

Figure S1. Molecular mechanism of SARS-COV-2 Mpro.

Table S1. Types of interactions of **RMH148** within COVID-19 Mpro active site, and distance (Å°).

Bond type	Distance Å°	Bond type	Distance Å°
Hydrogen bond with Tyrosine54	3.21	Hydrogen bond with Threonine 26	2.41
Hydrogen bond with Glutamic166	3.00	Hydrogen bond with Threonine 26	2.46
Hydrogen bond with Glutamic166	3.07	Hydrogen bond with Histidine 41	2.92
Hydrogen bond with Glutamic166	3.22	Hydrogen bond with Histidine 164	2.87
Hydrogen bond with Glutamic166	3.29	Hydrogen bond with Cysteine 145	2.75
Hydrogen bond with Glutamic166	3.05	Covalent bond with Cysteine 145	
Hydrogen bond with Glutamic166	3.02	Hydrogen bond with water 566	3.13
Non-classical Hydrogen bond with Glutamic166	3.15	Hydrogen bond with water 566	3.39
Hydrogen bond with Phenylalanine 140	3.20	Hydrogen bond with water 568	3.16
	3.20	Hydrogen bond with water 568	3.52
	3.23	Pi-Alkyl interaction with Methionine 49	5.22
		Pi-Sulfur interaction with Methionine 165	5.28

Hydrogen bond with Serine 144			
Hydrogen bond with Serine 144			
Hydrogen bond with Glycine 143			
Hydrogen bond with Glycine 143			

Table S2. The average distances of all the hydrogen bonds formed between the **RMH148** and Covid-19 Mpro through the entire 150 ns MD simulation.

Hydrogen bond name	Average distance (Å) +/- SD
Hydrogen bond with Tyrosine54	3.17+/- 0.06
Hydrogen bond with Glutamic166	3.05 +/- 0.12
Hydrogen bond with Glutamic166	3.05 +/- 0.08
Hydrogen bond with Glutamic166	3.21 +/- 0.1
Hydrogen bond with Glutamic166	3.31 +/- 0.12
Hydrogen bond with Phenylalanine 140	2.98 +/- 0.07
Hydrogen bond with Serine 144	3.17 +/- 0.11
Hydrogen bond with Serine 144	3.18 +/- 0.09
Hydrogen bond with Glycine 143	3.25 +/- 0.15
Hydrogen bond with Glycine 143	3.29 +/- 0.13
Hydrogen bond with Threonine 26	2.43 +/- 0.04
Hydrogen bond with Threonine 26	2.58 +/- 0.17
Hydrogen bond with Histidine 41	3.02 +/- 0.14
Hydrogen bond with Histidine 164	3.00 +/- 0.16
Hydrogen bond with Cysteine 145	2.71 +/- 0.07

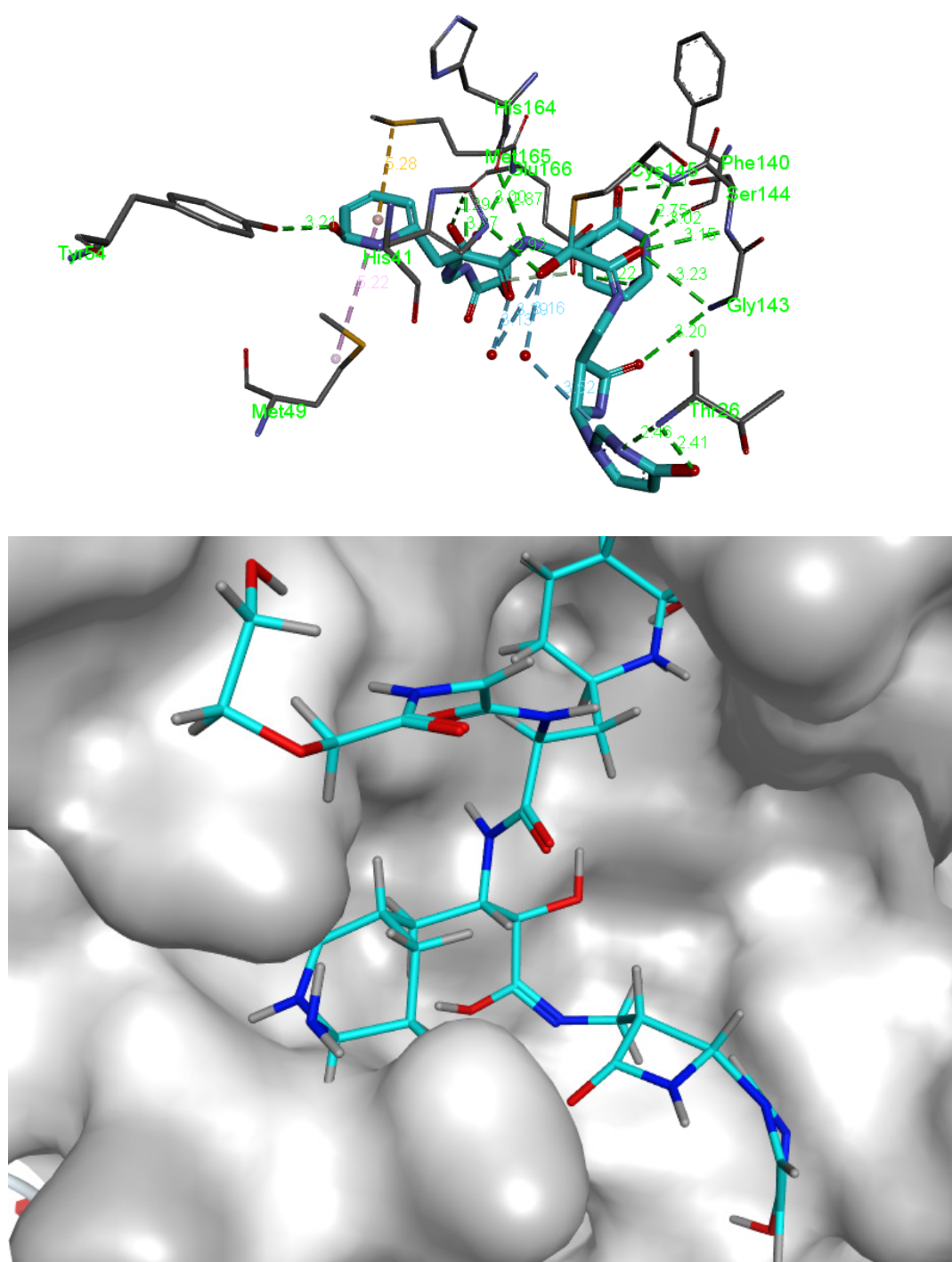
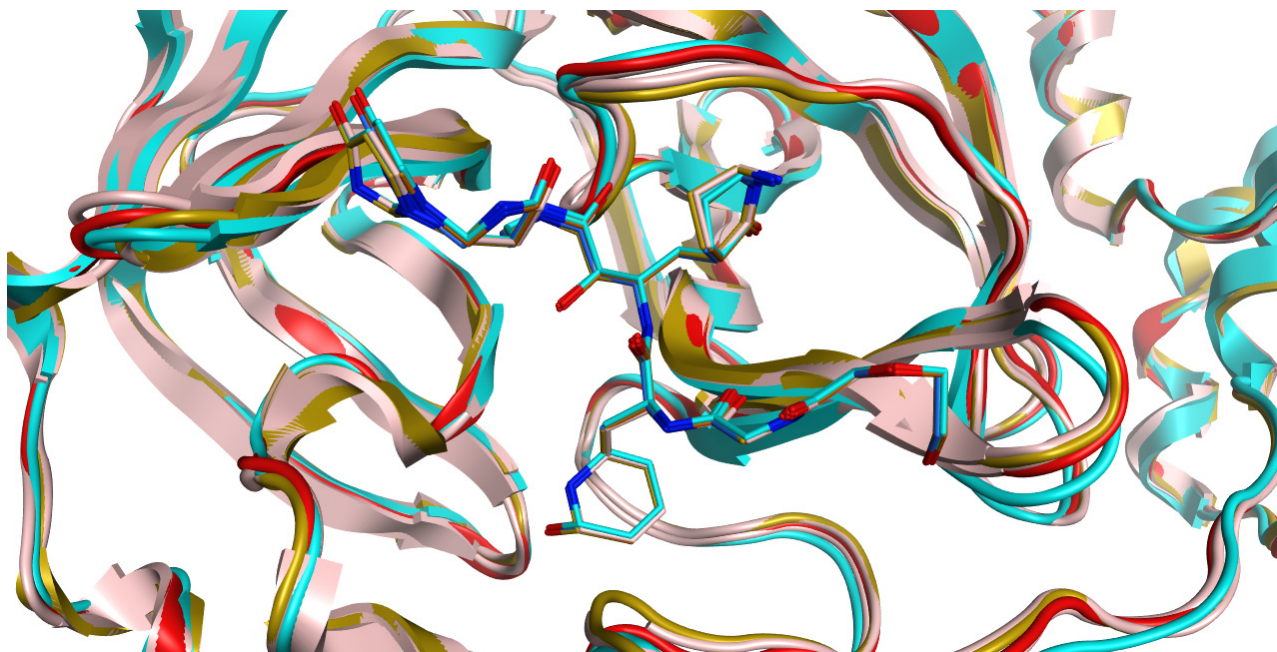


Figure S2. different 3D binding Views for RMH148 with the Mpro.

A.



B.

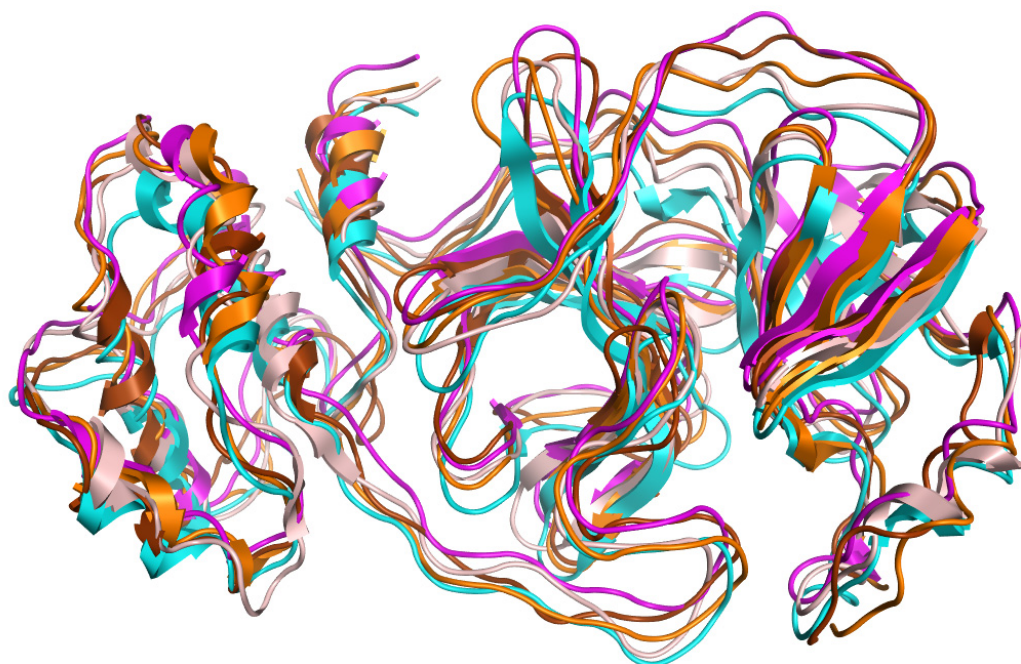


Figure S3. Five Conformational Samples showing (A) stable Mpro-RMH148 (B) dynamic free Mpro.