Supplementary information

Effect of Computationally Designed Fragment-based Analogs on the RBD-ACE2 Complex of SARS-CoV-2 P.1 Variant

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Supplementary Figure Legends

Figure S1. Protein and compounds interaction. Interactions are shown on a representative structure after 200 ns of MDS. (**A**) Compound 1 and residues from the complex. (**B**) Compound 2 and residues from the complex. Compounds are shown in orange color stick and interacting residues are in blue stick. Hydrogen bonds, hydrophobic interactions and halogen interactions are represented in blue, grey, and green lines, respectively. Interacting residues are labeled.

Figure S2. Hydrogen bond plots during 200 ns MDS. (**A**) Between RBD and ACE2 of the Apo and compound bond complexes (**B**) Between Compounds and ACE2 (**C**) Between Compounds and RBD. Plots of hydrogen bonds are shown as black, red and blue in Apo complex, Compounds 1 and 2 complexes, respectively.

Figure S3. Radius of gyration plot during 200ns of MDS. Radius of gyration plots are represented in black, red and blue for the Apo, compound 1-bound and compound 2-bound complexes, respectively.

Figure S1

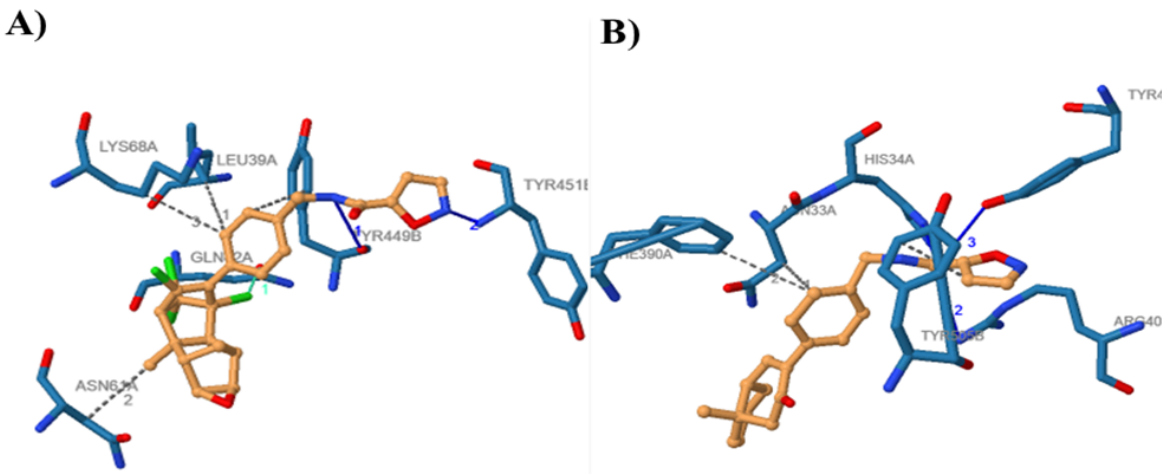
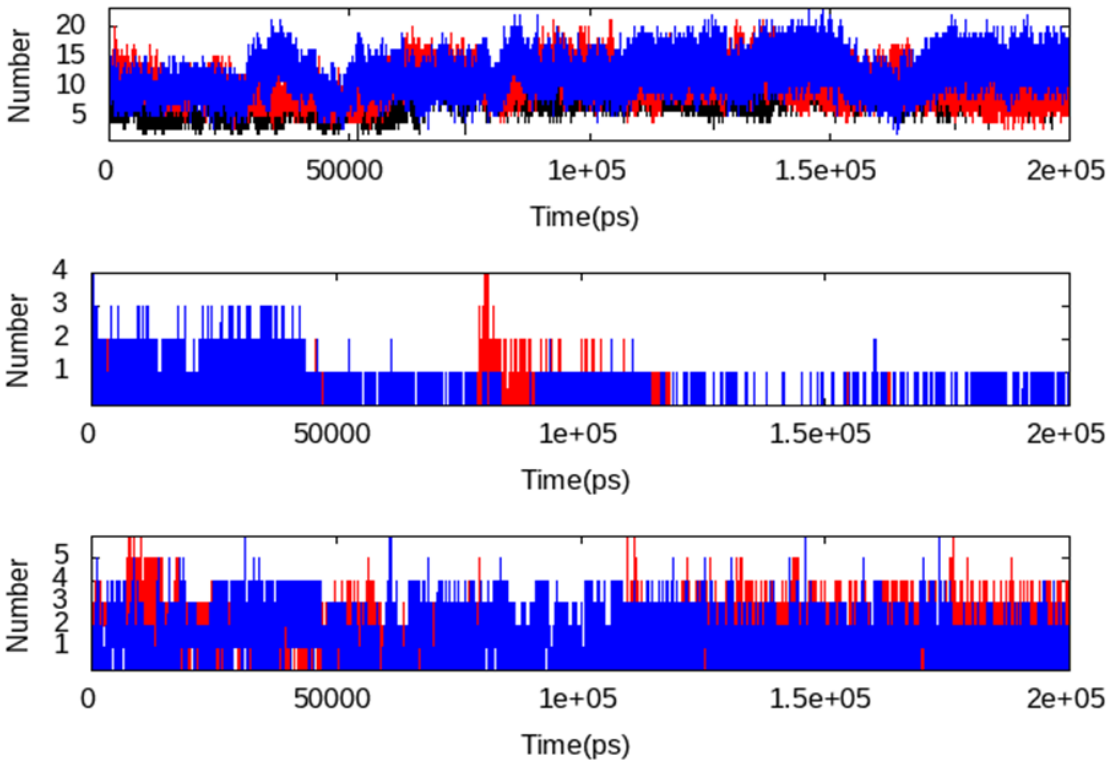


Figure S2


Number
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15
10
5
0
50000
1e+05
1.5e+05
2e+05
Time(ps)
Number
4
3
2
1
0
50000
1e+05
1.5e+05
2e+05
Time(ps)
Number
5
4
3
2
1
0
50000
1e+05
1.5e+05
2e+05
Time(ps)

Figure S3

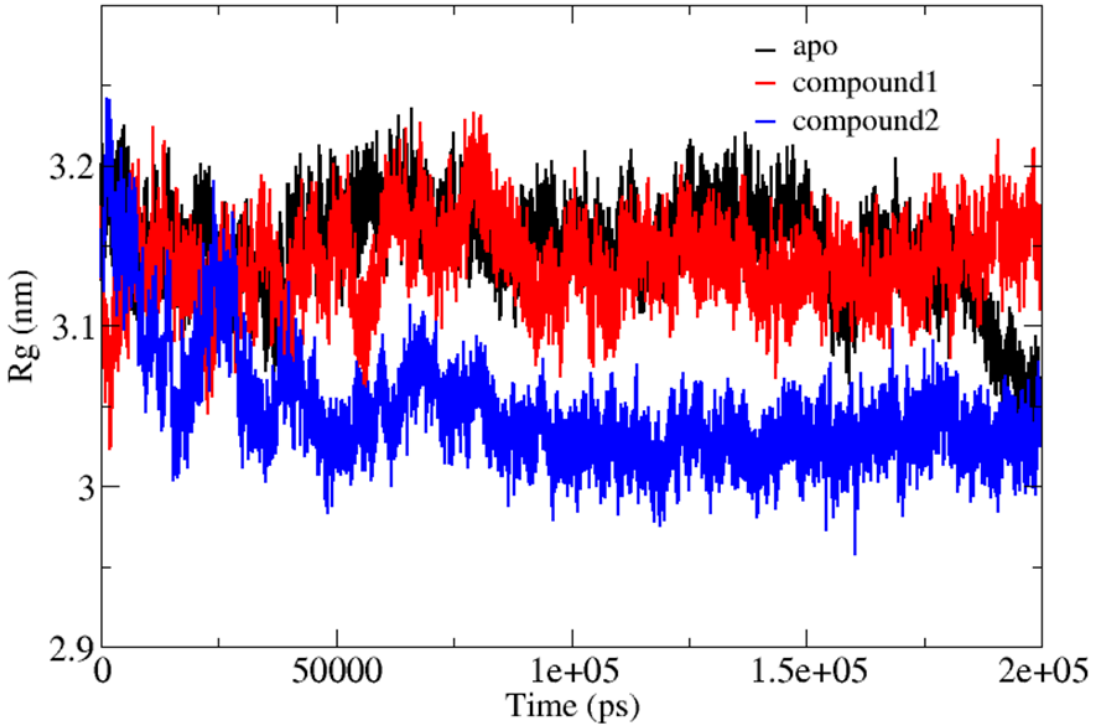
apo
compound1
compound2
Rg (nm)
3.2
3.1
3
2.9
0
50000
1e+05
1.5e+05
2e+05
Time (ps)

Table S1: Five top docking conformation with their binding energy

Conformations	**Binding Energy (kcal/mol)**		**RMS score**	
	Compound 1	**Compound 2**	**Compound 1**	**Compound 2**
Conformation 1	-5.83	-6.24	0.0	0.0
Conformation 2	-5.74	-4.43	0.17	0.0
Conformation 3	-5.61	-4.26	0.24	0.0
Conformation 4	-5.55	-4.05	0.97	1.26
Conformation 5	-5.41	-4.03	1.02	0.32