Lopinavir.

* No. of hydrogen bonds

No. of hydrophobic interactions