Supplementary Information

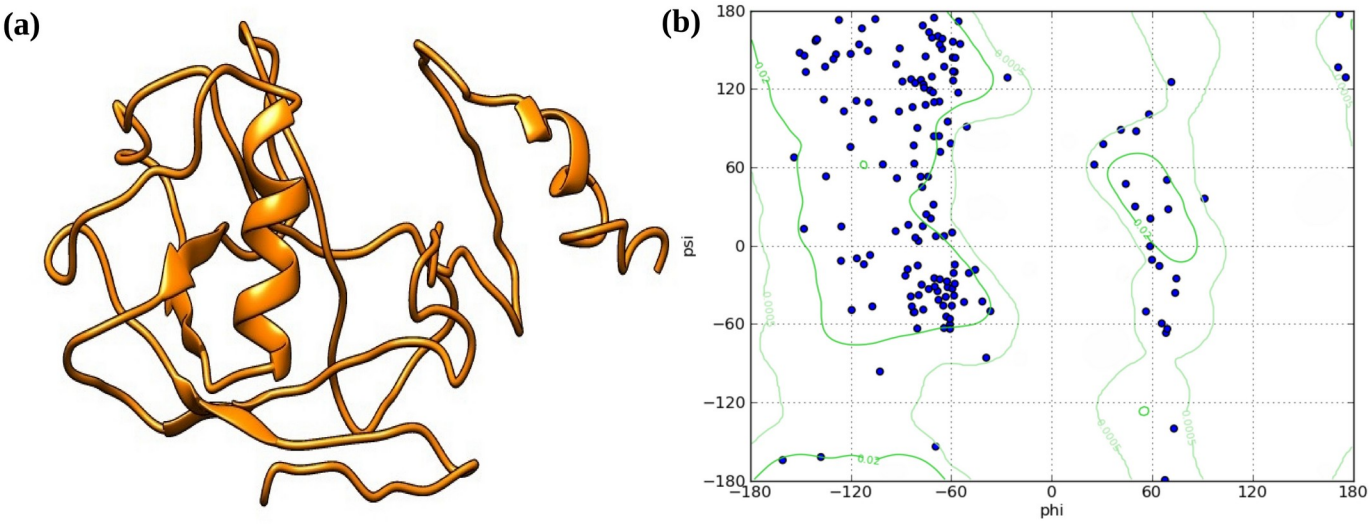

Figure S1: (a) 3D structure of modeled SARS-CoV-2 Nsp1. (b) Ramachandran plot generated by Chimera showing the stereochemical quality of the SARS-CoV-2 Nsp1 protein structure.

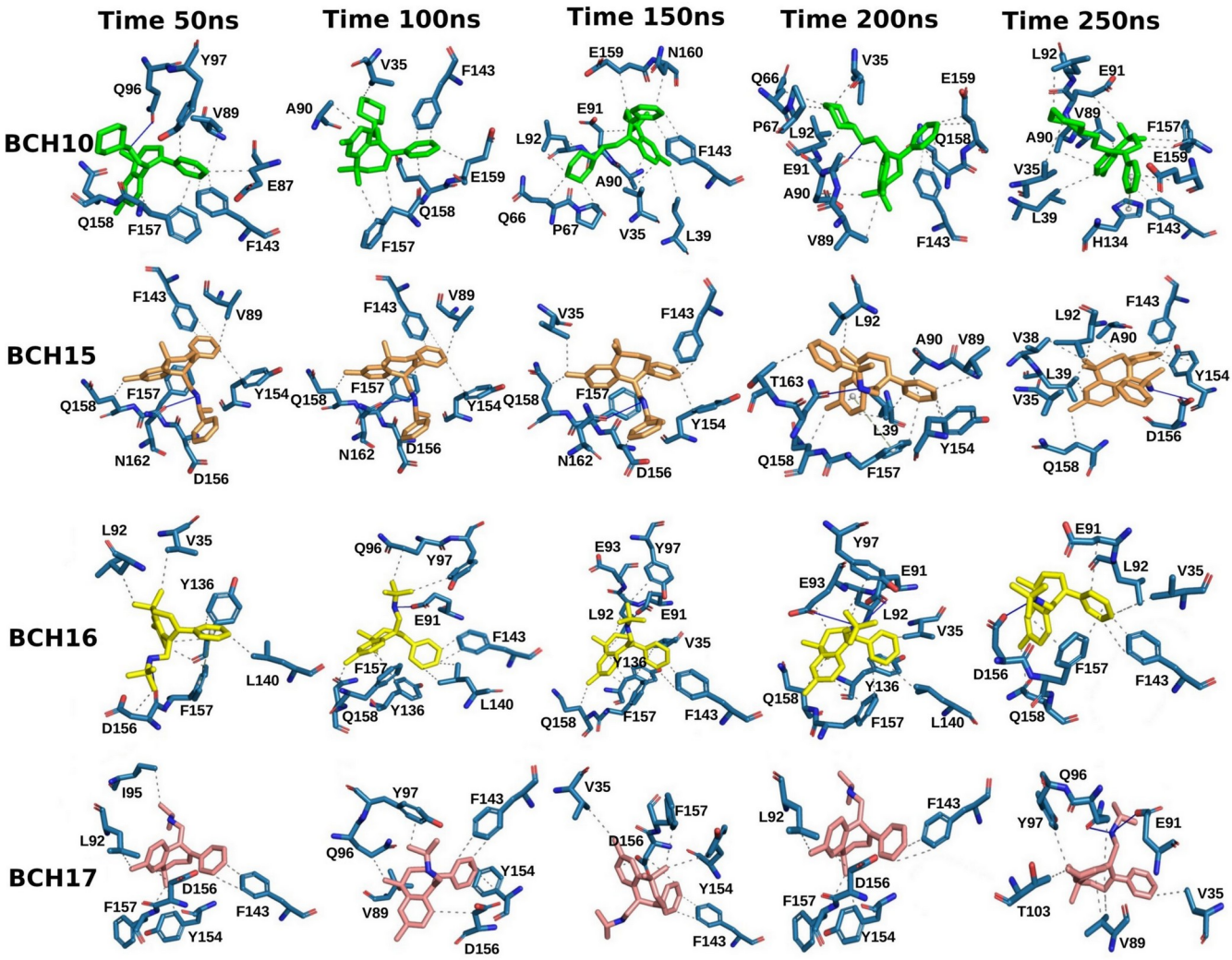

Figure S2: Interactions of selected molecules with SARS-CoV-2 Nsp1 complexes during MD-simulations at different time intervals.

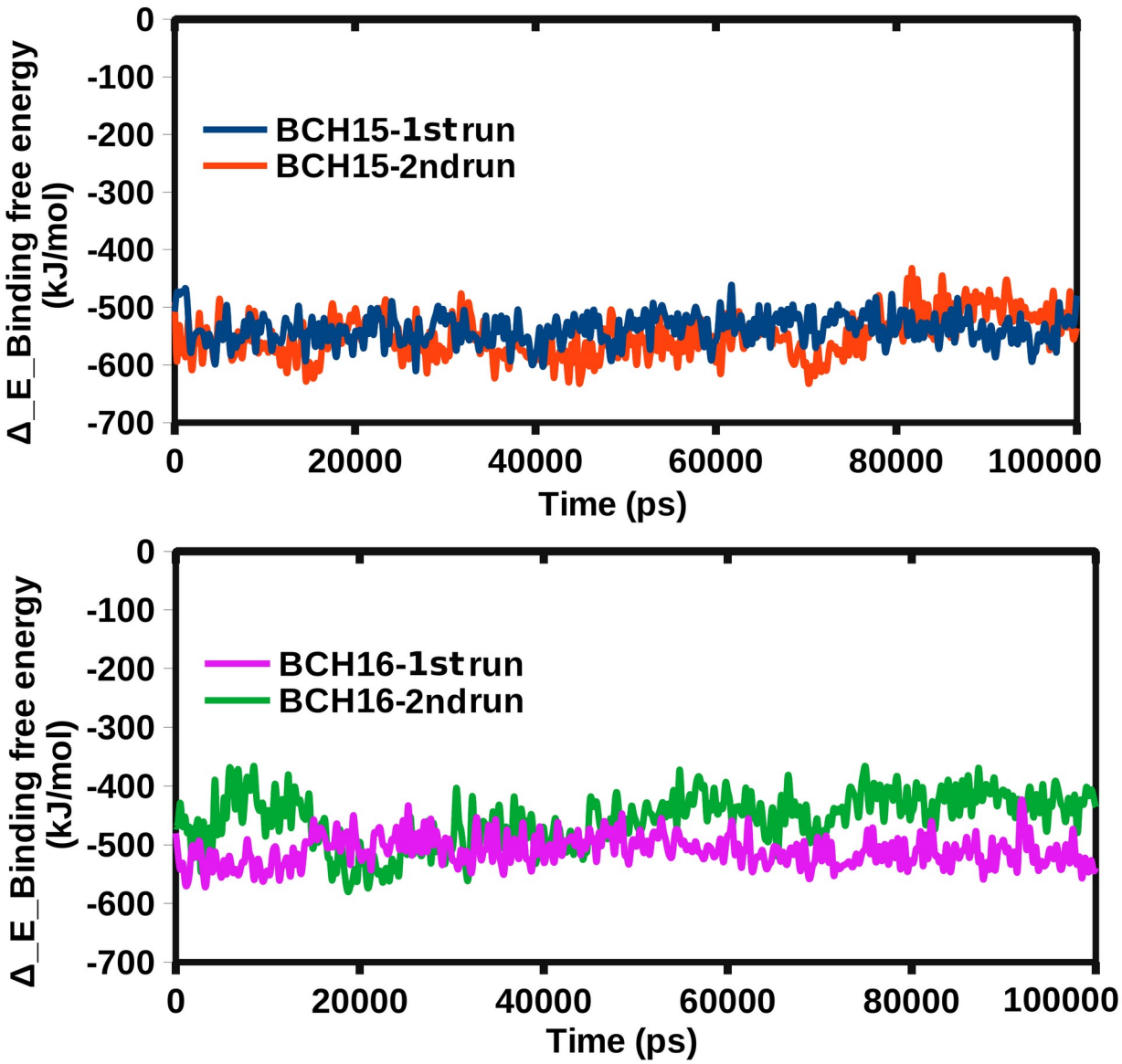

Figure S3: Graphical representation of binding free energy for top two complexes.

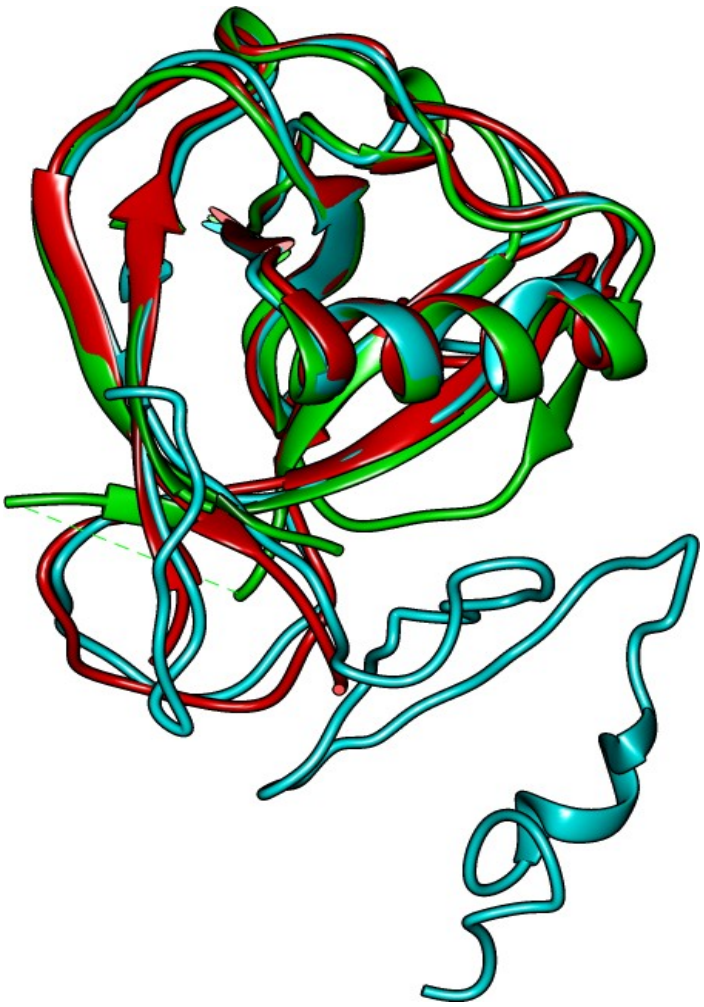

Figure S4: Comparison of modeled full length Nsp1 SARS-CoV-2 (cyan) with deposited short-length Nsp1 SARS-CoV-2 (PDBID: 7K3N in green) and Nsp1 SARS-CoV (PDBID: 2GDT in red) by superimposition.

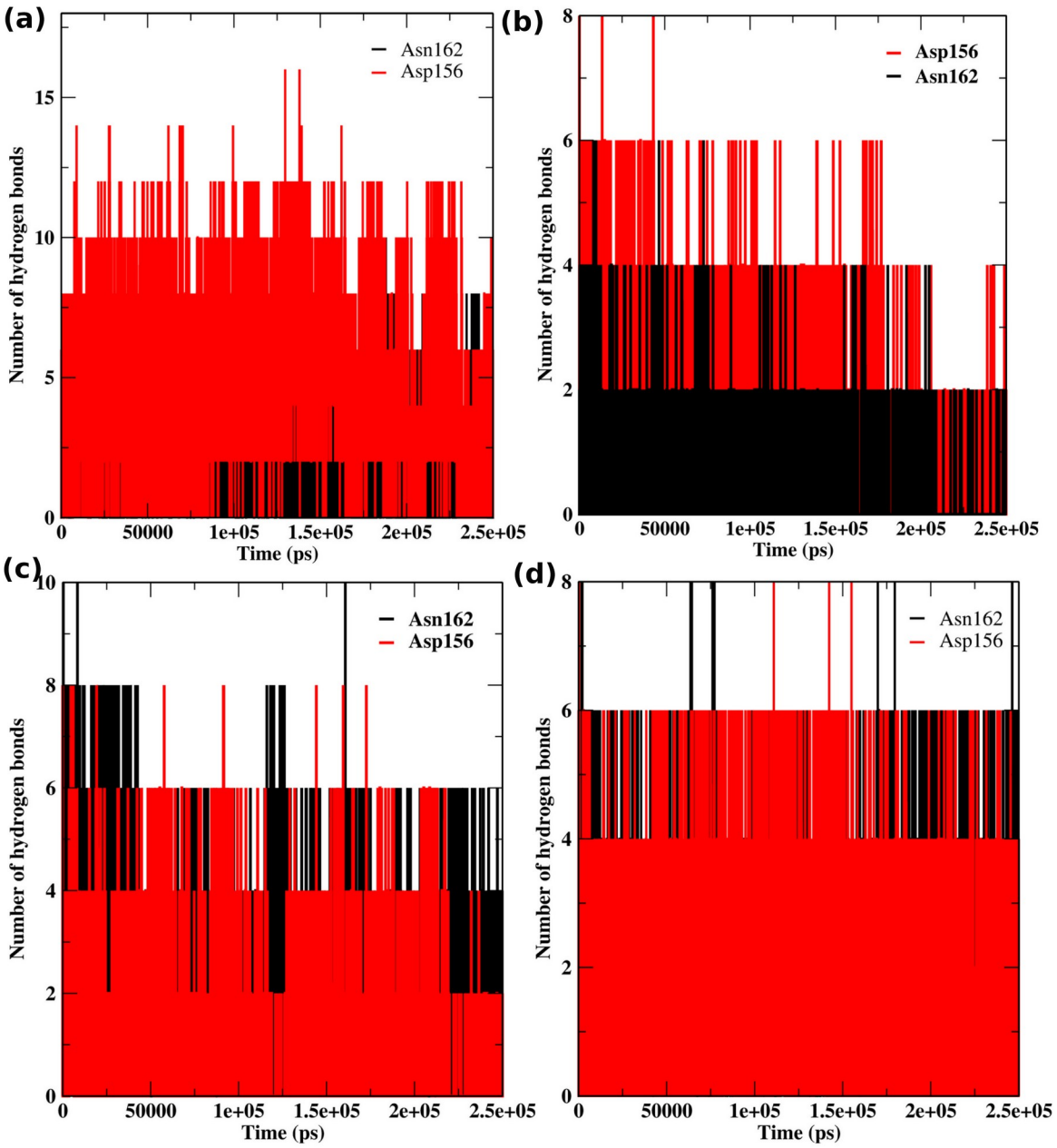

Figure S5: The analysis of Hydrogen bonds formed between protein and selected residues Asp156 and Asn162 during the simulation.

Table S1: Estimated Affinity, LE and Torsion values for selected seventeen AAB molecules.

Complexes	Estimated Affinity (Ki)	LE	Torsion
Nsp1-BCH1	12.45mM-125.3µM	0.18	
Nsp1-BCH2	86.82mM-873.9µM	0.10	
Nsp1-BCH3	2013.5mM-20.26mM	0.9	
Nsp1-BCH4	5243.9mM-52.77mM	0.7	
Nsp1-BCH5	156mM-1.57mM	0.12	
Nsp1-BCH6	91.9mM-925µM	0.14	
Nsp1-BCH7	11.4mM-115.3µM	0.17	
Nsp1-BCH8	92.64mM-932.4µM	0.15	
Nsp1-BCH9	7562mM-76.1mM	0.5	
Nsp1-BCH10	8.81mM-88.67µM	0.26	
Nsp1-BCH11	10.16mM-102.3µM	0.19	
Nsp1-BCH12	59.53mM-599µM	0.11	
Nsp1-BCH13	297.8mM-2.9mM	0.14	
Nsp1-BCH14	1307mM-13.15mM	0.10	
Nsp1-BCH15	0.22mM-2.24µM	0.30	
Nsp1-BCH16	0.95mM-9.62µM	0.29	
Nsp1-BCH17	0.90mM-9.07µM	0.30	

Below 0.20 LE is low

Table S2: MM-PBSA binding free energies of top two Nsp1 complexes calculated from the MD simulations performed in two repetition.

Complexes	Binding energy (kJ/mol)	Van der Waal (kJ/mol)	SASA (kJ/mol)	Electrostatic (kJ/mol)	Polar solvation (kJ/mol)
BCH15-2nd run	-537.468	-242.919	-21.108	-602.055	328.613
BCH15-3rd run	-549.833	-269.398	-21.200	-577.518	318.283
BCH16-2nd run	-510.643	-223.910	-17.119	-508.113	238.499
BCH16-3rd run	-456.137	-182.092	-16.315	-528.934	271.203

Table S3: Molecular properties of AAB molecules obtained from molinspiration server.

Molecules	LogP	MW	HBA	HBD	nRotb	nviolations	TPSA	Bioactivity
BCH1	5.76	375.56	2	0	3	1	12.47	0.25
BCH2	5.37	391.56	3	0	4	1	21.71	0.20
BCH3	5.21	403.57	3	0	4	1	29.54	0.18
BCH4	7.00	471.64	4	1	7	1	39.73	0.12
BCH5	4.56	388.62	1	2	4	0	16.61	0.27
BCH6	4.17	404.62	2	2	5	0	25.84	0.22
BCH7	4.94	402.65	1	2	4	0	16.61	0.24
BCH8	5.39	443.48	1	2	4	1	16.61	0.23
BCH9	4.01	416.63	2	2	5	0	33.68	0.19
BCH10	6.62	381.56	1	1	5	1	12.03	0.27
BCH11	7.07	395.59	1	1	5	1	12.03	0.26
BCH12	6.31	501.67	5	1	9	2	48.96	0.16
BCH13	5.31	361.53	2	0	3	1	12.47	0.26
BCH14	6.52	423.60	2	1	6	1	29.10	0.19
BCH15	4.16	396.60	1	2	5	0	16.61	0.15
BCH16	3.39	348.55	1	2	4	0	16.61	0.19
BCH17	2.94	334.53	1	2	4	0	16.61	0.24